SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24216	54584	A	24354	1	1201	MQPALLIVLNKVRQEARRAR
						ACRIRRASGIVQFGKVRRQLAA
						VELRQRQTPERFVLLRGTRQQA
	i					TGQRIVKTEQRVIIITQRSFRRPG
						EGRRINDHFRFPAHLPSIRPIGK
						HQTPFGISGHHFNFFTVAIGDDI
						AQLDRIGANQSVLKGFNKFVV
				1		QYATDSMTSQGKGLSQGSGVA
				ŀ		FDNEKFAYNI/SFNGHMLRILDH
		l		l		G\INWDNDNGTKWWTVGIRPM
		l		1		YKWTPIMSTVMEIGYDNVESQ
1						RTGDKNNQYKITLAQQWQAG
						DSIWSRPAIRVFATYAKWDEK
				1		WRYDYTGNADNNANFGKAVP
						ADFNGGSFG\RGDSDEWTFGAQ
		l				MEIWGLSRASGTLVTRAWRYK
		1	1	İ	1	TTPTRHCLLMNHYAGEAAMR
1					1	WKNYLKSTQKVQLQNFANWP
		1				KYSLSTLFHFPFSKSC
24217	54585	Α	24355	188	406	FIRSFDPSFVPSVLDRFFVLSTVF
ŀ		1				HSSSIFLVVIDRPSCVGEPSLF*V
		1				GGSCPTNSLYRCSGLAWYLMR
						SMD
24218	54586	Α	24356	1	1798	
24219	54587	В	24357	1465	7841	
24220	54588	Α	24358	174	3762	TLNDAMRREKCLARINRTAKS
						GVVMPKLVTWMNNQRVGELT
						KLANGAHTFKYAPEWLASRYA
	l					RPLSLSLPLQRGNITSDAVFNFF
			l			DNLLPDRTIVRDRIVKRYHAKS
						RQPFDLLSEIGRDSVGAVTLIPE
		1				DETQHHYESLTITDEGEFVVFV
1			İ			GPSGCGKSTLLRMIAGLETITTG
		1	i			DLFIGEKRMNDTPPAERGVGM
			l			VFQSYALYPHLSVAENMSFGH
						ATGLAQHKEVAEVLPSRRICWI
		_				ANRKRSPVVSVSVWRL
24221	54589	Α	24359	364	845	RPLLDHGSSPRLNFLRFWYVVH
		l				AHTLMRMTEGWAGFDILRPYR
		1				WRRVIAFVVAFYFRHLIALLVV
		1				QMHFKLVKGNVDVVFTAQLID
			i			STVQLIDSTTTVTQFTHIQTQLM
						IQRAGTKCRKEDFRHWFVHHP
		1				WVL/MSPPSVTLYALFPDRSHR
	L					PRRDGSPDA
24222	54590	Α	24360	781	1275	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24223	54591	A	24361	1	1185	MDKFDANRRKLLALGGVALG
24223	34391	^	24301	1	1100	AAILPTPAFATLSTPRPRILTLNN
				l		LHTGESIKAEFFDGRGYIQEELA
1						KLNHFFRDYRANKIKSIDPGLF
						DOLYRLOGLIGTRKPSCGYVT
				ļ		TAPAARSYRLTSKFIAVGOKAL
				1		SSLNIIHIAAPHLEALIIGESDTK
						NFASHDHAILIYKLEPTTGMLR
						TRAYIGOHMPLYCSAMGKIYM
				ŀ		AFGHPDYVKSYWESHQHEIQPL
1				İ		TRNTITELPAMFDELAHIRESGR
			ľ	ļ		TMDREENELGVSCIAVPVFDIH
		l				GRVPYAVSISLSTSRLKO/PROH
1						RFRLREROPAGGTPPAGTNSVT
						GGASLHHARCORRK*KPYRPER
						A/ESFLPARGKICWP*AGTLTVC
						IMASASRLISGCTPDSTCWSTA
				l		HAPICRRRGRAINRCHCSS
24224	54592	A	24362	I	801	
24225	54593	Α	24363	1523	1950	LLPA/AQKRRVDFLRATDFNAL
						MPGVVEIDGKNIYTQIIDLTTRE
1				1		AVVNRPEVHRRYIDIQFLAWGE
1						EKIGIAIDTGNNKVSESLLEQRN
				1	1	IIFYHDSEHESFIEMIPGSYAIFFP
1						QDVHRPGCIMQTASEIRKIVVK
						VALTALN
24226	54594	Α	24364	281	997	LTFARLKGITRKIGRLQSRRRKR
1				i	1	CKAMGVDVNRVYSLDELVRG
i				1		NDILFSATGVTGGELVNGIQQT
1					-	ANGVRTQTLLIGGADQTPMAT
						LTEDDVLEQLDAQDNLF\SFMK
						TAHTILLQGIRQFLPSLFVDNDE
	1					EIVEYAVKPLLAQSGQIDDIDV
						ALRLIYALGKMDKWLYADITH
1						FSQFWHYLNEQDETPGFADDM
1	1			1		TWDFISNVNSITRNAMLYDALK
-						AMKFADFSVWSEARFSGMVKT

NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino neid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24227	54595	A	24365	263	1410	AMISRRRFLQATAATIATSSGFG WHHY/CLNSDAIALGIEGRPDLI LLGGDYVLFDMSLNSSAYSDV LSPLAECAPTFACFGNIHDREVG TEKNHLIGETLKSAVITGMLNQ ATVIAYANRPFELVGTGDLWS CQCKSASASETNLSRLVLAHNS CSKEVMRDEPCDLMLGSHTHR WQLSVPMAGEPFCHVADERVV TEADLPCKGITVNPVQSTITEE TFQTLLVSRALEKLGYTVNKPS EVDYNVGYTSLASGDATFTAV NWTPLHDNNYEAAGGDKKFV NWTPLHDNNYEAAGGDKKFV QYKITNIRQLEDPEIAKLVDTNG DGK ADLTICNPGLOFFGAINH QUCAYELITNTVTHN
24228	54596	В	24366	1	2872	
24229	54597	В	24367	1	1704	
24230	54598	В	24368	1	1470	
24231	54599	В	24369	1	2301	
24232	54600	В	24370	1	900	
24233	54601	В	24371	26	856	
24234	54602	В	24372	1	1743	
24235	54603	В	24373	1	1410	
24236	54604	В	24374	1	957	
24237	54605	В	24375	1	2742	
24238	54606	В	24376	755	1816	
24239	54607	В	24377	1	1968	
24240	54608	В	24378	926	6441	



SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24241	54609	A	24379	1	1739	MTWTHEAVNRREPLRGCEPNW
						DVDVKPAGCMISRRNELPYTLG
						LRIDMLVDLGTPASLMGQSSVY
						NTTDRHSTHRMDGLEQLMQQA
						DFAADIAVVAPWDNWSPTAGR
						FGLIRLLDEQTAPYAWYTSPMH
						LMDEKCSCHRQRPVIGLNQPQ
l			ŀ			YQSGTIEVDNVSFAYRDDYLVL
			l			KNINLSVPSRNFVALVGHTGSG
	ŀ		ł			KSTLASLLMGYYPLTEGEIRLD
						GRPLSSLSHSALRQGVAMVQQ
						DPVVLADTFLANVTLGRDISEE
						RVWQALETVQLAELARSMSDG
			İ			IYTPLGEQGNNLSVGQKQLLAL
						ARVLVETPQILILDEATASIDSG
						TEQAIQHALRRDCSPLIDHCDA
ľ						DTILVLHRGQAVEQGTHQQLL
					l	AAQGRYWQMYQLQLAGEELA
		ł		i	1	ASVQPLPNSDRRGSMKLVTVII
						KPFKLEDVREALSSIGIQGLTVT
l						EVKGFGRQKGHAELYRGAEYS
						VNFLPKAAYTGKIGDG/KIFVAE
				l	l	LQRVIRIRTGEADEAALYLWHT
l						ATERDGPFRNFTAGAFRASLPH
			l		1	PARHGRRPILAAPFMPVNPSRLP
					1	PRRRHLASGRSLRFNCCTAGDE
						TCSARSGERRSLVF
24242	54610	Α	24380	547	684	

	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	lucation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24243	54611	A	24381	l	2208	MLLVSASVNAMSISGQAGKEY
24243	34011	<u>۱</u> ^	24301	ľ	2206	TNIGVGFGTETTGLALSGNWTH
						NDDDGDVAGVGLGLNLPLGPL
						MATVGGKGVYTNPNYGDEGY
						AAAVGGGLQWKIGNSFRLFGE
						YYYSPDSLSSGIOSYEEANAGA
					ŀ	RYTICVQVFVVVMLIRNQLFTP
						VNTAIDGFATNYAIMPAYAVG
						EGVATHGLQFELMRTTGGNTQ
			1			HVFHHPLPLFAMWRYAAEMF
						YQQMCQFVRYHFFNKSFTVFQ
		l		l		QQNGIEANFIAFQPGRSGGSA
						LGRNVFGFRYQPQCQQDKQYV
		l				QSRIHPEGVGVTQRVEHGQERG
		[				ANDHVQSSGTELMQEGVMSAS
		1				LKNQQGFSLPEVMLAMVLMV
		l				MIVTALSGFORTLMNSLASRNO
						YQQLWRHGWQQTQLRAISPPA
į		l			1	NWQSGAAMLRVYHSNRLDVL
		l				EALMEFIVERERLDDPFEPEMIL
		l				VQSTGMAQWLQMTLSQKFGIA
		l				ANIDFPLPASFIWDMFVRVLPEI
		l				PKESAFNKQSMSWKLMTLLPQ
		l				LLEREDFTLLRHYLTDDSDKRK
		l				LFQLSSKAADLFDQYLVYRPD
		1				WLAOWETGHLVEGLGEAOAW
ŀ		1			1	QAPLWKALVEYTHQLGQPRW
						HRANLYQRFIETLESATTCPPG
						YLRASLYAAIQHALASVREHTT
		1			l	LVVIAHRLSTIVDADTILVLHRO
		1				QAVEQGTHQQLLAAQGRYWQ
					i	MYQLQLAGEELAASKGHAELY
24244	54612	A	24382	2	729	DCSPLIDHCDADTILVLHRGQA
24244	34012	^	24302	-	1/29	VEOGTHOOLLAAOGRYWOMY
l						OLOLAGEELAASVOPLPNSDRR
			l			GSMKLVTVIIKPFKLEDVREAL
						SSIGIQGLTVTEVKGFGRQKGH
ŀ		1				AELYRGAEYSVNFLPKAAYTG
		1				KIGDG/KIFVAELQRVIRIRTGEA
		1			1	DEAALYLWHTATERDGPFRNF
						TAGAFRASLPHPARHGRRPILA
		l				APFMPVNPSRLPPRRRHLASGR
				I		
24245	51612	<del> </del> -	24202	683	1161	SLRFNCCTAGDETCSARSGERR
24245	54613	Α	24383	063	1101	RTGHCH/SAFSFSTVLTSCSLSRI
		1	į.	1		SFLAHRLQYLLRVAEPLPNSDR
				l		RGSMKLVTVIIKPFKLEDVREA
				1		LSSIGIQGLTVTEVKGFGRQKG
						HAELYRGAEYSVNFLPKVKIDV
	l .	ĺ		1	I	AIADDQLDEVIDIVSKAAYTGK
	I .	t				GDGKIFVAELQRVIRIRTGEADI

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24246	54614	A	24384	631	1149	FFGIKEOVITANNANSNRNKTD
						RCCRNWLEDHADNHCHKHSEV
						MPCLRRHTVGDRDKKHDTHH
		1			ŀ	HOWGO*FPYIIFWLVSPLIAISRS
		1				KVSTHGLRQRDFILLREASQSF
		l				RFVLRVYDVADHIAGKFTVHD
					1	LQFIGYHGGQAQLVAQVFSKES
	1	l			l	KAAGGNRHFPAORFOLEHOLR
24247	54615	Α	24385	833	1264	I I I I I I I I I I I I I I I I I I I
24248	54616	Ā	24386	1	1632	
24249	54617	Ā	24387	2078	2371	
24250	54618	A	24388	1	159	
24251	54619	Ā	24389	530	811	RPGTGTAAOVLNRRIKISRST*L
	0.1013	ľ.			1	TVVMGYWSHPSVSLLKWDRR
	1	1		į .		KSPKCSSALRVNISNTLLSTARR
		l			i	RKRYLIVIPALLVVRRCRPRGPS
	1	l				ACG
24252	54620	A	24390	1806	2115	AAFOEIELAFODPOCVGLLTAP
27252	34020	ľ` <b>`</b>	2.550	1000		MLMPLFLDQLILQCFFW/W/TN
		1				LERA*TSFSALFIDLOPPGYRTT
	l	1			1	TSKHKVSSSLIKGHVLLDHSFH
		l			!	DLNTOLWISTNAFREGN
24253	54621	A	24391	1476	1751	ALLLVSFASORFISA/TVGNONA
24233	34021	l^	2-371	1770	1731	GVDLLNLTLLVGGIFVLNNAGN
						FAVFTGDTSITGRIIQFHRQQTN
	ł	l				ATLRFSITOTLECFDRDORHVA
	1		i			VEH
24254	54622	A	24392	606	4519	EEVVRAISAKRNEPEWMLEFRL
24254	34022	ľ	24372	000	4515	NAYRAWLEMEEPHWLKAHYD
		1				KLNYODYSYYSAPSCGNCDDT
	[	1				CASEPGAVOOTGANAFLSKEV
	l .	l				EAAFEQLGVPVREGKEVAVDAI
		1				FDSVSVATTYREKLAEQGIIFCS
		1				FGEAIHDHPELVRKYLGTVVPG
	1	l	ĺ	1		NDNFFAALNAAVASDGTFIYVP
		l				KGVRCPMELSTYFRINAEKTGO
	1	l				FERTILVADEDSYAAKRLTDYP
		ĺ		Į.		HQLSGGERQRVMIAMALLTRP
		l				
21255	54622	١	0.4202	120	256	ELLIADEPTTALDVSVQ
24255	54623	A	24393	129	256	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
24256	54624	A	24394	1	1082	MAMSKVKSITRESWILSTFPEW
24230	34024	^	24334	1,	1002	GSWLNEEIEQEQVAPGTFAMW
		1		l		WLGCTGIWLKSEGGTNVCVDF
	İ	1		1		WCGTGKQSHGNPLMKQGHQM
		1		l		QRMAGVKKLQPNLRTTPFVLD
		1				PFAIRQIDAVLATHDHNDHIDV
						NVAAAVMQNCADDVPFIGPKT
		1				CVDSWIGWGVPKERCIVVKPG
		ı				DVVQVTALEIHAPDAFDRTAPI
		l				TWLADOKRRRTVKGRTTRPCN
l		l				RSVTVRPRRRDAVIGRFYRHQS
1	1	l	1			ITQKGLLLMVMPGCAFPLWIDS
		l				ELNLTFIDALFEGVSGITTTGAT
		i .				VIDDVSSLPRAYLYYRSQLNFIG
	l	l				GLGVIVLAVAVLPLLGIGGAKL
		1				YQSEMP/AAI*G*QTHSPPGRYV
		1				TDTVDNLFFIRCRT
24257	54625	Α	24395	49	281	ASDHRYLCSOSVPLRGIPACYL
						LQAPLTRWR/RIPPSRRICAAIDS
		1				AISRSPQRWLTAVCCGTVNFTN
		1				TCLLPDGVCA
24258	54626	Α	24396	737	1419	CIWRMYSHRLVAWRRCVKRR/
		1				RYLTRFAKTRGVAIVMVGHVT
		1	ľ			KDGSLAGPKVLEHCIDCSVLLD
		1	i			GDADSRFRTLRSHKNRFGAVN
1					i	ELGVFAMTEQGLREVSNPRGR
					ł	GKRKFISPKKTPALAKFRRNLL
						PPKVPGNGTSVRFRHSRICWMN
						PLPGAAWNCILTLKKPISPGVQ
		l				VFPESFTPARLEAFAGRSQACL
1						VPAQNILHQKSQAWLFDFPEQE
						KELRELSAWMAGA
24259	54627	A	24397	526	1693	STTGIRSIAMSNPILSWRRVRA\
		1				LCVKETRQIVRDPSSWLIAVVIP
1		1				LLLLFIFGYGINLDSSKLRVGIFL
		1				EQRSEAALDF\THTMTGSPYIDA
						TISDNRQELIAKMQAGKIRGLV
	1			İ		VIPVDFAEQMERANATAPIQVI
						TDGSEPNTANFVQGYVEGIWQI
						WQMQRAEDNGQTFEPLIDVQT
						RYWFNPAAISQHFIIPGAVTIIM
		1				TVIGAILTSLVVAREWERGTME
1	l	1				ALLSTEITRT\ELLLCKLIP\YYF\
		1				LGMLAM\LLCM\LVSVFILGVP
	1	l		1		YRGSVLILFFISSLFLLSTLGMG
l	l	l				LLISTITRNQFNAAQVALNAAF
l		1				LPSIMLSGFIFQIDSMPAVIRAVT
1	l	1				YIIPARYFVSTLQSLFLAGNIPV
	l					VLVVNVLFLIASAVMFIGLTWL
	L	<u></u>		L	L	KTKRRLD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
ĺ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \≔possible nucleotide insertion)
				sequence		
24260	54628	A	24398	655	915	IAVNVTLAFNGGKOLR*STSLL
						CCQEGLAFAVNLRQHFRVQTIS
						FFFLPVLRFWRPGIQQAKKCHP
						APRTAKGIPQQVIRAMRLLFK
24261	54629	A	24399	549	827	
24262	54630	Α	24400	472	626	WRFFRPRKDNIRRTLFADGHQI
l						AAQPGLNLSCTRTIF*IKRINTFP
						GRWRK
24263	54631	Α	24401	333	617	SDQSETDYRFADGERHLENQPH
İ					\	AGQTGRGGAGPGCTLYQRFAQ
		1				LCEVSEVERSGCRTLSAQHVEQ
		1				NLPAAICGGDDADGAVVHLWT
		1		I		TA*RTRIGTLRSGPKMNDSAISII
		1				TATDSGWKILLHMLS
24264	54632	A	24402	74	265	
24265	54633	Α	24403	I	1005	
24266	54634	Α	24404	1068	1185	SVAIRQASTGNRCQCLCPACA
						WA*VNADVK*SARVSRL
24267	54635	Α	24405	1	2292	
24268	54636	A	24406	720	2496	RRAGYRKAADAMTTIVPEKLS
		1				REVGSHFHALDRTTAVHRQPVI
		1				SATTTVHEFLRCHQFPLVVCDG
		1		l		GRMTPRAMFLFSSAHILMPLNY
l					ļ	HNSHINTLFPVAGTLMVEPTES
		1		l		ESKVELDRFIDAMLAIRAEIDQ
l		l				VKAGVWPLEDNPLVNAPHIQS
1						ELVAEWAHPYSREVAVFPAAL
ŀ		1				VTGGSRGIGRATALLLAOEGYT
1				l		VAVNYOONLHAAQEVMNLITO
		ŀ			ŀ	AGGKAFVLQADISDENQVVAM
l		i i		1	ł	FTAIDQHDEPLAALVNNAGILF
		l				TOCTVENLTAERINRVLSTNVT
		ŀ			1	GYFLCCREAVKRMALKNGGSG
		l		l		GAIVNVSSVASRLGSPGEYVDY
		1				AASKGAIDTLTTGLSLEVAAOG
		l				IRVNCVRPGFIYTEMHASGGEA\
						GRVDRVKSNIPMQRGGQAEEF
				İ		AVOTFPVWRVAOHCAVRPFRO
			l	I		RIGOLRDIFHLKGDOFTNPRKT
						GVTPQPPCSTYPDPSPPPVPAAG
						HIDRPALAPTFTPPIMCSKATVK
						PLSPSPPGTPDPASVLPFREQRA
				İ		
l			1	l		AVHRLRTVVTRHLLALRRDPF
						ANRHRQQDQRNGGFHHRQRHL
l				1		HTGKTRSLHHHQFAALRQHPK
2 12 (0	51627		24407	40	106	TKQRRKQSRHREEDLHIFRHAQ
24269	54637	C	24407	49	186	
24270	54638	A	24408	470	811	
24271	54639	A	24409	1	1006	
24272	54640	В	24410	1	2793	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nueleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ı		sequence		
24273	54641	IA	24411	463	1258	CCRSSWCNSDSETGLQIVASYF
24213	34041	^	24411	403	1238	EDRNGDS\LALRPEGTAGCVRA
	ľ					GIEHGLLYNQEQRLWYIGPMFR
						HERPQKGRYRQFHQLGCEVFG
						LQGPDIDAELIMLTARW\WRAL
l .						GISEHVTLELNSIGSLEARANYR
i i						DALVAFLEQHKEKLDEDCKRR
	i	١.	1			MYTNPLRVLDSKNPEVQALLN
						DAPALGDYLDEESREHFAGLC
		l		l		KLLESAGIAYTVNQRLLNYRLS
						ANLIENNLSLFDGEGIYRFYHPK
				l		PTKNAERENRQCRNDLFFRCGF
24274	54642	Α	24412	22 I	832	TMAENQSTVENAKEKLDRWLK
						DGITTPGGKLPSERELGELLGIK
						RMTLRQALLNLEAESKIFRKDR
						KGWFVTHPRFNYSPELSASFOR
						AAIEQGREPF\WGFTEKNRTSDI
						PETLAPLIAVTPSTELYRITGWG
	i .				l	ALEGHKVFYHETYINPEVAPGF
						IEQLENHSFSAVWEKCYQKEPV
1		1				VKKLIFKPVRMPGDISKYLGGS
		1				AGMP
24275	54643	A	24413	158	481	7.0
24276	54644	A	24414	2201	2350	
24277	54645	Α	24415	62I	1830	AGWKRGGAGEPDQGLQA\EME
						VLENLQELKDLNQRQAHAESKI
						FRKDRKGWFVTQPRFNYSPELS
		ļ				ASFORAAIEOGREPSWGFTEKN
		1				RTSDIPETLAPLIAVTPSTELYRI
1	1	1				TGWGALEGHKVFYHETYINPE
	ì			İ		VAPGFIEQLENHSFSAVWEKCY
		1			I	OKETVVKKLIFKPVRMPGDISK
		ı			l	YLGGSAGMPAILIEKHRADOOG
					I	NIVQIDIEYWRFEAVDLIINLCF
1					l	MVTINNARKILORVDTLPLYLH
ı		l				AYAFHLNMRLERVLPADLLDIA
						SENNLRGVKIHVLDGERFSLGN
1	1	1	1	1	I	MDDKELSAFGDKARRLNLDIHI
1	1	1		1	I	ETSASDKASIDEAVAIALKTGA
1	1	1			1	SSVRFYPRYESNLRDVLSIIAND
1		1		1	I	
1	1	1		i	I	IAYVRETYQDSRLTFNIEWGKS
1		1		I	1	SCCSPYVHPWAKLAAIYYRLQP HINDAF
24278	54646	A	24416	83	502	HINDAL
24279	54647	A	24417	15	95	
24280	54648	A	24418	500	786	LTORFGTVPLLLO\AYLYSAFFF
1	1	ľ.	1			TPEFLRPAPPLFSAAVLPEQRQR
1		1			i	AQGIGGLVIRPTVELHQALQLF
		1			1	FGHQPKIQSLHALLRGSTGFQA
	1	1			1	SFRLPL
		ь.		L		D1.40. D

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24281	54649	A	24419	1	2914	MYYSHASCVADQYACGMHRT
						PSRTGRPRIHAPRQARLKPQVK
						VASKKRNARDKMOPPNEOOKT
						RAHACTPSSRFRAVVRTLTCPV
						VANVTRIFPRYFSNTRVLRRRR
						KQARGTWWRLRHLHLYVQPH
						KHTSYYIYRLYRVTYVMSAQV
						VDTGIYEFTTRKHDIGTIELPNS
						EIRYHGNPAMSRPRKTPTPPNSP
1						ASERATGPTTLLPPIRORRYAA
						RHTSTIAYTNSTSDIFEAPYNKA
						APIMRYTSVYCSLFSP
24282	54650	A	24420	2	420	CPYPENRWRGKILARPLLFRAA
		ļ.,		ľ	1	*ASRFAGAGMPGRLIPTVRPRN
						SNSGRLVSASRCAKESLTVTTC
1						TPLPGSAVREASN
24283	54651	A	24421	212	497	TI DI GOTTI LETON
24284	54652	Α	24422	1	1149	
24285	54653	Α	24423	535	589	
24286	54654	Α	24424	1	1458	MFDPETLRTFIAVAETGSFSKA
						AERLCKTTATISYRIKLLEENTG
						VALFFRTTRSVTLTAVGEHLLS
		1				QARDWLSWLESMPERAATVW
		1				MFVPTPLSVASGLQRIGRAGHQ
		1				VGGVSKGLFFPRTRRDLVDSAV
		1				IVECMFAGRLENLTPPHNPLDV
		1				LAQQTVAAAAMDALQVDEWY
	1	1				SRVRRAAPWKDLPRRVFDATL
ŀ		1				DMLSGRYPSGDFSAFRPKLVW
		1				NRETGILTARPAAFAADSDIAD
i i	1	1			1	GQTQRFDFSILQSMAHDLSQTA
	1	1				WR/GIQYDAEKSLWHNVE\NRQ
		1				LDAQFFHMGMGFRRRVRMFSV
ŀ		1				DPATHLAREIHFRPELFKYNDA
		1				GVDTKQLEGQSDLGFAGFRVF
		1				KAPELARRDVVSFLGASYFRAV
		1				DDTYQYGLSARGLAIDTYTDSK
	1	1		1		EEFPDFTAFWFDTVKPGATTFT
				1		VYALLDSASITGAYKFTIHCEKS
1		1	ŀ			OVIMDVENHLYARKDIKQLGIA
		1				PMTSMFMPRKNASRLSKRCYDI
						RERDGREERK
24287	54655	Α	24425	157	650	PIRASTCLFKPLITQCFRQFGSE
1	1	1	l	1	1	GVNDHLLGILLIDPARAQIEYLF
1		1	l	1	1	IINTPHRRAVAAFHIICIDFQLRF
1	1	1	l	1	1	RIHFROFAHQQIVVGHLTIRFDG
1		1	l	1	1	VLRDVDQTVKYRAAFVADDSF
1	1	1	l	1	1	VQLSAVTKTFIVFQPGTGITHLV
		1	ĺ	1		FHRHRQAQ*PFKVPFSRRLRNGI
			l			нтнс
24288	54656	Α	24426	269	2024	
		-				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24289	54657	Α	24427	1	3548	MPRSNYFSERCKGEIFLKFENM
		1				QRTGSFKIRGAFNKLSSLTDAE
	ŀ					KRKGVVACSAGNHAQGVSLSC
						AMLGIDGKVVMPKGAPKSKVA
		1				ATCDYSAEVVLHGDNFNDTIA
		1				KVSEIVEMEARIFIPPYDDPKVI
						AGQGTIGLEIMEDLYDVDNVIV
						PIGGGGLIAGIAVAIKSINPTIRVI
						GVQSENVHGMAASFHSGEITTH
		l				RTTGTLADGCDVSRPGNLTYEI
		1			i .	VRELVDDIVLVSEDEIRNSMIAL
						IQRNKVVTEGA
24290	54658	В	24428	I	2691	
24291	54659	Α	24429	2174	3315	NLPKPDWARSAPHPASANYKS
						NTRRLPFAREQ/QDQHTLLAGT
l		1				LFIAKILIPMQIAQSAAYRRRCP
		1				DAQLHFLPLQLAPRGHRYKRV
l	1	1				CQVRYPPIIALIPVVFRLMNDAN
1		l				GLSQPADAGLAHHEMRNFLDF
1	İ					ASSNVAASRRRCVAALPCATG
1						KGRQANEQAENKCSKDPQTHR
						TDNKETKTPPARPTTTTQPHTK
		1				EEEPLSTPTQTKHPPTHVTGTGP
		1				HPTPASGQTEKHERKRPTQQKS
l						NARQNSKDKRTPNKSKTTKPN
	1					RGYNQHPAGEPTMSTHEKVKP
		1				HQQNRKIQAPPKRQKTDHRHT
						HNTHPHPPHRAASTTTQAAPPP
						RRATRSGTSATAHNNTEPHGTR
		l		İ		HTQPGDHKRAEEHDRTADEPT
						PPEHTLPSHTQLGP
24292	54660	Α	24430	I	2925	
24293	54661	Α	24431	341	689	RPLAFRQRCTFYWR\PGSANCR
		ı		l		LV*GASGTDPRLYSPCAAAADD
		1			i	CGRRQNAGRRRRATSGD*SPHR
		1			i	RWENALLFDSRHRHCPRRAKN
		l				AGGEYRQRGIAGSDLQQRFTA
		ı				AEKDHSRS

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24294	54662	Α	24432	1	1931	MGTLLGTLTVLTLVAEELPAET
						DVAADPAASPTCTAVNQTIGRA
1			ļ		i	IVAADFFIIFQLWQNTVRQLVT
l						HFKPHGQSEMSDTPELINRARY
						LTYLYCRQPAKAIRELSEQELA
		l		l		WKKQATHEYQVLVTRCKQTL
		1				HQVEPLREIEPGRKRLVFDENL
						RPKQNPIPHLLDTCWPLTVDEH
İ						ANRSSIGNNNISFVVNRAVVTN
						VLNTMRTACNSQATIQIYNADI
						ARDFGTRGIFSINSGFSTVIRGG
			1			VVTVDLSAGAAIGDSALAFVID
1						DGLVAVNLDTDGLRIGDGHGA
						LVIHRCAVAGDINTVTAAADM
1	ľ	l	1			DLEDPRHSARFGVPRTQVRTW
			1			VALYEKHGEKGLIPKPKGVSAD
						PECVLGRESCDRAAHVPYQAA
					l	AHFMLAGSGSVARWLKVYEER
						GEAGLRALKIGTKRNIAISVDPE
				i		KAASALELSKDRRIEDLERQVR
						FLETRLMYLKKLKALAHPTKK
				1		AAEIPRSTFYYHLKALSKPDKY
				1		ADVKKRISEIYHENRARYGYRR
	1					VTLSLHREGKQINHKAVQRLM
				1		GPSHLKQRLRSSDTALTEERDF
		l	i	l	1	KATRPNEKWVTDVTEFAVNGR
		l	l	l		KLYLSPVIDLFNNEVISYSLSER
		l			1	PVMNMRRSRPGVGYFYALTPV
İ	1	l			I	YLANRLQALLGVEQ/HHPDGEL
	1			l	I	FLTGYVADGGYHS
24295	54663	Α	24433	3	158	
24296	54664	A	24434	1	3432	

3211

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24297	54665	A	24435	1298	2649	TFITRPTSNGTSIFKLMNRRRLE
	1005		2.133	1.20		GGNVATLR/RLTIGMIFQDHHL
					i	LMDRTVYDNVAIPLIIAGASGD
						DIRRRYSAALDKYGLLDKAKN
						FPIQLSGGEQQRVGIARAVVNK
						PAVLLADEPTGNLDDALSEGIL
						RLFEEFNRVGVTVLMATHDINL
						ISRRSYRMLTLSDGHLHGGFGG
						RLDRFRKSVGGSGDGGRNAPK
						RAKSSPKPVNRKTNVFNEQVR
						YAFHGALODLKSKPFATFLTV
		1			1	MVIAISLTLPSVCYMVYKNVNQ
					}	AATOYYPSPOITVYLOKTLDDD
						AAAGDPDRPSLQLRWRVIPGFS
		1				IAVAIYFLNESLGRPLMITGYSA
						ECSLLAWPVRSGLRKAPMKTFP
						LOSLTHEAQOKOFALVDSICRH
						FPGSEFLTGGDLGLTPATELKPR
					l	RLPSGVEQVLADAFHAQAAAL
						VQGAGTGAIRAGLAALLKPGQ
					İ	RLLVHDAPVYPTTR
24298	54666		24436	546	707	KLLVHDAPVIPIIK
24298	54667	A A	24436	428	1464	RNSRSLAEISRLRGQTRSGLPM
24299	34007	A	24437	428	1404	LLNLOSMGAS/WYLSPVIDLFN
		1				NEVISYSLSERPVMNMDHHLL
	1	1				MDRTVYDNVAIPLIIAGASGDD
	ĺ	l				
		l				IRRRVSA ALDKVGLLDKAKNFP
		l				IQLSGACWHCRAVVNKPAVLL
		l				ADEPTGNLDDALSEGILRLFEEF NRVGVTVLMATHDINLISRRSY
		l				
		l				RMLTLSDGHLHGGFGGRLDRF
		l				RKSVGGSGDGGRNAPKRAKSS
		l				PKPVNRKTNVFNEQVRYAFHG
		l				ALQDLKSKPFATFLTVMVIAISL
		l				TLPTSCYMVYNIAKSERISDIST
		l	İ		ŀ	QLNAFPGCEVAVSDAPSGQLIV
		l				VVEAEDSETLIQTIESVRNVEGV
		ļ		ļ		LAVSLVYHQQEEQGEETP
24300	54668	A	24438	1	429	
24301	54669	A	24439	307	424	
24302	54670	٨	24440	300	468	V = GV-18 PPGP-V - 1 N 60
24303	54671	A	24441	946	1558	KGCVSIPFFSFSWA VMSNLTYL
		l	1			QGYPEQLLSQVRTLINEQRLGD
		l	1		I	VLAKRYPGTHDYATDKALWQ
			1			YTQDLKNQFLRNAPPINKVMY
		l			l	DNKIHVLKNALGLHTAVSRVQ
		l				GGKLKAKVE\IRVATVFRNAPE
		l	1			PFLRMIVVHELAHLKEKEHNK
	1					
	1	ı	l .			AFYQLCCHMEPQYHQLEFDTR
						AFYQLCCHMEPQYHQLEFDTR LCNRIRLNGHDHFRRRYALFRV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	eodon for last amino aeid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24304	54672	Α	24442	li -	774	
24305	54673	A	24443	1	452	MELKKLMEHISHPDYROAWKV
				[		EHKLSDILLLTICAVISGAEGWE
	1					DIEDFGETHPDFLKQYGDFENG
						IPVHDTIARVVSCICPAKFHESFI
						NWMLDYHSSDDKD/DHRN*W
		İ			l	KNTPAFL*QESP*GSDSCH*CVL
		l				NNAQSGHRTDQDG*EIQ
24306	54674	Α	24444	486	572	
24307	54675	Α	24445	1	683	MHSLVIGQIKTDKKSNEITAIPE
		l	ł			LLNMLDIKGKIIKTDAMGCQKD
	ļ	1				IAEKIQKQGGAVMNLQRFDDST
	1	l	Ì			LIRIFALHELHRLKEHGLTRGAL
	1		l			LDYHSRYKLVFL\AHPQPESRK
					i	LGPF\VADIHQWQNLDDYSPQY
		1				RQRVVVLLSHPANARDHTNVL
	l	1				MHVQGYFRPHIDSTERQQLRAL
		1				IDSYRRGEQPLLAPLMRIKHYM
	1	l				ALYPDAWLSGQRYFELWPRVI
						NLRHSGVL
24308	54676	A	24446	896	1066	WRLSPSSR*LMPKVPRIQAYFT
		l				T*YCS*VIQRSPC*FHCYSRSIPW
						AWGAGKQSLT
24309	54677	Α	24447	1	3660	
24310	54678	Α	24448	1	1530	
24311	54679	Α	24449	.1	1890	
24312	54680	Α	24450	746	1872	KHWRGSLISLSTPARFNGGPFW
		l				GANQGGDPKGRGGSQRALFRR
	i i			1		KNNRGGETVSGAEDACIVNNN
l				1	1	AAAVLLMLAATASGKEVVVSR
l	ŀ	l			1	GELVEIGGAFRIPDVMRQAGCT
l				ļ	1	LHEVGTTNRTHANDYRQAVNE
				1	1	NTALLMKVHTSNYSIQGFTKAI
				}	1	DEAELVALGKELDVPVVTDLG
					1	SGSLVDLSQYGLPKEP\MPHELI
					I	AAGVSLVSFSGDKLLGGPQAGI
ŀ					l	IVGKKEMIARLQSHPLKRALRA
l	1	1			1	DKMTLAALEATLRLYLHPEALS
		l			1	EKLPTLRLLTRSAEVIQIQAQRL
		l			1	QDPLAAHYGAEFAVQVMPCLS
		l			1	QIGSGSLPVDRLPSAALTYTPH
l	1	1			1	DGRGSQLESLADRWRELPVPVI
L		ļ.—				GRIYDERLWLDLRCLEDEQRFL
24313	54681	Α	24451	1358	1419	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide detetion, \=possible nucleotide insertion)
24314	54682	A	24452		1568	MKGRNIDAQEIQKRYGMVGDP VIIGVVLQLIFGLAAGGEFKGC SALMITVAAIMVLFPRMIRLIVE GLLPISDGARKFFQKYFKGREV GLLPISDGARKFFQKYFKGREV GLPISDGARKFFQKYFKGREV FYGLDTAVTIGHPTTIAVGLLLI PIMLILASILPGNSVLPLADLPV APFFICMATVIHRGDLVRTLISG VIVMITVLLIATQFAPYFTEMAL KGGFSFAGESAQISALSVGNMF GWSISELMSIGIGRVVAVGIVA SVVLFLRVLSMSWLKEVIGTEK AVIAMCHLRALPGDPSFDAQLG MNWVIDKAWDDLMALQNGG VDAVMFSNEFSLPYLTKVRPET TAAMABIGQUMSDIRIPFGVNV LWDPVASFDLAMATGAKFIEI FTGAYASDFGVWDTNVGETH HQHRIGAGEVKTLFNIVPEAAV YLGNRDICSIAKSTVFNNHPDA LCVSGLTAGTRTDSALLKRVKE TVPDTIVVLANTGVCLENVEEQ LISADGCVTATTFKKDGVFANF
24315	54683	В	24453	1	3352	VDQARSNNPSAIPAAFVKSIDG DRYQINPNRHGVNDG
24316	54684	В	24454	60	2284	
24317	54685	В	24455	1	2475	
24318	54686	В	24456	1	2890	
24319	54687	A	24457	1065	1139	
24320	54688	A	24458	282	615	
24321	54689	A	24459	2657	2919	
24322	54690	Α	24460	1	835	
24323	54691	Α	24461	167	338	
24324	54692	Α	24462	834	ISIS	LRWCSMPCCRWSKDRAAPSPA YSRLSSHVIIAGYVGGGVARG' HSWVFVALTLVLTAVLFSLAGL LNGVFAKTFDDISLVPTFVLTFL TVLGGVFYSLTLLPPFWQGLSH LNPIVYMISGFRYGFPWLNHNR PGVAVDINRLLLPRKQEKLGIK LDKDQLLAGVQDAFADKSKLS DQEIEGTLQAFEARVKSSAQAK MEKDAADNEAKGKEYREKFR QIPSVSSCOKQ
24325	54693	A	24463	3	557	
24326	54694	A	24464	255	693	
24327	54695	A	24465	3	242	QKAPVLANQRQPRRPTGALLLE /SLPLVAESSDG*EPMTNATEPH SRPLP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
24328	54696	A	24466	1	2636	MKNIIRTPETHPLTWRLRDDKQ PVWLDEYRSKNGYEĞARKALT GLSPDEIVNOVKDAĞLKĞRĞG AGFSTĞRK WILMPKDESMNIRY LLCNADEMEPĞTYKDRLLMEĞ LPHLLVEĞMLİSAFALKAYRĞY IFLRĞEYIEAAVNLRRAİAETTE AĞLLĞKNIMGTĞFDFELFVHTĞ AĞRYICĞEĞTPLLKPĞTĞĞWÜĞ RHSCWKLQELAMNDRDFMRY SRQİLLDDİALDĞQKİLDĞQV LIDİĞLĞDĞQKİLDĞQV
24329	54697	Α	24467	506	673	
24330	54698	С	24468	1	3411	
24331	54699	Α	24469	2455	2694	
24332	54700	A	24470	93	1081	MGGIRDPWLHKLRSLWGICE YGHKEGYDHIRELNLAPGOTT LVPTGLAIHIADPSLAAMMLPR SGLGHKHGIVLGNIVGLIDSDY GQQLMISWWNRGQDSFTIQPGE RIAQMIFVPVVQAEFRILVEDFD ATDREGGGGISGRYFCNED KOTAKRNRREEILQSLALMLES SDGSQRITTAKLAASVGVSEAA LVRHFPSKTRMFDSLIEFIEST TRINLILKDEKDTTARLRLIVLL LGFGERNPGLTRILTCHALL EQDRLQGRINQLFERIEAQLRQ VLREKRMREGGGYTTDETLLA SQILAFCEGMLSFFVSEFKYRP TDDFDARWPLIAAISCSIMMTD TDGYGRAGGESTEVEFKYRP TDDFDARWPLIAAISCSIMMTD
24333		A				RCKCADAATRGKSRRDLPDVQ NSARQYG/W/GCATHARSG+HI VEAVQSG/TPPQPLRPRGTSRKV STDRYWRAASQLPAQYQDLTSI YDVYTVPDRVAKRAFKSPPDD GPVMWRMGHQPHLIPRNVLAQ
24334	54702	A	24472	254	1150	RELTCRYOPOMAEDMOSLVGG TYTRSG'LSVVNNNNGELLAK ELSVQVGIRPEYLDRLLHAFSG GQRQRIALARALSSQPDVIVLDE HGLTYVLISHNVSVIRHMSDRV AVMYLOQIVELGDAQQEIAQA ANLKLESKLAIMEQVYGKKVID AVIVGPKVDVSAVKERIVIQEV LEASDIPYRHDRQLLHNALEKA LQALGGLEVIQLYRDSNLVPG QLKTSEMGKTRLYAADSRLIA AKGSPIQPTLDSLK

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
24335	54703	A	24473	1874	2927	KEDOVKGGMVCPKKLLCOGTR
2-1555	34703	l'`			[-/-/	*RGGVVGGISQASVTSVIGYSA
		l			1	SCOPTPAIMOLHL/ANAASRRL
		1			ł	OPDRNRPNPGWHRPPIHAFTTP
		1				GLVSVSFLGYPCSTPTCLPFSES
		1			ł	SVGESVNLWPOSNENLRRTLV
		1				GEGNLLLTFIGNGKHEIIASIFFA
		1				FSEGISAQSHWQPRYISPASVCT
		ı				LVTEIDIKANKITFSIFDENAGA
		i				WLPPFCKAVVPGWVYKPNLGH
		l			1	EIACVDHWLMPNRLIENLCDIM
ł		l				LPIWVLTKFNDCCAGCVPCCVII
		l				VDDALHGAPKRMCCCITRGMR
		l			1	LLKLSVHAATRSTLQQASHGH
		l				CAWSAPGWLDTSGMDGDRLW
		1				WTLHEVLRDLCTSHGNIVESAR
24336	54704	В	24474	1	672	
24337	54705	В	24475	1	2496	
24338	54706	A	24476	3260	3363	RPDSGGP*RQRRYLRCADHRRR
		_				AVRNQQQLTACA
24339	54707	A	24477	112	224	
24340	54708	Α	24478	1614	2326	CTYSRKCRPDKRSASGNFALSS
1		l				LKSSPLTKNRRYWKVSPTHLLL
l		l				SKRPKISLNAYFGACSLVRPVL
		l				AAASDWTLQGAWSPTRAKALP
		l				ICESWRIPYADSLSSLAASCDAV
		l			İ	FVHSSTASHFDVVSTLLNAGVH
		l				ICVDKPLAENLRDAERLVEG\M
		l			l	REWREERGQGVVHKPIPGWQS
		l				TLEQRGFVGCARHFIECVQNQT
		l	İ			VPQTAGEQAVLAQRIVDKICSS
		_				FNVVRVAPLGDPIQSKPVV
24341	54709	A	24479	19	885	
24342	54710	В	24480	1	1704	
24343	54711	A	24481	974	1156	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Step codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24344	54712	Α	24482	162	1602	HRRKRARGTPKATTTRKPARTI
		1		l		ETLSPLLAILAFAPKLAICTRSPL
	1			1		L/DDMTPFTQCTNAYSHSGIRNP
		1		1		TAISSAAYPRRITGY/KLGPTGE
	İ	1				ERTVYGIYGISESNLAECEKGV
1						KSAVALTPALOPIDGVAVSYID
1		1				AAVALGNTINEMDKYYTQENY
		1				KDDAFAKGKTLHOTFLKNLEA
						FEPVAESYHAAIQEINDKRQLA
						ELKNIEEREGKTFHYYSLAVMI
1						SAKQINNLISQDKFDAEAAMKK
						VSELETLVAQAKEADKGGMNF
		1				SFINSAGQYQLEAKKYVRRIRD
		1				KVPYSDWDKEOLODANSSWM
	1					VEDSFPRALREYNEMLMTRIGG
1						GAGDODMVNDFSYSPOLVGRG
1	l					
		1				WFNDQVATGCTRDSTFNQQQV
		1		ì	ŀ	ALSVNAYYVVNRFGKIDWKPM
						YAEADKLLAKPNMRFKSDKLV
1	1	1				GDLSIGDQQMVEIAKVLSYESK
		1		i		VIIMDEPTDALTDTEAESLFRVI
		_				REMKSQAPRYCLYLPPHENNL
24345	54713	В	24483	1	1263	
24346	54714	В	24484	148	894	
24347	54715	В	24485	1	1071	
24348	54716	В	24486	168	1088	
24349	54717	В	24487	1	1236	
24350	54718	В	24488	1	849	
24351	54719	В	24489	1	1548	
24352	54720	В	24490	1	1372	
24353	54721	В	24491	1	2469	
24354	54722	В	24492	1	1917	
24355	54723	В	24493	1	1159	
24356	54724	В	24494	1	2294	
24357	54725	В	24495	217	2476	
24358	54726	Α	24496	477	916	SLPECEDRVQYRRSLFADPSYR
1		1		i		YGLARHGDPRRAGRLRDV*PL
		1				HE*YRHWHDQS/RLLIASVLPQ
1				l		VWHGACNAMTSSCIARQVS*N
		1		l		TALIIRMRKGDLSAVMSSQTGL
		l		I		INIVRRGLLLSCFRLTAMKISTV
		ı		1		SPFRPQMPSIVRSVWC
24359	54727	Α	24497	1136	1317	
24360	54728	Α	24498	3	317	
24361	54729	Α	24499	1	1245	
$\overline{}$		_				

SEO ID	SEO ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24362	54730	A	24500	85	1293	ITVATTQHQAGLTLRRAGIRQP
						DMAVORDHLPFRVAGVIRHIM
	-					LMLHSORRTGLLITAKNRLLFF
						ORRSVPKFHSKLNOAYCLIAAT
						DCPRRLLLICRYPHHFLHQLIIL
	ŀ		l			AIGIGSAVFEPHQIIGVSRCCPR
						HLGVERVLFLFLNDFIEOVIIRC
						HVVCQSAPAAANIQYAHPWF*
	ŀ					LOFFTNHFELRLLGRFOIIGIFPV
						SAGILHEGIKHAAEQVITQIVML
				i		FADYPGTFFTL/RD*RDERROY
				i		AACL*NDGGVGSRDLRVRLC*
	l					KTYPVGHIPTSHPYN/CSPNPKE
			Ì			PSCRTRLKKSGFFTRISAGAEPL
						MAIPARLSNSLACGARDSAAKE
						VLLWFRFVLLLKQTLLNWTTK
						NVTSLWRTLGSPVGVKEVRAW
				l		TIPV/VSNRAAGSGQNPY*F*KR
24363	5473 I	Α	24501	2794	353 I	SPRDSPTFWTKGGPGGSRGKAL
						RLVVGTDFHQAADNIPDHMMY
						KSIRFNIYHHIRTVTRDINMHNV
						APRGSGLALHRTERGEIILAQQ
		1				ALRSPMHPFSVQRFVKMGYPFT
		1				QYRRAQPMIVDDVAITASRGA
		1	ŀ	ł		KSGMKIIRYSFNPTHSDVTR*IRI
	i			1		YAQGPRRVFAQRGCFEMHNLP
						GTVYPCVSTPGAEDGDGFVRH
		1				LGERLFQLLLHTADFVLPLPAVI
						LTGGVLNAQRNFINRRLLPYVE
24364	54732	A	24502	1	1767	
24365	54733	A	24503	1	1275	SNPTAIGGRPRRPYQAEDRSLD
		1				FVDTALNRKILKDSIFHALQTIM
		1				VGIKDFLRLTQVFFDLATRIPRH
		1				LYHPVDITTHYGRFCRHRRHHF
						QLLQLCFRFLFCLFRHLRRVDF
			ŀ			ALQGFVFVRRVVHFTEFFLNSF
	1			l		HLLVQIVLTLGFLHLLFNAVAN
	İ		1			AFLNLQQIDFRFHHCHQIFQTFV
				İ		NVGHLQNRHRKIGIVIFRSDVL
				l		EHPHRNNTIKLVVQVTIILQQN
						GDIQAFTAFLSHFLLFGRNGDA
						HHAYVIIRCHVVCQSAPAAANI
						QYAHPWF*LQFFTNHFELRLLG
				1		RFQIIGIFPVSAGILHEGIKHAAE
			1			QVITQIVMLFADYPGTFFTLQIE
				I		ETSAGNTQRVFEMMGELVLET
						RLRSPAGFTQWIPHQGCRWSCL
		1		I		PVPRGTLALLSPWVVDGTGRR
24266	54734	١.	24504		2052	GAGGGTPQGGSSCTGAHGGGG
24366	34/34	A	24504	I	2032	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nuelcotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24367	54735	Α	24505	1	1060	MNARQQVAALRVPGVEKATIV
						YRRSLQEMPAWREEYEEALHD
		1		İ		GFRFLNNPERFDADGTLTLRVM
		l				SLGEPDEKGRRRPVETNETVTL
				l		LVDSLITAIGEQQDTEALNAMG
				l		VPLDKNGWPDVDHNGETRLTD
		l				VFMIGDVQRGPSSIVAAVGTAR
l		1	İ			RATDAILSRENIRSHQNDKYWN
		ł				NVNPAEIYQRKGDISITLVNSDD
1						RDAFVAQEAARCLECNYVCSK
						CV\DVCPNRANVSIAVPGFQNR
						FQTLH\LEA\YCNECGNCAQFCP
		1				WNGKPYKDKITVFSLAQDFDN
ļ	}					SSNPGFLVEDCRWVPHRGLYH
l						RLYREPTWRSEWPRRHICPEGS
	Į					TFPERHCDHLSANNSRNKLLPL
		_				QKPGFIN
24368	54736	Α.	24506	1316	2678	NUMBER OF THE PARTY OF THE PART
24369	54737	Α	24507	2172	5242	IYFSERLPALCTPDAHYREPCQ
l		1		l		YNCTRLDYDSALNIRELKKVAL
ŀ	ŀ	1				EKGWDEYKQRWHKPAGSGSR
	ļ	1				HPVAVIGAGPAGLAAGYFLAR AGHPVTLFEREANAGGVVKNI
l				1		
		l				VPQFRIPAELIQHDIDFVAAHGV KFEYGCSPDLTIEQLKNQGFHY
				1		VLIATGTDKNSGVKLAGDNON
		ı		Į.		VWKSLPFLREYNKGTALKLGK
1		1				HVVVVGAGNTAMDCARAALR
l	1	l				VPGVEKATIVYRRSLOEMPAW
	1	l				REEYEEALHDGVEFRFLNNPE
24370	54738	Ā	24508	192	484	RGLVHRGRYRWRQKWSAGSP
2.0.0	5.750	ľ		1		ARHPV/SQSTTDTPATHALSTKII
l		l				SPIPNAPISALARTTATRL*RSM
		1				NQPPVKRPTVIPRVKPA*ISEPE
		l				VGPIILGP
24371	54739	Α	24509	1	1713	
24372	54740	Α	24510	I	651	
24373	54741	Α	24511	3	783	PVLSKTPLTAKAIDAAQPQDKP
		l				YKLTDSLTPGLFLLVHPNGSKY
		1				WRFRYWLNKREFLQAIGVYPLI
ŀ		1				TLKEARRRATESRSLIANGINPV
						EQARKEKAIDALNMAAGFKKV
!			1	1		AEDWFATRVGGWSESYAKQV
1	1		1	1		RSALEKDVYPVLGKRSIVDITA
1	1	1	ŀ	1		RDVLALLQKKERTAPEQARNV\
1			l	1		AGASVRSSSLPLSPNWGGWLA
1						RAAFPHHITIAARMTKHPPCW
1			1	1		WCTILACRQASLAVRGSTHYSL
		L				ELLIRRHILSLLRSPICASPLTV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24374	54742	A	24512	746	2387	WTALPARLKQIRSGRKLPLTVM
		1				PALRETDTFDTFMESSWYYAR
	1	1		İ		YTCPQYKEGMLDSEAANYWLP
i		1				VDIYIGGIEHAIMHLLYFRFFHK
	1					LMRDASMTNPSSVPRAGGPAL
	1	1				LFENPKGYSMPVLCNLFGTPKR
					1	VAMGMGQEDVSALREVGKLL
		l				AFLKEPEPPKGFRDLFDKLPQF
	ı					KQVLNMPTKRLRGAPCQQKIV
						SGDDVDLNRIPIMTCWPEDAAP
	i			i		LITWGLTVTRGPHKERQNLGIY
				l		RQQLIGKNKLIMRWLSHRGG\A
				l		LDYQEWCAAHPGERFP\VSVAL
	1					GAVPATILGAVTPVP\DTLSEYA
						FAGLLRGTKTEVVKCISNDLEV
	1	l			1	PASAEIVLEGYIEQGETAPEGPY
	1	1			-	GDHTGYYNEVDSFPVFTVTHIT
						QREDAIYHSTYTGRPPDEPAVL
		1			l	GVALNEVFVPILQKQFPEIVDFY
		1				LPPEGCSYRLAVVTIKKQYAGH
						AKRVMMGVWSFLRQFMYTKF
	Į.	1				VIVCDDDVNARDWNDVIWAIT
		1			l	TRMDPARDTVLVENTPIDYLDF
	i					ASPVSGLGSKMGLDATNKWPG
						ETQREWGRPIKKDPDVVAHIDA
24375	54743	A	24513	576	878	NLGSVWHYFRRSPEPATHHDA
					1	ANLERSPAA*RLSGARYRILAV
	ŀ					*ADQSQTGSGDGSPDLQTGRV
					İ	GDEARHRKRGLHVPQPRSEPPV
						GARGFPYRFATRWR
24376	54744	Α	24514	2	878	
24377	54745	A	24515	1	735	
24378	54746	A	24516	I	1992	
24379	54747	A	24517	721	1239	

3220

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
				l		
24380	54748	Α	24518	1	1954	RQLNGVQLAFRESFHTVTRVTE
		1				QHAAGAVAIHQHRNQLLTGAL
1		ı	1			GIFAVAVCCLQQRLDILLADHL
		l				AEHVQFVIAQFVTCQQHGNGV
		1				RNRTIIFLLFNELRKIVETVRVQ
						QTQTGEVAFHPQLFRGRVVYG
		1				PDLNARRGNGVINCSTLEDPQF
		1				GLILFVYTIGIQVGPGFFASLRV
		1				SGLRLNLFAVLIVIIGGLVTAIL
		1				HKLFDIPLPVVLGIFSGAVTNTP
1		l				ALGAGOQILRDLGTPMEMVDQ
						MGMSYAMAYPFGICGILFTMW
		1				MLRVIFRVNVETEAQQHESSRT
		1				NGGALIKTINIRVENPNLHDLAI
		1			ŀ	KDVPILNGDKIICSRLKREETLK
		1				VPSPDTIIQLGDLLHLDSRGSPL
		1				DTQDIDLQINSSVEKQFGDAIRT
		1				TILDVLARYNVRGVQLNVDDK
		1				GALDCILRARLEALLARASGLP
						MISASLOORKTRTRRSMLFVPG
						ANAAMVNNSFIYPADALMFDL
						EDSVALREKDTARRMVYHALO
		1				HPLYRDIETIVRVNALDSEWGV
						NDLEAVVRGGADVVRLTKTDT
		l		l		AODVLDIEK\EILRIEKACGREP
	İ	l			1	GSTGLLAAIESPLGITRAVEIAH
		l				ASERLIGIALGAEDYVRNLRTE
		l				RSPEGTELLSARCPIWQAARSA
						GIQAFDTVYSDANNEAGFL/QE
24381	54749	Α	24519	5121	5492	
24382	54750	A	24520	2520	3525	
24383	54751	A	24521	I	1263	MAINSPLNIAAQPGKTRLRKSL
		1		1		KLWOVVMMGLAYLTPMTVFD
		1				TFGIVSGISDGHVPASYLLALAG
		1			i	VLFTAISYGKLVRQFPEAGSAY
		1	İ			TYAQKSINPHVGFMVGWSSLL
						DCLLAVVIIAAIYVGFSLAGFHV
l						YIGMLEVPGANAAMVSNSFIYP
						ADALMFDLEDSVALREKDTAR
						RMVYHALOHPLYRDIETIVRVN
1		1				ALDSEWGVNDLEAVVRGGAD
1		1				VVRLPKTDTAQDVLDIEKEILRI
l		1				EKACGREPGSTGLLAAIESPLGI
						TRAVEIAHASERLIGIALGAEDY
1						VRNLRTERSPEGTELLFARCSIL
1					1	QAARSAGIQAFDTVYSDANNE
						AGFLOEAAHIKOLGFDGKSLIN
		1		1		PRQIDLLHNLYAPTQKEVDHAR
1					1	RVVEAAEAAAREG\LGVVSLN
2.120.4	5.4750	<u> </u>	24522	-	405	GKMVDGPVIDRARLVLSRAELS
24384	54752	В	24522	62	1403	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1		l		sequence		
24385	54753	A	24523	891	3240	RYRKSPGSWR/CMSCILTSWITT
24303	34733		2.4323	05.	52.10	MFPI*RLGQWC*NPCVTMAL/L
		l				APIDVHLMVKPVDRIVPDFAAA
ŀ				l		GASIITFHPEASEHVDRTLOLIK
		l				ENGCKAGLVFNPATPLSYLDY
						VMDKLDVILLMSVNPGFGGQS
	1			l		FIPOTLDKLREVRRRIDESGFDI
	1			i		RLEVDGGVKVNNIGEIAAAGA
l		1	İ			DMFVAGSAIFDQPDYKKVIDE
		1		ĺ		MRSELAKFEDIRGVAFDLDGTL
		1		1		VDSAPGLAAAVDMALYALELP
						VAGEERVITWIGNGADVLMER
		l				ALTWARQERATORKTMGKPPV
		l				DDDIPAEEQVRILRKLFDRYYG
1		l				EVAEEGTFLFPHVADTLGALQA
1						KGLPLGLVTNKPTPFVAPLLEA
						LDIAKYFSVVIGGDDVQNKKPH
	ŀ	l				PDPLLLVAERMGIAPQQMLFVG
		1				DSRNDIOAAKAAGLDAOARRK
		1				NAGYYYYLRLAKRQMRAGVA
		1				EALRODLLAAKLNVKLVNAGD
						YKFKQIASEKLLIVVTSTQGEGE
						PPEEAVALHKFLFSKKAPKLEN
						TAFAVFSLGDSSYEFFCOSGKD
						FDSKLAELGGERLLDRVDADV
						EYQAAASEWRARVVDALKSRA
1	ŀ					PVAAPSQSVATGAVNEIHTSPY
						SKDAPLVAWRLPNVEGRARAG
		1				GASSFLADRVEEEGEVRVFIEH
				1		NDNFRLPANPETPVIMIGPGTGI
						APFRAFMQQRAADEAPGKNWL
		l				FFGNPHFTEDFLYQVEWQRYV
24386	54754	A	24524	950	2124	MSLISSVIAATWLHVKSYRLSC
24300	34734	1	24324	550	2127	GFYACQSLVLVS/IFPTLSCLFA
		l		i		AEQLLIWSASAFITKVLLVPLIM
		Į				TYAARNIPQNIPEKALFGPAMM
i						ALLAALIVLLCAFVVQPVKLPM
1			1			ATGLKPALAVALGHFLLGLLCI
1		1				VSQRNILRQIFGYCLMENGSHL
1						VLALLAWRAPELVEIGIATDAIF
		i				AVIVMVLLARKIWRTHGTLDL
						TPLLFSLLCFACRKRRLSATRTV
	l	1		1	1	TVLHSLGITLLLILALWVVQTA
		1			1	ADAGEIFAAGLWLHIDGLGGLF
	İ	1	1		1	LAILGVIGFLTGIYSIGYMRHEV
	1	1			1	AHGELSPVTLCDYYGFFHLFLF
	1	1		1	1	TMLLVVTSNNLIVMWAAIEAT
	1	1	1		1	TLSSAFLVGIYGORSSLEAAWK
						YIIICTVRVAFGLFGTVLVYANA
		1	1			ASVMPQAEMAIFWSE
	<u> </u>				J	MOVIME VACINIAIT WOE

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequen <del>ce</del>	deletion, \≔possible nucleotide insertion)
24387	54755	Α	24525	1	757	RWRLPGVPPFNGFFSKFPLFAP
						GFALSVEYWILLPAMILLMIESV
						ASFAWFIRWFGRVVPGKPSEAV
						ADAAPLPGSMRLVLIVLIVMSLI
						SSVIAATWLHVKSYRLSCGFYA
					l	COSLVLVSIFATLSCLFAAEOLL
		1				IWSASAFITKVLLVPLIMTYAAR
		l				NIPQN\IPEKALFGPAMMALLA
		ı				ALIVLLCAFVVQPVKLPMATGL
					1	KPAL/AGLATDAIFAVIVMVLL
	,	ı				ARH\IWRTHGTLDVNNLHALK
		l				GIMSCSYSS
24388	54756	Α	24526	249	3943	
24389	54757	A	24527	1	1278	
24390	54758	В	24528	48	I44	
24391	54759	В	24529	27	239	
24392	54760	Α	24530	1	551	
24393	54761	Α	24531	3	258	MLFDEPTSALYPEMIN*VLDVM
						VELANEGMTMMVVTHEMGFA
					i	RKEANRVIFMDEGKIVEYSPKD
0.1001			0.500		0.00	AFFDDPKSDRAKDFLAKILH
24394	54762	Α	24532	2	979	
24395 24396	54763 54764	A	24533	1	4116	MLIAEGLMTAKNITVITNSLPA
24390	34704	^	24334	'	1193	AFALSENKDITLVVCGGTVRHK
		١.				TRSMHGSIAERSLODINADLMF
		1	Ì			VGADGIDAVNGITTFNEGYSIS
		l				GAMVTAANKVIAVLDSSKFNR
		l				RGFNOVLPIEKIDIIITDDAVSEV
		1				DKLALQKTRDTSLVYVLSLADF
		l				FRTASTIGERDGTOVEMILFAGE
						VYLVISLSASLLVLTDCSTEVK
						KGEVVVVCGPSGSGKSTLIKTV
						NGLEPVQQGEITVDGIVVNDKK
		1				TDLAKLRSRVGMVFQHFELFPH
		1				LSIIENLTLAQVKVLKRDKAPA
		l				REKALKLLER/VSGFFAHANKF
		l				PAQLSGGQQQRVAIARALCMD
		1				PIAMLFDEPTSALDPEMINEVLD
		l				VMVELANEGMTMMVVTHEM
		l				GFARKVANRKHTTRSTIALQSL
		l				ATCT
24397	54765	Α	24535	383	962	TDNDRPGLGTDMKKASAIVTN
		l				VAVVLSGRYRRERASGEWAAL
		l	ĺ	1		SFLRPHTLTVFVIPHIQWDDPQ
		1	1	1		MSRP\SGRHLFRCRTVQRKHAL
	l	1	1	1		QVVEKFRPFFPSDRYRYGAPGD
	l		1	I		YAQSFGGQIDDVVKAIQTPSKF
		ĺ				RRFLRVSFD*IRLPILHSGKSPLR
	l	1	ı	1	1	
						RMPNLMRRHSHTARHYPALGT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
24398	54766	Α	24536	1477	2387	
24399	54767	Α	24537	I	1560	
24400	54768	Α	24538	305	718	
24401	54769	A	24539	1	2161	MNDVDRVGGKNASLGEMITINL SGMGVSVPNGFATTADAFNOF LDQSGWNQRIYELLDKTDIDDV TQLAKAGAQIRQWIIDTFOPEL ENAIREAY AQLSADDENASFAAV RSSATAEDMPDASFAACTLVFG QNLSTSNKDVIELPDNQVDLDK WNVIYPYTFGLIDQLRAKPIMS QANPELEQQIANYEYRIGIGDV LMTVVWDHPDLTTFAGQYRSA SDTGNWVNADGAIFYPYIGILK VAGKTLTQVRNEITARLDSVIE SQVDVSVAAFRISQKAYVITA EVSKSGQQPITNIPLTIMDAINA AGGLTADADWRNVLTQNGV KTKVNLYALMQRGDLRQNKLL HPGDILEIPRNDDLKVFVMGEV KGSTLKMDRSGMTLAEALGN AEGMNQDVADATGIFVIRATQ MKQNGKLANIYQLNAKDASAM ILGTEPQLEPYDIVYTTAPLAR WNENSILKKLERFYEDVKEMPL GEALEQHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEQHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGVSFENSKEMPL GEALEGHTGMT GEALEGHTGVSFENSKEMPL GEA
						GSPLSKAADILFPVISDSIRQQA
		L				LPAYSQHISVESTQFSNQGTMA
24402	54770	С	24540	I	1389	
24403	54771	Α	24541	405	576	CEMGAPPWPGCWLS\LFDVDG RFVLAWMLFQGSYLAGALGDQ PVHIHLGQLLALWRPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24404	54772	A	24542	I	1127	MARTLAHELIDFGEIKRGLLGIK GTEMSADIAKAFNLDVQRGAF VSEVLPGSGSAKAGVKAGDIIT SLNGKPLNSFAELRSRIATTEPG TKVKLGLLRNGKPLEVEVTLDI STSSSASAEMITPALEGATLSDG QLKDGGKGIKIDEVVKGSPAAQ AGLQKDDVIIGVYMDRVNSIAE MRKVLAAKPAIIALQIFPVDHR GAIGGQTTDIPPDPSGINIDRC MKGLSFAGEMTYTNTAHRRA FTNQPRDFMSVAWLGKGIALP SVOWCYKSPVAGRIASLFATLHAI GUESDDGVEULHVGIDTVKLDG QIFSAHVNGEAGLKRVVKKEH ADVQRHAESVYRGQAGQTT DGIRRQDNRVQPGCERCTHQLLR
24405	54773	А	24543	95	599	QIMMLNGSSTPNTSLPTPQAF DRSLPINATSARPSSTSTRHSAE SSISRDCVSNVS/HSGG*TGGIK G*CHAHPADLTACHEADSRGSP SHAYAAVALHVID/GWYLGDQ TAAYATGSAVSCPSSGNQFSRP SAAGRFSAVSAPQGAQRHPGR ARREPRERTAGGCER
24406	54774	A	24544	640	890	LANAQLGSNEISIFQCFAAIQRFI KLHRDASVINHPLAE/TRK*YPV SVYHLRHPPAIIR*PAIRDNA**I LPVTPGYSCSRHQ
24407	54775	А	24545	3	257	ETDIFICDSREFFHHFAKASVHI* PVVSIANFAIQSGKILALGAENI ATTSDRRAQRQKAVCKAHDAS SVSFRTLSVRPTNDCP
24408	54776	A	24546	332	1047	RTRPYCPGMGNEPMTGWMAA AVVTLMIRMCFSVYTMLSESC QRMVIVGYGRCFADRQNLMVC LRSMPNVFTGSCARMRCCLSEN LLYRHRNGHIQAEWP*KKAISD KQYRTSCWERWNAASATIFR/ LSPVEWLTDNGSCYRANETRQ FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDVISIMPKPDGLT AAKNLAEAFEHYNEWHPHSAL GYRSPREYLRQRACNGLSDNR CLEI
24409	54777	Ā	24547	1200	1544	LTGVADGNVDKPCYKFARLW YWIYPAFPPIRRVKVAYREYRP PTTPRVRQVRDLTFCHRPAIPDR MHRY*SSHRALPGCWSKVPAQ KSSRTVSGTD*VDLLSPRAQRA PSPLQG

SEQ ID NO:	nf peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24410	54778	A	24548	263	625	
24411	54779	Α	24549	742	851	VSAQQRVILNKIAVLNRK*RYG CWRLWICPYISRHLLSLNPLQA RCRRYSRGER
24412	54780	A	24550	I	532	MKTLLIIDANLGTIRLYGEDPAG AAARKAKLEIIDNPNDAEMAIV LGDSIPNDSALNGKNVWLGDIS RAVAHPELFI.SERKGHAKPYTA CPTGVAHTFMALKPLKPKKN VAGIPDTGQVCETVQTSCW/AA VETPLRQRSSVVSSGVADG*WF MLPG
24413	54781	В	24551	1	888	
24414	54782	Α	24552	1	2283	
24415	54783	A	24553	992	1662	KKAISDGALTGSSSA VITERDC VSRSRWTAVIRHCTGRSLPAA STVKQYRTSCWERWNAASATI FRLSPVEWLTDNGSCYRANET ROPARMLGLEPKNTAVRSPESN GIAESFVKTIKRDYISIMPKPDG LTAAKNLAEAFEHYNEWHPHS ALGYRSPECYLRIGILVSFISSLQ KFNDFAFEDGLFSGYDAEKRQ YEKSSWNYQLDENGYAKRDET LTHPRC
24416	54784	Α	24554	1	2262	
24417	54785	Α	24555	158	410	
24418	54786	В	24556	1	2607	
24419	54787	A	24557	715	1016	KSAAVPRSGASSQSDSAHFAQP EYAAFSRFPRGSFRHPRAA*YF GRLNHHVRSERGINP*YHRFNL HWRYVADAISADGAFRTVSGG GGRRSGAGRVDWQ
24420	54788	A	24558	652	1214	RTDHCVSRSRWTAVIVRHCTG RSLPAASTVKQYRTSCWDRWN AASATIFR/LSPVEWLTDNGSCY RANETRQFARMLGLEPKNTAV RSPESNGJAESFVKTIKRDYSW PKPDGLTAAKNLAEAFEHYNE WHPPSALGYRSPREVLGQRACT GHAIGSGPSAFFGAPVRRVSRT SVTAKACPRGLL
24421	54789	Α	24559	647	1976	
24422	54790	A	24560	289	574	ETPASSPTLRTSIPSISWMTRGSL RRVMLLCPFPSESGTVSEKAWP EWSSFSSSPPSCRTSASSPPSHLR /NIDVSPKHVVFATIPRNYTMSF LPR
24423	54791	A	24561	816	1375	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
24424	54792	A	24562	li	3993	I IMSOKLKVVTIGGGSSYTPELLE
24424	34/92	A	24302	l'	3993	GFIKRYHELPVSELWLVDVEGG
		1			1	
		l	l			KPKLDIIFDLCQRMIDNAGVPM
		1				KLYKTLDRREALKDADFVTTQ
		1				LRVGQLPARELDERIPLSHGYL
		1				GQETNGAGGLFKGLRTIPVIFDI
		ı				VKDVEELCPNAWVINFTNPAG
1						MVTEAVYRHTGFKRFIGVCNIS
1		1	ĺ		\	IGMKILKTRTLDTTGSTSTGDTI
İ						LTQSLLMELSALCRVEVEEGLA
		1		1		LVALIGNDLSKACGVGKEVFG
		l				VLEPFNIRMICYGA
24425	54793	Α	24563	1136	3608	KKAISDGALTGSSSAVITERDC
				1		VSRSRWTAVIVRHCTGRSLPAA
		1			İ	STVKQYRTSCWERWNAASATI
						FR/LSPVEWLTDNGSCYRANET
						RQFARMLGLEPKNTAVRSPESN
					i .	GIAESFVKTIKRDYISIMPKPDG
						LTAAKNLAEAFEHYNEWHPHS
1		1				ALGYRSPREYLRQRACNGLSD
		1				NRCLEIYGQIQLGTGELNITTGV
	ľ					VVTARDTHIALNFOKRRTTGLA
						TOSRORCONRRRVMGKIVIYRE
I					1	AIRFTTQLQTATSINKRTQRVSG
		i				ICRRYTNMASRCNRHOAIVHIM
				1	ł	FAYORPFHFAHFFAIQONFPFGS
1		1			1	IGGQLFRLPVTLLTHQLLLAPA
1		1			l	AHRHGLFQVDVIFRPDNTALPR
1		1			1	NDTHOMVELFLDRFOVVKDIG
	1	1			1	VIELKVVEDORTRAVMNKFRA
		1			i	FVEKGAVILIRFDKKKDIFLQYR
1		1				FHTRISTGHGVANNHQIRLRLE
i					1	LAGIVPLNOLNPLPLNSVPMINI
		1			1	MNGGENADNNVDIQEFMIQPV
		1				GAKTVKEAIRMGSEVFHHLAK
		1			i	VLKAKGMNTAVGDEGGYAPN
		1				LGSNAEALAVIAEAVKAAGYE
1	i					LGKDITLAMDCAASEFYKDGK
		1				YVLAGEGNKAFTSEEFTHFLEE
1	1	1	1			LTKOYPIVSIEDGLDESDWDGF
1		1				,
			l		İ	AYQTKVLGDKIQLVGDDLFVT
	1		1		1	NTKILKEGIEKGIANSILIKFKAQ
			<b>[</b>			HAGLLHMYTCAMLGVGGQCW RYCMSQAFKEDRFAQDQRVAV
24426	54794	В	24564	83	2851	K I CHISQAF KEDIG AQDQK VA V
24426	54795	В	24565	1 I	1578	
24428	54796	A	24566	574	753	
24429	54797	A	24567	1	2112	
24429	54798	В	24568	27	969	
24431	54799	A	24569	1	1773	-
24471	24/1/	1~	2 1202	1.	r	L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24432	54800	A	24570	822	984	PSALCGCHSL*CSNASARFFAA VNPSGAFGCRADHPDGELFLTG YVADGGYHS
24433	54801	Α	24571	1	4287	
24434	54802	Α	24572	1	2384	
24435	54803	A	24573	3	3682	ACSARPSEAELELLOTLANADN TIDGILVQI-PAGIDNYKVLER HPDKDVDGFHPYNVGRLCQR APRLRPCTPRGIVTLLERYNIDT FGLNAVVIGASNIVGRPMSMEL LLAGCTTTVTHRFTKNLRHHWE ADALLINAVGRPGFHEDBWIKE GAIVIDVGINRLENGKVVGDVV FEDAAKRASYITPVPGGVGPMT VATLIENTLQAMSNMATFSLGK HPHVELCDLLKLEGWSESGAQ AKIALBGGOVKVD
24436	54804	A	24574		1382	MLRCVNVLADAVKYTLEPKG RNVVLDKSFGAPTITKDGVSVA REIELEDKFENMGAQMVKEVA SKANDAAGDGTTTATVLAQAII TEGLKAVAAGNNPMDLKRAIS RSRKGYGPARIROELNOKGISR EATEKAMRECDIDWCA**RF*S DKHHHRT*RQ/PTRHRYPDESV PGSHNMRSAHALSSAQGYILLP RAVLSGWREENVHPTPGYDSA SGSVEVPPPMTSRRLPAPDNFA APHRYRVLKTGLLSPGCHVRN ADTL
24437	54805	Α	24575	466	1215	
24438	54806	A	24576	1104	1923	LAIPMKDETTEAWLRANHTLISE GAEHIHADSRITPSARELLESR HLRIKFIDEOGRLFYDDEOQOP QPVHGLTSSDEHPQACCELCRQ QPVHGLTSSDEHPQACCELCRQ PVAKKUPDIT.THLSAEKMYAKS DPRLOFRAVLDSTIALAVWLQI ELAFPWQPWLADIRSRLGNIMR ADALGEPLGCQAIVGLSDEDLH RLSHQPPLRYLDHDHLYPEASHG RDAALLNLLRTKVRETETVAA QVFITRSSPEVLRPDILQALNRL SSTYVYMMILSYTKQPLTVKQI QQRLGETQ
24439	54807	A	24577	243	644	HAGSVCPSLYRCQRTAKRSGFY LLLKRLWSFSGNI*IHSGQQNPG RNQQLGLPRSRKGESSRAHPSC QRRPQVWPHPLAGSRPPRPWA ACARLGPIAPARQIPERWPGQV PVLADAHVLPCLAGSLRPALYD F

NO: of peptide hod in USSN location of first codon for last amino a	
sequence 09/540,217 codon for peptide of peptide sequence	deletion, \=possible nucleotide insertion)
24440 54808 A 24578 237 454	RSRLPEGVPVCWCNHSVR*RDC
	RFPVGKLHRLWL/LALPGVRLIF
	RASTKRITGYINARSASIASASA
	RNRLV
24441 54809 A 24579 377 1155	KAYSFATMKSLAISCRWQNA*S
	HVSTFVMVRW/LKGVQFRNHEI
	IGDIVPLAKRYAEEGADELVFY
	DITASSDGRVYPTLITRLADRFG
	VQCIVVGIDTWYDARNLKDISV
	VGLLGAQVPSVRAGMPQSRRQ
	TEGAQGMVRNEEGGSLRLSHH
	QACKATHTQQWTLEVTAQSSY
	NLFPEQWVKLFWGIRQGDLPL
	AFSQKLSRQTFQQQQTQTPRPI
	VGQAPKDLQTGTGTPQTHAVH
	SGDHAAGEQSCKSCKAPIYPLT
	AQFSLETRSFWGSEWGYSTHG
	ELRRRDKGRRRFY
24442 54810 A 24580 1107 1458	RTFWWTTCNSLAPCAGGYPST
	GAALPVSRKLPGRGLLLSGWG
	EHNARYRAGTFLWALFCAAAV
	AYWRRC\WGQYGMWFLRIRRG
	TLGDGTIRRVFVGSLWAAVVIV
24443 54811 A 24581 171 352	EIGVEHIGVFKA PPAPPAESDGLPAHTTRARTTA
24443 54811 A 24581 171 352	DDLRNKRROHVGC*YRTRGSP
	RPNRTWWRVCRYRSPHR
24444 54812 A 24582 5 226	RFINKIWWKVCKIKSFHK
24445 54813 A 24583 476 1939	RPESOHNTAKPAMKVLEOARR
	FLGIRWLSAPASLAN/PVILLVV
	GNILNIVLDVWLVMGLHMNVQ
	GAALATVIAEYATLLIGLLMVR
	KILKLRGISGEMLKTAWRGNFR
	RLLALNRDIMLRSLLLQLCFGAI
	TVLGARLGSDIIAVNAVLMTLL
	TFTAYALDGFAYAVEAHSGQA
	YGARDGSQLLDVWRAACRQSG
	IVALLFSVVYLLAGEHIIALLTS
	LTQIQQLADRYLIWQVILPVVG
	VWCYLLDGMFIGATRATEMRN
	SMAVAAAGFALTLLTLPWLGN
	HALWLALTVFLALRGLSLAAI
	WRRHWRNGRPGTGCLNTKGS
	QQQHRHDSTTQHIHLQLLVIRV
	KTTTTNNSQQTPQYPCQQYHT
	DSRQHRQQNRMVCQRIPHALPS
	PRFRQISRGSTAKVPCAKARAF
	LRVKSDPTLITRLADRFGVQCIV
	VGIDTWYDAETGKYHVNQYTG
	DESRTRVTQWETLDWVQEVQK
	RGAGEIVLAYVSE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24446	54814	Α	24584	1	50	
24447	54815	Α	24585	354	456	HLFSEACCSPGVLRELCRPF*SP
						GTDRNLVMHGH
24448	54816	A	24586	494	835	ITWLPGFRPPFQGSEQFCLAGVP
		1				GATGGSESVLHTRNSYKMLEV
		1				RREVAALISALKVSAKCRNCGS
						SHALTEP/ASSPCWRETSTRPTG APAPTIPPPAASPSPGPMCVOPH
						GED
24449	54817	A	24587	3	726	GED
24450	54818	A	24588	i	1635	
24451	54819	A	24589	1614	2454	RTTHAPASTPNTGTMLCRPYPC
21131	3.017	ľ.	2.507	1.011		CWRRKTP\IIFRATPQWFVSMD
		l				OKGLRAQSLKEIKGVQWIPDW
ŀ		l		1		GQARIESMVANRPDWCISRQRT
						WGVPMSLFVHKDTEELHPRTL
		1		ļ		ELMEEVAKRVEVDGIQAWWD
						LDAKEILGDEADQYVKVPDTL
						DVWFDSGSTHSSVVDVRPEFA
		l				GHAADMYLEGSDQHRGWFMS
		1			l	SLMISTAMKGKAPYRQVLTHG
		l			1	FTVDGQGRKMSKSIGNTVSPQD
					i	VMNKLGADILRLWVASNDYTG
						EIAGSDENLKRACHYNACSISL ARRRH
24452	54820	A	24590	362	517	TKSLISSMSSISSPPVVLICRNSS
24432	34620	^	24390	302	F"'	PEV**RKI*LGTELEFVIMVIAVS
		l				AWP
24453	54821	A	24591	250	930	
24454	54822	A	24592	1388	1912	VCPAAMTGFAGSPFCTAVVTFP
		1			1	DITPLLWILMC*LAILMAESEPK
İ		1				AISPPTISVVP*YAAESLLRVRIP
	ľ	1				VPSFVTSPLPLILCVIAQLRSVE
		1	ì			MVSRPLLITEASPRFFCSLTLSA
		ı	ĺ			LPVSMLNCPTKRLLSPSNSTSVL
		ŀ				AVALTIPFPLMLLRSSPVTFFSV
		_				NRPSWAIFPLPNP
24455	54823	В	24593	1	6018	WALOA BOWLINIERDI DESIRENT
24456	54824	A	24594	510	1003	VALQADQKHKHERPLPPPIPTM FOLAQPGVQLHAKPVYQVP/V
	1				1	MMOATEPTGI*VRIPVLSISTNA
						PSITSIWPLFVRKISVLTLASVV
					1	AASHAASSPRQCAIRCKIWGRW
					1	AGSLRRDDGFGVRSRGSRYGA
					1	SVSISNFSAGINGKSSRSSSPRRS
		1			1	SOTOPVMPI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24457	54825	A	24595	197	4314	RASTELSLRCCAPSLQ'ALLHFL YLACETWMLLEGI.HLELTVRN LKYANYTSTERFEKREMYPVG YGIPAVIIAVSAIVGPONYGTET HCWLKLDKGFIWSFMGPVAVII LINLYFYFQVLWILRSKLSSLNK EVSTIQOTRYMTEKAISQLEILG CSWGLGFFMVEEVGKTIGSIIA YSFTIINTLQGVLLFVVHCLLNR QINSLLTWTLWTLWTLRQRLSSVN AEVSTLKDTRLLTFKAFAQLFIL GCSWVLGIF
24458	54826	Α	24596	1409	1573	
24459	54827	Α	24597	1283	1563	
24460	54828	A	24598	281	839	CVPTTDL VVQSQI PR WRNWPR CSCSHVSMKAASSPERTFTYCS GIYWLISGSGIGVSVPLLISIGES VINLAVRPVIAHAIRVAITTRQT TRYAVTVVVALPVFRA VEHV FQHLTQTRTGFRWHQFFFNRRQ REOSTTQGEOGRWANFONGKV VNHOLAQRLRRLIGRVRFENQ RFVVFDHLA
2446I	54829	В	24599	I	5652	
24462	54830	A	24600	559	1665	RVERKATIEMKSQRTTSDSWLII LAKQTGIIRAAKKGKTFILHD PROFPYANGSIHIGHSVNKILKDII VKSKGLSGYDSPYVPGWDCHG LPIELK VEQEYGKPGEKFTAAE FRAKCREVAATQVDGQRKDFI RLGVLGDWSHPYLTMDFKTA RIKALGKILONGHLHKGAKEP HWCVDCRSALAEAEVEYYJDK TSPSIDVJAHPFMGFDVPAILGD YVIGQKYGLETANPVGPDGTY LHGTYPTLDGVNVFKANDIVVA LLQEKGALLHVEKMJHSYPCC WRIKKTPIIFRATPGWFVSMDQK GCDIGFHASSNGKRADDSTDD HVRKILCARQRGQPHPHQFQRT

3231

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
24463	54831	A	24601	1	1190	MITDFRESDTMSLFDKKHLVSP ADALPGRNTPMPVATLHAVNG HSMTNVPDGMEIAIFAMGCPW GVERLFWQLPOVYSTAAGVTG GYTPNPTYREVCSGDTGHAEA VRIVYDPSVISYEQLLRKYRCV AVALLGYFKCFPILLNESYKSM QDDLAFIARFIFKDLKFRRFSL KADQKSRIYERVLSIAGVNSWK DKQHQPRLVEHLLVCAESWVA PRALFDAAIEVLAHGKIAIPAYL VAFLVLGPLVLSLIPSQMLPSTL WSSITYSIVVIVEAGVQYHSRLR RFGRVEVNEQIEYLINPIRITRA RAVNFVDNNNRLQAPRILRQDS WWITRPLFGLTWAIIGSPGILPQ VYKSARVMKQAVAVLEPFEA SKEQGKTNGKMVIATVKGDVH DIGKNIYGVVLQCNNYEIVDLG WYMPAEKILR*RLGGIPFTL*R SNRVPGPPEDRISCLFGCVYW SNRVPGPEDRISCLFGCVYW SNRVPGPEDRISCLFGCVYW RCLSSLRRCCR*RGQAS RQ*VLLSSKLAISTILLGLRFGR
				:		VEVNEQIEYLIHNPIR/IARQGG QLC**QQSASGPTDITAGFMVD HQTFTGADVGDNRVARNPATG GQIGARHETGGGLPRTVY*SQQ RAGQNQRQDGDRHREGRRPRH

3232

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24464	54832	A	24602	1	1591	MGILVSPLLAPLIGGLLDTMWN
		l				WRACYLFLLVLCAGVTFSMAR
						WMPETRPVDAPRTRLLTSYKTL
		1		·		FGNSGFNCYLLMLIGGLAGIAA
		1				FEACSGVLMGAVLGLSSMTVSI
		l				LFILPIPAAFFGAWFAGRPNKRF
		l				STLMWQSVICCLLAGLLMWIP
						DWFGVMNVWTLLVPAALFFFG
						AGMLFPLATSGAMEPFPFLAGT
						AGALVGGLQNIGSGVLASLSA
						MLPQTGQGSLGLLMTLMGLLI
						VLCWLPLARGYRLSSWTSTTAS
						EDIDCEEGDGEGNETHGLQLAV
				1		EPEGLQPNYMGRGKIRFRDTCL
		İ				LFCTQSRGSQWGFARTELVALL
						PPFLSGAADYRAGLALWLARG
						ADCDVDERHRADRQSNLARSS
						GGFIALAAGAKSDRRLRELNQS
						LQKELARNQHLAERLLETEESV
						RRDVARELHDDIGQTITAIRTQ
						AGIVQRLAADNASVKQSGQLIE
						QLSLGVYDAVRRLLGRLRPRQ
						LDDLTLEQAIRSLMREMÉLEGR
						GIVSHLEW\QSMNQR*AKTSA*
						RCFVSARKG
24465	54833	A	24603	1	1752	
24466	54834	A	24604	1	699	
24467	54835	Α	24605	965	5516	
24468	54836		24606	84	3760	
24469	54837	A	24607	27	278	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		<u> </u>				
24470	54838	A	24608	311	2529	REWGSTRRCERRISLSRNIARW
						RTIWRITRPCRRCVFRFIASTLR
					. 8	LHLHLIMNDLPLEEYPCVRDLV
						PGRFLKFL/HRDPKGTTLVLASI
						LPGRIPVDPRSIIVMLFLAVRWL
						QRQLAGQELLETRATRILNGER
		1	1			GSNVLGTIYEWPPRTSSALDTL
	1	1			\	LREIQNAREQHSRLDTLIRSYA
		1				AQDVKTGLNNRLFFDNQLATL
	ł	I	1			LEDQEKVGTHGIVMMIRLPDFN
						MLSDTWGHSQVEEQFFTLTNL
			1			LSTFMMRYPGALLARYHRSDF
		ŀ				AALLPHRTLKEAESIAVFRALS
						RLPDLWHRSIGTLTEALPOTDK
				l		RQEQIAVALTSYSGLYGLGYGS
						KEIOLTYSGTAGDLISPGLSAIH
						GRCILNTLVFIVKLRWMENTLH
		l				RFGTHHGCSAVRSSHLDSGSPR
		İ				RSSWHMARARNHIHVLEENMA
		1				LLMEQAIANEGLFYRLLYLORS
		l				LTAASSLDDMLMRFHRWARDL
		1				GLAELLVVLPEAKAVGSVAMS
						MLGSDADWGVVLFTSRDASHY
						OOGOGTOLLHEIALMLPELLER
		1				WIERGWEOOVWRYGFLRYVAF
		1				LTGWSAQNELKANPAKGVSAP
		1				
		1			i	KAPRHLPKNIDVDDMNRLLDID
		1				INDPLAVRDLMYGAGLRLSELV
		1				GLDIKHLDLESGEVWVMGKGS
		1				KERRLPIGRNAVAWIEHWLDL
		1	2			RDLFGSERERRQHAGTNVLQT
		<u></u>				ADQRASRARQEGERLHRAAGR
24471	54839	A	24609	1	1749	
24472	54840	Α	24610	1	2911	MNIDAKILNKILANRIQQHIKKL
1		1			1	IHHNQVSFIPGMQGWFNIHKSM
		1				KVIQHINRTKDKNYMIISIDAEK
		l				AFDKIQQPFMLKTLKKLVAGM
i		ı			1	MAVAAPDDPPPPSVSSSKPSTV
1		l			l	APPGRISPSGRALCTSLPSALSSS
	1	1			ĺ	SKFSLLRIFQVPAKLGMVAVAA
						AAGVNAMLRKVAVAAASKPH
	1	1		1		VEIRODGDOFYIKTSTTVRTTEI
		l			l	NFKVGEGFEEETVDGRKCRVR
		1	1		i	PQSHYSVPVSPLGAHGPLLLEE
		Į				PVSPFAACGAPS
24473	54841	A	24611	249	609	QIEVCVRIKPKAGTVLAYS*RSR
[		1				QERPPAPGMTSLSLAAVSSDNP
1		1		I		VSGDEHIRLARASGRFGIGRVA
1		1		1		OPKRIORRSSTPRAATDLGNPG
1		1	1	1		HRPCTVRKSALLVVSVCRRHSS
		1		I		RSLRFRSC
	L					KOLIG KOC

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
24474	54842	Α	24612	942	1121	
24475	54843	Α	24613	1010	1658	EISSSKRSRTVCKRRAPMFSVDS
			İ			FTCHAASAMRLIPESVNSIFTPS
1				ŀ		VAISALYCTVIEAFGSVRIRSKS
		l			l	LVVSACSSTRIG\DDLAVPGSGQ
		1			i	TVSQSGTRQKR*TECGQF*PSR
						VWWKRCNLLPAAAGHAERLH
1						EKHPDRKTRRVRLVWLAGPPT
ļ		1				RLLGTMGAGTLVLGACCLPWP
		1				REGAHNVATAACGGWRARCD
						LRFRLSCKLGLSRQFFGWNA
24476	54844	A	24614	1	1995	
24477	54845	Α	24615	1	2853	
24478	54846	A	24616	1	1755	
24479	54847	A	24617	2942	3454	SVPDWLMCTAFLSLSRINSPRL
		1				LKAELLLTSSIPVLLPSLLLPRFQ
		1	l			VPSLFATAVPVSAAPLIIAPSV*L
		l				LKTPPADIIRPVTLPLLLNTPAFC
			l		i	TILLMVPVLFTNELSAPAFMVIC
		l			ł	AVISPALLRIPPLTSTLFVITPAF
		ı				LMTAPLSSFTKLLMMPPLVFSR
						RPLDTVI
24480	54848	A	24618	1	2959	MKRYRPREILPWKVPPGNYTPK
		1				IFKIKGTGHNPMSAIENFDAHTP
		l				MMQQYLRLKAQHPEILLFYRM
						GDFYELFYDDAKRASQLLDISL
			1			TKRGASAGEPIPMAGIPYHAVE
					1	NYLAKLVNQGESVAICEQIGDP
						ATSKGCCRSGNRNGGRKIVAVS
						LKKVSGAAKPCGHFRSTRYRV
ì						AYSTIINNKAGIWSAFEGVSAT
						RPNPTPRASPAVRTLSRGTPEPR
						KISTDADNLAQGSLKERLPAWL
21101	44040	<del>ا</del> .	24610	443	1405	WGKKENSKWEVLD
24481	54849 54850	A A	24619 24620	1441	1425 2574	
24482	54850	A B	24620	1	1725	
24484	54851	A	24621	160	390	
				892		
24485	54853	A	24623 24624	1	1183 2493	
24480	54855	A	24625	435	829	ASDVLVSEGCR/YRGASALTST
2448/	J4833	l <sup>A</sup>	24023	1433	027	SVICINTDKALRKIIRLPLNGLR
						KPLNAMTPLPGITWPLCITTEKE
1	1	1		I	i	DLSISDRLSTCIVKFSHPEPEMS
1	1	1	l	1	I	
1		1	l	1	1	VRKFVPPAILLCSVCLRFSCPTR
24486	54056	ļ	24626	762	1962	HQKAPAKWILKSCSAWMR
24488	54856	Α	24626	763	1863	
24489	54857	Α	24627	1423	1712	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24490	54858	A	24628	1	2792	MTYLSAODHELIQVVONGHLO
		1				MCGKSETGNEASPVKCIVLOVL
		1				RGLOYLHRNFIIHSQEOTIPDPSI
						SDQQETPLLAGDMAQRGRRGG
		1			•	FYYVTAYIYVDKKAPVHMRTA
	l					AQGLITLCCQGFG\$LLGYRLGG
						VMMEKMFAYQEPVNGLTFNW
						SGMWTFGAVMIAIIAVLFMIFF
1						RESDNEITAIKVMEDSMSSATT
						LTTPQEQVDSLIMQIAEENGLE
		ļ				VLDQLSQLPEGASAVGESSVRS
						QEDQLSRSFICLMAMM
24491	54859	С	24629	213	345	
24492	54860	A	24630	1	474	MHQTTAKTPHTSYPNNYEEHN
						RRANRSKNYDRIRHTTIILKRTN
						PAQTITNLLKSRFNRYNYVQPR
						SCRSIFIHIPGERDLNLCIAPNPP
1	i	l		1		AIFPTSIGYLGPDLNNLPTYAPFI
		ł				TTNLTGPAPTTTHPVGNLGTTG
l						NPEPGGCGILIVWCCVNWACL
		l				WDSVVAAPREPYMPAGLLRHR
	İ			ł		RHYRHRREDLIAVPAARQTDE
						NRRPALCHEYAVGHRKIKTNV
	Į.	ı				EHTEPYILPLITHSQPLNRGAFF
		1				CPGVRFLVVSVLDFEKRL**RR
		ı		i		WRRSPAGI*GSRGAATTLSQRQ
		1		ŀ		AQLTQHQTIRIPHPPGSGLPVVP
						KFPTGCVVVGAGPVRFVVING
24493	54861	Α	24631	I	924	
24494	54862	В	24632	177	468	
24495	54863	В	24633	592	883	

PCT/US01/08631

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
24496	54864	A	24634	1	1926	MATAKANOEIŌEWLGKYGTAR
24450	34004	ľ	24034	ľ	1520	VKLNVDKDFSLKDSSLEMLYPI
	1	1				YDTPTNMLFTQGAIHRTDDRTQ
						SNIGFGWRHFSGNDWMAAVIT
l		1				FIDHDLSRSHTRIGVGAEYWRD
		1				
						YLKLSANGYIRASGWKKSPDIE
		1				DYQERPANGWDIRAEGYLPAW
	1	1				PQLGASLMYEQYYGDEVGLFG
	l	1				KDKRQKDPHAISAEHSPEFRSE
1		1				ALKLVNASVLLPQPVNSACMN
1		1				HNSTTGAVNSKISRRLLNVNW
		1				RCLPRLHVSNASWQNGMKSWL
		1	i			SSKRPRHTSEAPEMKYVFIEKH
						QAEFSIKAMCRVLRVARSGWY
					ł	TWCQRRTRINIAVVRRADGSRT
						SFVYTSYLAKVNEEWKNNVGT
	1	ŀ				GSTVKWPIGLGGKGNDGIAAF
	l					VQRLPGAIGYVEYAYAKQNNL
		1				AYTKLISA*NEVCLY*KTSG*V
		1				QHQSNVPR/RSGWPAAAGIRGV
	1	1				SGGQG*TLL*YAAQMAPELPSS
l				1		TPATWRK*TKSGKTTLV/HGST
		1		1		VKWPIGLGGKGNDGIAAFVQR
		1				LPGAIGYVEYAYAKONNLAYT
1		1				KLISADGKPVSPTEENFANAAK
		1				GADWSKTFAQDLTNQKGEDA
		1				WPITSTTFILIHKDQKKPEQGTE
	1	1				VLKFFDWAYKTGAKQANDLD
		1				YASLPDSVVEQVRAAWKTNIK
	1	1				DSSVNFDMANVFFRVTPGNFL
	l	1		İ		VNREASHORRVFAVRAGVDFI
1		1				YRASSDGLRRCRDRRTRFKRIN
0.1407	54066	<del> -</del>	24625	1387	1620	
24497	54865	Α	24635	1387	1639	ESKPLNLGRGSGFLLTRALSAQ
l	1	1				PLWQSPDQHLTPQAGLRSRL*A
1		1				QRQA*QKTASRVV*PKPLWAL
		┞		ļ		VKATSEDISVVL*ESACQC
24498	54866	Α	24636	1570	2516	IEVAMSIVVKNNIHWVGQRDW
	1	1				EVRDFHGTEYKTLRGSSYNSYF
		1				IREEKNVLIDTVDHKFSREFVQ
		1				NLRNEIDLADIDYIVINHAEEDH
l .		1				AGALTELMAQIPDTPIYCTANAI
		1	*	1		DSINGHHHHPEWNFNVVKTGD
l		1				TLDIGNGKQLIFVETPMLHWPD
				1	1	SMMTYLTGDAVLFNYDAFGQH
				1		YCDEHLFNDEVDQTELFEQCQ
	1	1		1	1	RYYANILTPFSRLVTPKITEILGF
		1	1		1	NLPVDMIATSHGVVWRDNPTO
1		1		1		IVELYLKWAADYQEDRITIFYD
	1					TMVNNTPMMADAIAOGIA\ETG
		1	l			PRLAGENFNV\ARNDKHEDPDL
		1				LSFRSERGA
	L	1	L		<u> </u>	EDI KOLKOA

WO 01/075067

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24499	54867	Α	24637	24	363	
24500	54868	A	24638	2	366	RATPRHIIVRFTKVEMKEKMLR AAREKGRVTLKGKPIRLTADLS AETLQARREW*QNLSAFACL*R ILFLLHL*SLVWLDMKCWVENS FL*EC*ILAPTLFWLVGFLPRDP LLV*WASL*G*PDLSLWLPLAF FPSFQLW*I*QLCVLELL
24501	54869	Α	24639	232	292	
24502	54870	Α	24640	4	911	
24503	54871	A	24641	2795	3226	SWWISFLMCCWIWFASILLRIFA SMFIKDIGLKFPFLVVSLPGFGI RMMLAS*NELGRIPSFSIGWNSF RRNGTSSSLYLW*NSAVNPSGP GLFLVGKLLVIASISEPVIGLFTD STSSWFSLGRVYVSRNLSISSRF SSLFA
24504	54872	A	24642	1	3285	
24505	54873	Α	24643	1	4368	
24506	54874	A	24644	200	335	YALLNKDSSPWYPFSVPVLASN TRYLWPLSST**GSLSVWLSPD V
24507	54875	Α	24645	174	263	
24508	54876	Α	24646	1244	1354	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
ļ	sequence	1	09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
				sequence		
24509	54877	Α	24647	194	2481	GMFRMNLMEPLTQCINAGHEM
						TKAIAIAOFNDDSPEARKITRR
i		İ				WRIGEAADLVGVSSQAIRDAEK
						AGRLPHPDMEIRGRVEORVGY
1		l				TIEOINHMRDVFGTRLRRAEDV
						FPPVIGVAAHKGGVYKTSVSVH
1		l	İ			LAODLALKGLRVLLVEGNDPO
		1				GTASMYHGWVPDLHIHAEDTL
	ŀ	l				LPFYLGEKDDVTYAIKPTCWPG
		1				LDIIPSCLALHRIETELMGKFDE
1						GKLPTDPHLMLRLAIETVAHDY
		l				DVIVIDSAPNLGIGTINVVCAA
		l				DVLIVPTPAELFDYTSALQFFD
		1				MLRDLLKNVDLKGFEPDVRILL
						TKYSNSNGSQSPWMEEQIRDA
					i	WGSMV\IKNVVRETNEVGKAA
						PMVDSLIARVGVMARGNAITLP
					i	VCGRDVKFTLEVLRGDSVEKTS
						RVWSGNERDQELLTEDALDDLI
				}		PSFLLTGOOTPAFGRRVSGVIEI
		Į.				ADGSRRRKAAALTESDYRVLV
					i	GELDDEOMAALSRLGNDYRPT
		1				SAYERGORYASRLQNEFAGNIS
		l				ALADAENISRKIITRCINTAKLP
		1				KSVVALFSHPGELSARSGDALO
		1			1	KAFTDKEELLKQQASNLHEQK
		i i	l			KAGVIFEAEEVITLLTSVLKTSS
		1				ASRTSLSSRHQFAPGATVLYKG
		l				DKMVLNLDSPQSFSPGAGDHA
1		l		1	1	NSPQSSSPSTGVHINSPQLSSLS
		l		1		AGVHTISPQSSNPSVGVTALSHP
1		l .		l		DLVWVFTLTAHSRPVLVWVFT
24510	54878	Ā	24648	1361	1694	
24511	54879	Α	24649	1	3852	MKLMETLNHCINAGHEMTKAV
		l				AIAOFNDDSPEARKITRRWRIG
		l		l		EAADLVGVSSQAIRDAEKAGR
l		l				LPHPDMEIRGRVEQRVGYTIEQI
i		1		l		NHMRDVFGTRLRRAEDVFPPVI
		l		l		GVAAHKGGVYKTSVSVHRAQ
		1				DLALKGLRVLLVEGNAPQGTA
		I		l		SVYHGWVPDLHIHAEAALLPF
		I		i		YLGEKDDVTYAIKPTCWPGLDI
		1		l		IPSCLALPRIEPELMGK/FDEGRS
1		1	i	l		FMPGPP/HHHPLGRSSO*OVSNS
		I	1	l		LDRAAKGN*KPLCHC
			L		L	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
24512	54880	IA	24650	1	1720	MEKLLLENDSLSKDVSRLETVF
1						VPPEKHEKEIIALKSNIVELKKQ
						LSELKKKCGEDQEKIHALTSEN
İ	ŀ					TNLKKMMSNOYVPVKTHEEV
1						KMTLNDTLAKTNRELLDVKKK
1		l				FEDINOEFVKIKDKNEILKRNLE
		l				NTONOIKAEYISLAEHEAKMSS
1		l				LSQSMRKVQDSNAEILANYRK
		l				GOEEIVTLHAEIKAOKKELDTIQ
		l				ECIKIMKRAPVIPKHTLNTOPVE
		1				DTSLSTPAAPMVDSLIARVGVM
	İ	l				ARGNAITLPVCGRDVKFTLEVL
		l				RGDSVEKTSRVWSGNERDOEL
		l				LTEDALDDLIPSFLLTGQQTPAF
		1				GRRVSGVIEIADGSRRRKAAAL
		l				TESDYRVLVGELDDEOMAALS
						RLGNDYRPTSAYERGORYATR
						PONEFAGNISAMADAENISRKII
		ŀ				TRCINTAKLPKSVVALFSHPGE
		ļ.			ŀ	LSARSVIDSAPNLGIGTINVVCA
					ľ	ADVLIVPTPAELFDYTSALQFFD
		1				MLRDLLKNVDLKGFEPDVRILL
1		1				TKYTNINASQSP\WMREKFGMA
		1				WESMVLKNVVRETDEVGKGQI
		l			1	RMRADFV\QAIDQRSSTGAWRN
	1					ALSIWEPVCNEIFDRLIKPRSEIT
24513	54881	A	24651	1094	2271	APFHRPHTKQSLQEQTDVVSIN
1		1				EFLKQMAF*AQKLKE/WRTSAA
					l .	SDITPAGFCSCRAIKDAEKPGRL
		ł	İ			PHPD\MEFRDRVDQ\RVVSPFGQ
1					1	II\HMRNVFGPRLPRAKDVFPPV
						IGVAAHKGGVYKTSVSVHLAQ
		1				DLALKGLRVLLVEGN\DP\QGT
		l			ŀ	ASMVSREGDPALHI\YQEAPFLP
		1			Į.	FYLGEKDDVTYAIKPTCCPGLN
i						IIPSCLALPRIETELMGKFDEGK
						LPTDPHLMLRLAIETVAHAHDY
						DVIVIDSAPNLGIGTINVVCAAD
1	l			1		V\LIVLTPVE\MFDYTSARQFFD
						MLRDLLKNA\DLKGFEPEVRIL
	1	1				LTKYSNSNGSQFP\WMEEQIRD
l						AWGSMVLKNVVRETG\EVGKG
				1		\QIRMRT\VFEQAIDQRSSTDTSL
						STPAAPMVDSLIARVGVMASR
24514	54882	Α	24652	I	1415	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24515	54883	A	24653	3008	8165	ILIPFFIGLQNRFTQFRLSETKEIT
						NPYAMRLYESLFQSSKTNGSGI
						VSLKIDWIIERYQLPQSYQRMP
				İ		DFRRRFLQVCVNEINSRTPMRL
						SYIEKKKGRQTTHIAIRDAEKA
						GRLPHPDMEIRGRVEQRVGYTI
					i .	EQINHMRDVFGTRLRRAEDVFP
			1			PVIGVAAHKGGVYKTSVSVHL
						AQDLALKGLRVLLVEGNDPQG
						TA\SMYHEWVQNLHIHAEDTLL
					1	PFYLGKKDDVTYAIKPTCWPGL
						DIIPSCLALHRI
24516	54884	A	24654	1	848	
24517	54885	A	24655	2354	3640	NVICNQELVYSSRHQFAPGATV
						LYKGDKMVLNLDRSRVPTEYR
						YGVFLNVLLPATKYFQLHDPSL
						RNMELNYSLASEDI.VLKGLRV
						LLVEGNDPQGTASMYHGWVP
						DLHIHAEDTLLPFYLGEKDDVT
						YAIKPTCWPGLDIIPSCLALHRI
						ETHLMGKFDEGKLPTDPHLML
						RLAIETVAHDYDVIVIDSAPNL
						GIGTINVVCAADVLIVPTPVE\L
						FDYASARQFFHMLRPLLKNVD
						LKGFEPDVRILLTKYSNSNGSQ
						SPWMEEQIRDAWGSMVLKNV
		1				KEFAGNISALADAENISRKIITR
						CINTAKLPKSVVVFFLTPVNYL
		1				PGDALQKAFTDKEELLKQQAS
		1		1	l	NLHEQKKAGVIFEAEEVITLLTS
			ļ.			VLKTSSASRTSLSSRHQFAPGA
		1				TVLYKGDKMVLNLDRSRVPTE
		_				CIEKIEAILKELEKPAP
24518	54886	A	24656	667	870	QIVSSEPKYTDFLSKIPFEQRVR
		1				DVQRNGDHTEGAVR*LSIAFFS
		_				ALLKLLAFFTEEVRAAAVVRFV
24519	54887	В	24657	1	1086	
24520	54888	A	24658	2	250	WRTKSLDIPPLIYPNGIVKNILR
	1				[	HLSQLLNVPITRPFSWILRPF*RP
					i	*RKISTSFIRPLFTFLPA**MLIRS
	1	1		l		SVWQ*KTVSW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24521	54889	A	24659	1	1608	MAETAVINHKKRKNSPRIVQSN
	1007	ľ	-1007	ľ		DLTEAAYSLSRDQKRMLYLFV
		1				DOIRKSDGTLLYMTYRKPDGS
		l				GIVSLKIDWIJERYQLPQSYQRM
l		ı				PDFRRRFLQCINAGHEMTKAIA
		i .				AOFNDDSPEARKITRRWRIGEA
		1				ADLLGVSSQAIRDAEKAGPLPH
l	1	İ				PDMENRGRVEORGGYTIEPNN
		1				HMRDGVGTRWRRAEDVF\PPLI
ł		1				G\VAGHKGGR\YKTSVSVHLAQ
		1				DLALKGLRVLLVEGNDPQGTA
		1				SMYHGWVPDLHIHAEDTLLPF
i		l			1	YLGEKDDVTYAIKPTCWPGLDI
		ı			1	IPSCLALHRIETELMGKFDEGKL
	i	1				PTDPHLMLRLAIETVAHDYDVI
		1	- 0			VIDSAPNLGIGTINVVCAADVLI
		1		1		VPTPAELFDYTSALQFFDMLPD
		ı				LVKNRDLKGVEPDMRKORHR
						KAKDLLAQDPTAMTTDELLKE
						ATROPICTAYLEKPMSLECECV
						FCLSCTNSLQKEPQGEGVLCPF
		1				CLEASQKNNIRLNRQLGRLVSH
		1				IKELEPKLKKILKMNFKDAEVP
		1			1	RFSSPKPCSSFFSTCYLSKNCSN
					İ	HPCYSPYPGSGWG
24522	54890	A	24660	1	1128	III C 151 11 G5GWG
24523	54891	A	24661	1035	1208	SLIDRIEALGIFRFAAV*GSAAY
1.025		1		1.000		HGV*YERRRTFLCMLFGYFLSR
						RLESLLLPEVQS
24524	54892	A	24662	1	1316	MEIRGRVEORVGYTIEOINHMR
		1		ľ		DVFGTRLRRAEDVFPPVIGVAA
						HKGGVYKTSVSVHLAQDLALK
				i		GLRVLLVEGNDPQGTASMYHG
					İ	WVPDLHIHAEDTLLPFYLGEKD
					İ	DVTYAIKPTCWPGLDIIPSCLAL
				l		HRIETELMGKFDEGKLPTDPHL
						MLRLAIETVAHDYDVIVIDSAP
						NLGIGTINVALQNFQRYTGIQH
-				l		VHRIGMAERMWCDRNRERHT
		1		l		VSSSGGNRLPNPGPDRSDLALK
1				1		GLRVLLVEGNDPQGTASMYHG
		1				WVPDLHIHAEDTLLPFYLGEKD
			1			DVTYAIKPTCWPGLDIIPSCLAL
			1			HRIETELMGKFDEGKLPTDPHL
	1	ı		I		MLRLAIETVAHDYDVIVIDSAP
1		1	1	1		NLVFRICFVIWAQERIDIKGFEP
		1		1		DVRILLTKYSNSNGSQSPWMEE
		l				QIRHAWGSMVLKN/VVRETDE
	1					VGKDTGVRSKSIWCHRNSRWE
	1	1	i .	1	L	A OVDIO A VSVSI M CHK NSK ME

SEQ ID	SEQ ID NO:	Met	SEQ tD NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24525	54893	Α	24663	504	1254	SYVKYFPHQPAQKYFQQIHSAI
		l				GLHNADHVHKHLLGDNRYPIW
		l				IMQPSAHHPARQPEHDIAFGKC
		1				SSSVSVHLAQDLALKGLRVLLV
		1				EGNDPQGTASMYHGWVPDLHI
		ı				HAEDTLLPFY\DPHLMLRLAIET
	ļ	l			l	VAHDYDVIVIDSAPNLGIGTINV
	1					VCAADVLIVPTPAELFDYTSAL
		İ				QFFDMLRDLLKNVDLKGFEPD
						VRILVVRVSQRMVVAGCIIAFID
						KLLNVLICFPFSVKNRFVIFHSV
						DFECVIRF
24526	54894	Α	24664	1	3216	MKLMETLNQCINAGHEMTKAI
	1					AIAQFNDDSPEARKITRRWRIG
				I		EAADLVGVSSQAIRDAEKAGR
	1	l				LPHPDMEIRGRVEQRVGYTIEQI
				İ		NHMRDVFGTRLRRAEDVFPPG
		l			1	FGDFADFGTTIKQDFRLLGQTS
						VDRLLQLSQGQAVKGNQLLPV
						SLVKRKTTLAPNTQTASPRALA
						DSLMQLARQVSRL/VKRAPTC
		l				WPGLDIIPSC\LALPRIETELMGK
						FDEGKLPTDPHLMLRLAIETVA
						HDYDVIVIDSAPNLG
24527	54895	A	24665	1	419	MSSSDKDFDFSVANMVNFFAP
						VFPMGKYYTQADKVLIPLAIQE
İ					ŀ	HDGICEIHVAKYAEIFGLTSAEA
	1				I	SKDIRQALKSFAGKEVVFYRPE/
		1			İ	VGCRR*KRL*IFSLVYQTCAQSI
				I	1	QRALQCTYQPISHSLLYRVTEP
						VYAVSA
24528	54896	Α	24666	1	2598	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24529	54897	A	24667	1	2027	MRGHREKAAACKPRTRASEGT
						TPASTFILDFOPPNCNYTSGDNH
l		1				TLRDPHYVEDKGHKYLVFEAN
		1				TGTENGYQGEESLFNKAYYGG
		1				GTNFFRKESQKLQQSAKKRDA
1						ELANGALGIIELNNDYTLKKVM
						KPLITSNTVTDEIERANVFKMN
1						GKWYLFTDSRGSKMTIDGINSN
	1					DIYMLGYVSNSLTGPYKPLNKT
						GLVLOMGLDPNDVTFTYSHFA
						VPOAKGILCEEDNYTAGDNHM
						MRAPHCEEDRAHKFVVFDANA
1						GTESGHOGESSLFNRACGGGGT
1						FFFSKESQKLQQSAKKRDCINA
i		ŀ				GHEMTKAIAIAQFNDDSPEARK
						ITRRWRIGEAADLVGVSSQAIR
						DAEKAGRLPHPDMEIRGRVEO
ļ.						RVGYTIEQINHMRDVFGTRLKR
						AEDVFPPVIGVAAHKGGVYKT
						SVSVHLAQDLALKGSLLLPKND
						FLFKLGLEGHLPLGKIHSPPTGA
						DVARGSSGLPKSELFLPERNTO
						ELQQDSEEGPLALQVLQSNLM
						DFADFGTTIKODFRLLGOTSVD
1		l				RLLQLSQGQAVKGNQLLPVSL
1		1				VKRKTTLAPNTQTASPRALADS
		1				LMQLARQVSRLESGQNNDGIC
		1				EIHVAKYVEIFGLTSAEASKDIR
ŀ						QALKSFAGKLVVFYRPE/VGCR
						R*KRL*IFSLVYOTCAOSIORAL
	-	1				QCTYQPISHSLLYRVTEPVYAV
24530	54898	A	24668	1	989	PWISAPVPVDVVEGAMDSVTV
		1				LSFGGLMLYFCAGWPPARRWC
						FPESISCGSMERDQWWGLQVA
						KRAGLAGGQSGRTVLRERVRIE
		1				IASTHIALAARHSDWRCCRNGR
		1				YPARGPAALONFORYTGIOHV
		1				HRIGMAERMWCDRNRERHTVS
						SSGGNRLPNPGPDRSCDNLKTC
1		1				HTSHGSVMAETAVINHKKRKN
		1				SPRIVQSNDLTEAAYSLSRDQK
		1	1			RMLYLFVDQIRKSDGTLQEHD
		1				GICEIHVAKYAEIFGLTSAEASK
		ı				DIRQALKSFAGKEVVFYRPE/V
1		1	1			GCRR*KRL*IFSLVYQTCAQSIQ
		1				RALOCTYOPISHSLLYRVTEPV
		ــــــــــــــــــــــــــــــــــــــ	L			

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codun for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
10.	sequence	liou.	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24531	54899	A	24669	350	1203	LLTARLTWVSARLMSDFADFG
						TTIKQDFRLLGQTSVDRLLQLS
						QGQAVKGNQLLPVSLVKRKTT
						LAPNTQTASPRALADSLMQLA
						RQD/LALKGLRVLLVEGNDPQG
						TASMYHGWVPDLHIHAEDTLL
l						PFYLGEKDDVTYAIKPTCWPGL
		İ				DIIPSCLALHRIETELMGKFDEG
						KLPTDPHLMLRLAIETVAHDYD
		l				VIVIDSAPNLGIGTINVVCAADV
		1			ĺ	LIVPTPAELFDYTSALQFFDMLR
					į .	DLLKNVDLKGFEPDVRILLTKY
						SNSNGSQSPWMEEQIRDAEGSR
24532	54900	Α	24670	1	936	
24533	54901	Α	24671	1070	1324	LGTPGGCSRMTCALVPLIPNDD
1	1	ı				TPTRRTRPLLGQGVFSVRS*TVP
	į.	l				ADQSTSGDGDSTCNVRGSCPCR
		_				IAITILITPATPAAACV
24534	54902	Α	24672	1	1212	
24535	54903	A	24673	2373	3381	FKRGQYGQLLRPRFHHGQILYA
ŀ		1	1			RRQGADAAGDSGIW/HGIWTEP
	1	1		l		MTM*KKDER*PSPTQAS*DNW
i		l				KSIRGSCWQALSITRN/CKNSPRI
		i		1		VQSNDLTEAAYSLSRDQKRML
		l			1	YLFVDQIRKSDGTLQEHDGICEI
		l		l		HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD
		l				EKGYESFPWFIKRAHSPSRGLY
1		1				SVHINPYLIPFFIGLONRFTOFRL
		1				SETKEITNPYAMRLYESLCQYR
		1			i	KPDGSGIVSLKIDWIERYQLPQ
		1		l		SYORMPDFRRRFLOHIFVLRER
		1		l		PETVLIDLIORTKDAVRELDNL
		1		l		QYRKMKKLLFQEAHNGPAVEA
						OEEEEDD
24536	54904	A	24674	31	811	RRGLLGTRLRLSEDVFPPVLGV
2 1554	1,00	1			l	AAHKGGVDKTSVSVHLAODLA
	l	1		l		LKGLRVLLVEGNDPQGTASMY
		1				HGWVPELHIHAEDTLLPFYLGE
		1				KDDVTYAIKPTCWPGLDIIPSCL
		1				ALHRIETELMGKFDEGKLPTDP
		ı			l .	HLMLRLAIETVAHDYDVIVIDS
1		1				APNLGIGTINVVCAADVLIVPTP
				l		AELFDYTSALQFFDMLRDLLKN
						VDLKGFEPDVRILLTKYSNSNG
				I		SQSPWMEEQIRDAWG\SMVLK
				1	1	NVVAFQNLEFLFILLRIWL
24537	54905	Α	24675	1004	1105	-
24331	154705	111	12-7073	1.00-	1	L

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	1	09/540,217	codon for peptide sequence	or pepude sequence	deletion, (-possible nucleotide insertion)
		1				
24538	54906	Α	24676	1	1139	MEKKITGYTTVDISQWHRKEHF
						EAFQSVAQCTYNQTVQLDIKK
		l				KLKTVKKNKHKFYPAFIHILAR
		l			İ	LMNAHPEFRMAMKDVAEYNG
		l				YHVVFALAGSPKDADDTSIYM
						FYQKVGDNSIDSWKNAGRVFK
		l				DSDKFDANDPILKDQTQEWSGS
1						ATFTSDGKIRLFYTDYSGKHYG
			i			KQSLTTAQVNVSKSDDTLKING
						VEDHKTIFDGDGKTYQNVQQFI
						DEGNYTSGDNHTLRDPHYVED
	1	1				KGHKYLVFEANTGTENGYQGE
		l				ESLFNKAYYGGGTASSIRKSDG
						TLQEHDGICEIHVAKYAEIFGLT
1					ŀ	SAEASKDIRQALKSFAGKEVVF
						YRPE/VGCRR*KRL*IFSLVYQT
ļ			1			CAQSIQRALQCTYQPISHSLLYR
		ļ. —		ļ. —	000	VTEPVYAVSA
24539	54907 54908	A	24677	1	930 2486	MNMNIKKIVKOATVLTFTTALL
24540	34908	l <sup>A</sup>	24078	1	2480	AGGATQAFAKENNQKAYKETY
İ			ì			GVSHITRHDMLQIPKQQQNEKY
	i					QVPQFDQSTIKNIESAKGLDVW
ļ	l	I				DKWPLANADGTVAEYNGYNV
l						VDKFDANDPILKDOTQEWSGS
l						ATFTCDGKIRLFYTDYSGKHYG
	l	1				KQSLTTAQVNVLKSDDTLKING
		ĺ				VEDHKAIFDGDGKTYONVOOL
	1					IDEGNYTSGDNHTLRDPHYVED
	l					KGHKYLVFEANTGTENGYQGE
1				1		ESLFNKAYYGGGTNFFRKESQK
						LQQSAKKRDAELANGALGIIEL
l					1	NNDYTLKKVMKPLITSNTVTDE
			ľ			IERANVFKMNGKWYLFTDSRG
						SKMTIDGINSNDIYMLGYVSNS
			l			LTGPYKPLNKTGLVLQMGLDP
						NDVTFTYSHFAVPQAKGNNVV
						ITSYMTNRGFFEDKKATFAPSF
						LMNIKGNKTSVVKNSILEQGQL
	1		l			TWLQVAKRAGLGGGQSGRTVL
						RERLPNYKNFKGTIQELGQNQY
1	İ					AVSGEIFVVDRNTVEITELPVRT
1	1		1			WTQVYKEQVLEPMLNGTDKTP
1						ALISDYKEYHTDTTVKFVVKM
l			1			TEEKLAQAEAAGLHKVFKLQT
İ			1			TLTCNSMVLFDHMGCLKKYET
1						VQDILKEFFDLRLSYYGLRKEW
i					1	LVGMLGAESTKLNNQARFILEK
1	1	1	1			IQGKITIENRSKKDLIQMLVQRG
1	1		l			YESDPVKAWKEAQEKCDNLKT
1	1	1	l	1	i	CHTSHGSVMAETAVINHKKRK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	į.	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24541	54909	A	24679	5	253	I SAPKVWRGLROOGAGISVLP*V
		1		ľ		CAQP/VQVAKAPELILNFDLPK
	Ì	1				KYFDKL/R/DTHFFSPHTGKFPT
		1				VKILMAPFANSASRGVALC
24542	54910	A	24680	334	842	PDKEGNEIWVDMYTVKPSGWT
	31710	Γ.	2.000	1		VRTFDKPRKRFIAFFIAGILFRAI
		1				KNHFLPRETLQCLPYILTGFRRG
		1				OSEYFSIFSNMDLADTVMFLVG
		1				GHKIFVFHCHTELRMSIHQAGK
		1				NVNKGRIKLVLIFLYGL*/QRP*
	ľ					YPAERSGYRYIEQLTEMPONVL
1						YDAIGIYORWYIO
24543	54911	A	24681	676	1169	DNLKTCHTSHGSVMAETAVIN
24343	34911	Ι^	24001	070	1109	HKKRKNSPRIVQSNDLTEAAYS
						LSRDOKRMLYLFVDOIRKSDGT
		1				LOEHDGICEIHVAKYAEIFGLTS
l		1		ļ		AEASKDIRQALKSFAGKEVVFY
ŀ		1				RPE/VGCRR*KRL*IFSLVYQTC
1		1			ì	AQSIQRALQCTYQPISHSLLYRV
1	ì	1				TEPVYAVSA
24544	54912	A	24682	1	783	TEL VIA VOA
24545	54913	A	24683	i	1884	
24546	54914	A	24684	1	1131	
24547	54915	A	24685	1	2856	
24548	54916	A	24686	528	725	
24549	54917	Α	24687	1	898	
24550	54918	Α	24688	1879	2343	
24551	54919	A	24689	1	1254	
24552	54920	Α	24690	1	1113	
24553	54921	В	24691	1	1156	
24554	54922	В	24692	1	1980	
24555	54923	В	24693	1	1932	
24556	54924	Α	24694	1	663	
24557	54925	A	24695	1123	1764	
24558	54926	Α	24696	2	1772	MELKTKARELREECRSLRSRCN
24559	54927	A	24697	1	1040	QLEERVSAMEDEMNEMKREG
	ľ					KFREKRIKRNEOSLOEIWDYVK
1		1				RPNLRLIGVPESDVENGTKLEN
	i					TLQDIIQENFPNLARQANVQIQE
ł						IQRTPQRYSSGRETPRHIIVRFT
l		1				KVEMKEKMLRAAERKCDNLK
1	1	1				
1	1	1				TCHTSHGSVMAETAVINHKKR
		1		1		KNSPRIVQSNDLTEAAYSLSRD
1		1				QKRMLYLFVDQIRKSDGTLQE
1		1				HDGICEIHVAKYA EIFGLTSAEA
1	1	1				SKDIRQALKSFAGKEVVFYRPE
		1				EDAGDEKSYEQPSKDIRQALKS
				1		FAGKEVVFYRPE/VGCRR*KRL
		1			1	*IFSLVYQTCAQSIQRALQCTYQ
		1	L	L	L	PISHSLLYRVTEPVYAVSA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24560	54928	A	24698	1683	4289	RVFKDSDKFDANDPILKDQTQE
						WSGSATFTSDGKIRLFYTDYSG
		ı				KHYGKQSLTTAQVNVSKSDDT
		1				LKINGVEDHKTIFDGDGKTYQN
	1	1			1	VQQFIDEGNYTSGDNHTLRDPF
		1				YVEDKGHKYLVFEANTGTENG
	į.			1		YQGEESLFNKAYYGGGTNFFR
				ı	l	KESQKLQQSAKKRDAELANGA
				1	i	LGIIELNNDYTLKKVMKPLITSN
						TVTDEIERANVFKMNGKWHSK
				1		ILVSGTHRARTEVEVTDPIHQQ
		1		1		RMGCCFTVGAGEICEKPTGCFF
	1	1		1		TPLPNCNCQWTGSAILDRRSHS
				1		HPHSPASGSWVKVVTGSYQLT
				1		HSPGIGLRDFADFGTPHQTGFSF
		ı				AGANQRGPLVATLSGPGGEGQ
				1		SAVARLTGEKKNHPGAQYANR
- 1		1				LSPRVGRFINAAGTTGFPTGKR
		1				AVSATQLMHFKILVSRAHRART
						ELEVTDPGSSAENGLLFPVVLL
						LRKARKTLMPPHSTCFIKRSAP
	1			1		TQSTAGKTRPRVLKDSDKFDA
		1				NDPILKDQTQEWSGSAPFTSDG KIRLFYTDYSGKHYGKOSLTTA
						QVNVSKSDDTLKINGVEDHKTI
				1		FDGDGKTYONVOOFIDEGNYT
		l		1		SGDNHTLRDPHYVEDKGHKYL
		1	ľ			VFEANTGTENGYQGEESLFNKS
		1	ļ			VLRRRHELLPDFADFGPTIKQD
		ŀ		1		FRLLGQTSVDRLLQLSQGQAV
		i	ŀ	1		KGNOLLPVSLVKRKTTLAPNTO
						TASPRALADSLMQLARQVSRLE
24561	54929	В	24699	1	2034	
24562	54930	Α	24700	1	1038	
24563	54931	Α	24701	1	1149	Was out a complete to the comp
24564	54932	Α	24702	2	823	WPLQNADGTVAEYNGYHVVF
	i					ALAGSPKDADDTSIYMFYQKV
	ĺ	1				GDNSIDSWKNAGRVFKDSDKF
		1				DANDPILKDQTQEWSGSATFTS
		1	ļ			DGKIRLFYTDYSGKHYGKQSLT
		1		i		TAQCDNLKTCHTSHGSVMAET
		1	l			AVINHKKRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR
	1	ı				KSDGTLQEHDGICEIHVAKYAE
		ı				IFGLTSAEASKDIROALKSFAGK
	1	1				EVVFYRPEEDAGDEK/ML*IFSL
		ı	1			VYQTCAQSIQRALQCTYQPISH
		1	1			SLLYRVTEPGYAVSA
24565	54933	В	24703	1	1206	
24566	54934	Α	24704	2	1037	
24567	54935	В	24705	I	1389	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24568	54936	A	24706	1	602	I MGTGDFICISMTGGAPWGFRLO
24308	34936	Ι^	24700	'	002	GGKEQKQPLQVAKWANLKPGP
İ		1	ŀ			PSHGSVMAETAVINHKKRKNSP
		1			i	RIVOSNOLTEAAYSLSROQKRM
ŀ						LYLFVDQIRKSDGTLQEHDGIC
			İ			EIHVAKYAEIFGLTSAEASKDIR
		1				QALKSFAGKEVVFYRPE/VGCR
						R*KRL*IFSLVYQTCAQSIQRAL
		l				QCTYQPISHSLLYRVTEPVYAV
24569	54937	A	24707	1	774	QCT QTISHSEET RETTER TTAT
24570	54938	A	24708	1479	1947	
24571	54939	A	24709	1	696	
24572	54940	A	24710	1	1773	
24573	54941	A	24711	1	1509	
24574	54942	A	24712	1	891	
24575	54943	A	24713	156	242	VAGRGIGYRLSPNKGL*TWSAL CKPIAE
24576	54944	Α	24714	1441	1866	
24577	54945	Α	24715	1	1098	
24578	54946	Α	24716	Ī	1989	
24579	54947	В	24717	126	848	
24580	54948	В	24718	58	688	
24581	54949	Α	24719	]	542	
24582	54950	Α	24720	1	675	
24583	54951	Α	24721	1	1209	MKMPEKHDLLAAILAAKEQGI
				l	ŀ	GAILAFAMAYLRGRYNGVLEA
}			i			RSLKSRCQQSHALAEGSRGGPP
					İ	VTGRFKSTFTADSWNRYSLPSL
		1				TGGGNILHSRTHRRTVSRLLGR
		ĺ				RWQELLRDVFGTRLRRAEDVF
		l				PPVIGVAAHKGGVYKTSVSVH
		l				LAQDLALKGLRVLLVEGNDPQ
		l				GTASMYHGWVPDLHIHAEDTL
		1				LPFYLGEKDDVTYAIKPTCWPA
		l			İ	LDIIPSCLALHRIETELMGKFDE
		1				GKLPTDPHLMLRLAIETVAHDY
		1				DVIVIDSAPNLGIGTINVVCAAD
		1				VLIVPTPAELFDYTSALQFFDM
						LRDLLKNVDLKGFEPDVRILLT/
					İ	KYSNSNGSQSPWMEEQ\IRDAW
						GSMGLKNV/VRETDEIG\KGQIR
						MRTVFETAMDKRLLTGAWEK
						AFFFLEPGFEEKSNR

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide scquence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24584	54952	A	24722		743	MIGMELPGLEGTELEGCHEREY VYDRWAVPEKRGEARHVEARS PGGGSEKRGWGGARHQRMCR KGADNGGAGRARFARLRQL ASRAIGRRKGAVLYQTPVINHK KRKNSPRIVQSNDLTEAAYSLS ROOKRNLTLYFVDQIRKSDGTL QEHDGICEHVAKYAEIFGLTL WREASKDIRQALKSFAGKEVV TCAQSIQRALQCTYQPISHSLLY RVTEPVYAVG
24585	54953	A	24723	1157	1471	
24586	54954		24724	1	824	MEENERDLEINMINMSKELKVE NIKKHIGMLEKDEIEIVYKSILI EIEIPTQCLRNLNTLHLAASAGN HMSNTACWYGCEDETSVSTFA HQGVGSWDAYEPAASLLSCD NLKTCHTSHGSVMAETAVINH KKRKNSPRIVQSNDLTEAAYSL SKDQKRMLYLEVDQIRKSDGTL QEHDGICEIHVANYAEIYGLTS ACASKDIRQALKSFAGKEVVFY RPEVYGCRR*KRL*IFSLVYQTC AQSIQRALQCTYQPISHSLLYRV TEPUYAVSA
24587	54955	A	24725	996	1169	SLIDRIEALGIFRFAAV*GSAAY HGV*YERRRTFLCMLFGYFLSR RLESLLLPEVQS

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
i	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
	1	_	24726		1743	DSPE\ARKITERWRIGEAADLV
24588	54956	Α	24726	3	1743	
						GVSSQAIRDAEKAGRLPHPDME
		l			1	IRGRVEQRVGYTIEQINHMRDV
1						FGTRLRRAEDVFPPVIGVAAHK
						GNDPQGTASMYHGWVPDLHIH
						AEDTLLPFYLGEKDDVTYAIKP
						TCWPGLDIIPSCLALHRIETELM
	İ					GKFDEAQPNLGIGTINVVCAAD
1					ł	VLIVPTPAELFDYTSALQFFDM
	l					LRDLLKNVDLKGFEPDVRILLT
ł						KYSNSNGSQSPWMEEQIRDAW
İ					ì	GSMVLKNVVRETDEVGKGQIR
l	1					MRTVFEQAIDQRSSTDTSLSTP
						AAPMVDSLIARVGVMARGNAI
1	ļ					TLPVCGRDVKFTLEVLRGDSVE
	1					KTSRVWSGNERDQELLTEDAL
l						DDLIPSFLLTGQQTPAFGRRVSG
	ĺ					VIEIADGSRRRKAAALTESDYR
ŀ						VLVGELDDEOMAALSRLGNDY
l	ļ					RPTSAYERGORYASRLONEFAG
ł						KYFLRWLMRKIFHIITRCINTAK
İ	l					LPKSVVALFSHPGELSARSGDA
	1					LQKAFTDKEELLKQQASNLHE
ł	1					OKKAGVIFEAEEVITLLTSVLKT
						SSASRTSLSSRHOFAPGATVLY
						KGDKMVLNLDRSRVPTECIEKI
						EAILKELEKPAP
24589	54957	A	24727	1	1623	
24590	54958	A	24728	1	1863	
24591	54959	A	24729	i -	2622	
24592	54960	A	24730	ī	1338	
27372	124700	<u></u>	24730	1.	11000	L

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24593	54961	A	24731	1	1823	MNMNIKKIVKOATVLTFTTALL
						AGGATQAFAKENNQKAYKETY
		l		l		GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
		1				VFALAGSPKDADDTSIYMFYQ
						KVGDNSIDSWKNAGRVFKDSD
				1		KFDANDPILKDQTQEWSGSATF
						TSDGKIRLFYTDYSGKHYGKQS
	İ	1				LTTAQVNVSKSDDTLKINGVED
		1				HKTIFDGDGKTYQNVQQFIDEG
		1				NYTSGDNHTLRDPHYVEDKGH
1	ļ	1				KYLVFEANTGTENGYQGEESLF
		1		1		NKAYYGGGTNFFRKESQKLQQ
		1				SAKKRDAELANGALGIIELNND
		l				YTLKKVMKPLITSNTVFIRDKL
		l				MERRNRRTGRTEKARIWEVTD
		ı				RTVRTWIGEAVAAAAAADGVTF
		l	l	ĺ		SVPVTPHTFRHSYAMHMLYAG
		l		1		IPLKVLQSLMGHKSISSTEVYTK
		l				VFALDVAARHRCDNLKTCHTS
		l				HGSVMAETAVINHKKRKNSPRI
		1				VQSNDLTEAAYSLSRDQKRML
		l				YLFVDQIRKSDGTLQEHDGICEI
		1				HVAKYAEIFGLTSAEASKDIRQ
		1	1			ALKSFAGKEVVFYRPE/VGCRR
						*KRL*IFSLVYQTCAQSIQRALQ
21501		ļ				CTYQPISHSLLYRVTEPVYAVS
24594	54962	Α	24732	1476	2221	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24595	54963	A	24733	1	815	MRVGRKAVGAIWWSSKQELFQ
						QLFLRTELEDIGPGIVKRELGRE
						GSKDTGSSDDWEQLPDWKTKR
						VGNERDQELLIEDALDDLIPSFL
						LTGQQTPAFGRRVSGVIEIADG
			ŀ			SRRRKAAALTESDYRVLVGEL
		l				DDEQMAALSRLGNDYRPTSAY
						ERGQRYASRLQNEFAGNISALA
						DAENISRKIITRCINTAKLPKSV
						VALFSHPGELSARSGDALQKAF
			i			TDKEELLKQQASNLHEQKKAG
						VIFEAEEVITLLTSVLKTVQSKN
						LSHFTWICHAETAVINHKKRKN
			ŀ			SPRIVQSNDLTEAAYSLSRDQK
						RMLYLFVDQIRKSDGTLQEHD
						GICEIHVAKYAEIFGLTSAEASK
						DIRQALKSFAGKEVVFYRPEED
						AGDEKGYESFPWFIKHWVTISP
	1					QTSAYERGQRYASRCKNEFAG
						NISALADAENISRKIITRCINTAK
						LPKSVVALFSHPGELSARSGDA
						LQKAFTDKEELLKQQASNLHE
					i	QKKAGVIFEAEEVITLLTSVLKT
						SSASRTSLSSRHQFAPGATVLY
						KGDKMVLNLDRSRVPTECKRK
						LRPF*SGQRTDTAYVFDPGRDY

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
24596	54964	Α	24734	2	1249	DFADFGTTIKQDFRLLGQTSVD RLLQLSQQAVKQQLLPYSL VKKKTTLAPNTQTASPRALADS LMQLARQVSRLESGQLAISGRI LLPMLNSINIKLAAPSQCTEPF FRRDPTLHPKSEVRLPPKVTTIT VISNPILITPQEKSVAQCTYNQT VOLDITAFLETVKKNKHKFYPA FIHILARLMNAHPEFRMAMKD GELVIWDSVHPCYTVFHEGTET FSSLWSEYHDDFRQFLHIYSQD VACYGENLAYPPKGTETF FSSLWSEYHDDFRQFLHIYSQD VACYGENLAYPPKGTETF FSSLWSEYHDDFRQFLHIYSQD VACYGENLAYPPKGTETF FSSLWSEYHDDFRQFLHIYSQD VACYGENLAYPPKGTEMFMV AQUENLAYPTMGKYYTQGDKVLMPL AQUENLAYPTMGKYYTQGDKVLMPL AQUENLAYPTMGKYYTQGDKVLMPL SAPPWFIKRAHSPSRGLYSVHIN PYLIPFFIGLONRFTQFRLSETKE ESFEWFIKRAHSPSRGLYSVHIN PYLIPFFIGLONRFTQFRLSETKE ITNPYAMRLYSELCQYRKPDGS GIVSLPIDWIIERYQLPQSYQRM PDFRRRFLQVCVNEINSRTPMR LSYIEKKKGRQTTHIIRISGTL QBHDGIGEHWAKYAEIFGLTSA EASKDIRQALKSFAGKEVVYFYR PEEDAGDERGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLON RFTGFRLSETKEITNPYAMRLY ESSCLYSVHINPYLIPFFIGLON RFTGFRLSETKEITNPYAMRLY ESSCLYSVGTLRNSRFGEHY AKYAEIFGLTSAEASKDIRQAL KSFAGKEVYFYRPEVGCRR*K 4"FISLYYOTCASOIGRALOCT

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	tocation of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or peptide sequence	deterion, (-possible nucleonide insertion)
24597	54965	A	24735	1	2286	MLTLILLDLOFMAOLAGYOMS
		l				FNSTKSKQTKNNFAVGYRTGD
						FOLHTNVNDGAEFGGSVYOKV
						CEELDALINLAWTSSTSCTRFG
	İ					LAAKFOLKPIAFISTKVNHWLT
						GVSYTPPLEAGVKLNLSALCDN
1						LKTCHTSHGSVMAETAVINHK
						KRKNSPRIVQSNDLTEAAYSLS
	i				1	RDQKRMLYLFVDQIRKSDGTL
1					i	QEHDGICEIHVAKYAEIFGLTSA
1						EASKDIRQALKSFAGKEVVFYR
						PEEDAGDEKGYESFPWFIKRAH
						SPSRGLYSVHINPYLIPFFIGLQN
ĺ						RFTQFRLSETKEITNPYAMRLY
l						EIPVVSIRKPGMGSGIVSLKIDW
l			ŀ			HERYQLPQSYQRMPDFRRRFLQ
						CINAGHEMTKAIAIAQFNDDSP
						EARKITRRWRIGEAADLLGVSS
						QAIRDAEKAGPLPHPDMENRG
			}	ł		RVEQRGGYTIEPNNHMRDGVG
						TRWRRAEDVF\PPLIG\VAGHKG
						GR\YKTSV\$VHLAQDLALKGLR
				ŀ		VLLVEGNDPQGTASMYHGWV
						PDLHIHAEDTLLPFYLGEKDDV
						TYAIKPTCWPGLDIIPSCLALHR
		1				IETELMGKFDEGKLPTDPHLML
				ŀ	ł	RLAIETVAHDYDVIVIDSAPNL
		1		1		GIGTINVVCAADVLIVPTPAELF
		1				DYTSALQFFDMLPDLVKNRDL
		l		l		KGVEPDVFIRDKLMERRNRRT
		1		1		GRTEKARIWEVTDRTVRTWIGE
				1		AVAAAAADGVTFSVPVTPHTF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nuclcotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
24598	54966	A	24736	1	1400	MDAKMHSGGTAPPGTLSQRQP
24370	34900	ľ^	24730	ľ	1400	SSNSKTNGSKLNPLKDTLLSTPS
			l			CPEGELVNAARRSNGSGNAITL
		1				
		ł				PVWGRDVKFTLEVLRGDSVEK
		l				TSRVWSGNERDQELLTEDALD
1		1			ŀ	DLIPSFLLTGQQTPAFGRRVSGV
		1				IEIADGSRRRKAAALTESDYRV
						LVGELDDEQMAALSRLGNDYR
		l				PTSAYERGQRYASRLQNEFAG
1						NISALADAENISRKIITRCINTAK
						LPKSVVALFSHPGELSARSGDA
						LQKAFTDKEELLKQQASNLHE
						QKKAGCDNLKTCHTSHGSVMA
		ļ				ETAVINHKKRKNSPRIVQSNDL
		1				TEAAYSLSRDQKRMLYLFVDQI
		1		1		RKSDGTLQEHDGICEIHVAKYA
		1				EIFGLTSAEASKDIRQALKSFAG
						KEVVFYRPEEDAGDEKSYEQPS
						KDIRQALKSFAGKEVVFYRPE/
		l	1			VGCRR*KRL*IFSLVYQTCAQSI
						QRALQCTYQPISHSLLYRVTEP
24599	54967	Α	24737	1	1628	MLHITNDQGNASQNHNAMPPY
				1		SCKNGHNLKTVDGGMDAVNG
						EHFYTAGLSQGPLKGSFLLFFNI
		i				LILVCPPIFRVSGNEVFIRDKLM
						ERRNRRTGRTEKARIWEVTDRT
						VRTWIGEAVAPLLLTCDNLKTC
						HTSHGSVMAETAVINHKKRKF
		1				SPRIVQSNDLTEAAYSLSRDQK
				İ		RMLYLFVDQIRKSDGTLQEHD
1						GICEIHVAKYAEIFGLTSAEASK
		l				DIRQALKSFAGKEVVFYRPEED
						AGDEKGYESFPWFIKRAHSPSR
				1		GLYSVHINPYLIPFFIGLQNRFT
						QFRLSETKEITNPYAMRLYESL
						CQYRKPDGSGIVSLKIDWIIERY
						QLPQSYQRMPDFRRRFLQVCV
						NEINSRTPMRLSYIEKKKGRQT
		1		1		THICDNLKTCHTSHGSVMAETA
1		1				VINHKKRKNSPRIVQSNDLTEA
1						AYSLSRDQKRMLYLFVDQIRKS
				1		DGTLQEHDGICEIHVAKYAEIF
1						GLTSAEASKDIRQALKSFAGKE
1				1		VVFYRPE/VGCRR*KRL*IFSLV
				1		YOTCAOSIORALOCTYOPISHSL
1		l		1		LYRVTEPVYTISAY
		_		L		

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24600	54968	Α	24738	1295	1675	SVTSCLKVTSVCLTSGRRFLQIR
		1			1	ISDGTLQEHDGICEIHVAKYAEI
		1		ŀ	İ	FGLTSAEASKDIRQALKSFAGK
						EVVFYRPEEDAGDEKGYESFP
				i		WFIKRAHSPSRGLYSVHINPYLI
		1				PFFIGLQNRFTQFRLSETKEITNP
		ĺ				YAMRLYESLCQYRKPDGSGIVS
		l			ł	LKIAWVIERYQLPQSYQRMPDF
		1		i		RRRFLQVSDFLMAPYRNIDGIC
						EIHVAKYAEIFGLTSAEASKDIR
i		1				QALKSFAGKEVVFYRPEEDAG
						DEKGYESFPWFIKRAHSPSRGL
		l				YSVHINPYLIPFFIGLQNRFTQFR
		1	1		İ	LSETKEITNPYAMRLYESLCQY
		l				RKPDGSGIVSLKIDWIIERYQLP
l						QSYQRMPDFRRRFLQVCVNEIN
ŀ						SRTPMRLSYIEKKKGRQTTHIE
		1				HDGICEIHVAKYAEIFGLTSAEA
						SKDIRQALKSFAGKEVVFYRPE
						EDAGDERGYESFPWFIKRAHSP
						SRGLYSVHINPYLIPFFIGLQNRF
						TQFRLSETKEITNPYAMRLYQS
						LCQYRKPDGSGIVSLKIDWIIER
l		l				YQLPQSYQRMPDFRRRFLQIRK
		l				SDGTLQEHDGICEIHVAKYAEIF
						GLTSAEASKDIRQALKSFAGKE
		1				VVFYRPEEDAGDEEGYESFPWF
	İ			l		IKRAHSPSRGLYSVHINPYLIPFF
		1		l		IGLQNRFTQFRLSETKEITNPYA
				l		MRLYESLCQYRKPDGSCIVSLK
						IDWIIERYQLPPRYQRMPDFRRR
				i		FLRVWVQEINSRTPMPPLLPWE
24601	54969	Α	24739	1	1986	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		١.		sequence		
24602	54970	l <sub>A</sub>	24740	1	398	MVDSLIARVGVMARGNAITLP
24002	34970	l^`	24740	<b>'</b>	376	VCGRDVKFTLQVLRGDSVEKT
	i	l		į.		SRVPPGNERDQEMLTEDALDD
		1				LIPSFLLTGQQTPAFGRRVSGVI
	1	1		i .		HTADGSRRRKAAALTEKFCIVD
	ı	1				NPPGEIRKRACLFIPTHALNLNR
		1				FEDICYAHOLPDGGLLSARVGV
		1				MARGNPILSPVCGRNVKFTLKV
		l				LRGDSVENPSRVWSGNERAQE
	I	l				
	1	l				LLTEHALDDLTLSFLLTGQQTP
	l	l				AFGRRVSGVIEIADGSRRRKAA
		l				ALTESDYRVLVGELDDEQMAA
	I	l		1		LSRLGNDYRPTSPYERGQRYAS
	1					RLQNEFAGNISALADAENISRKI
						ITRCINTAKLPKSVVALFSHPGE
	1	l				LSARSGNERDQELLTEDALDDL
		l				IPSFLLTGQQTPAFGRRVSGVIH
		l	1			TADGSRRRKAA/DTYRKILYR**
21500	54971	١	24741	1450	3699	PPGGD*KKSVPFYSNTCAQSQP
24603	349/1	A	24/41	1430	3099	RNPLQIPKQQQNEKYQVPQFDQ
		İ				STIKNIESAKGLDVWDSWPLQN
		l				ADGTVAEYNGYHVVFALAGSP
		l				KDADDTSIYMFYQKVGDNSIDS
	i			1		WKNAGRVFKDSDKFDANDPIL
	1					KDQTQEWSGSATFTSDGKIRLF
				1		YTDYSGKHYGKQSLTTAQIFQ MITVFITSLCNTTSSHICLHISWV
		l				TTMHGAMPHPGHIPTAPASLPA
				İ		KVKGSGKVCWLAFPLSELTPPS
			l	1		
						ALQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQHFIDEGN
		1	1	ı		YTCGDNHTLRDPHYVEDKGHK
		1		ļ		YLVFEANTGTENGYQGEESLFN
		1		l		KAYYGGGTNFFRKESQKLQQS
		1				AKKRDAELANGALGIIELNNDY
	1		l	1		TLKKVMKPLITSNTVTDEIERA
		1				NVFKMNGKWYLFTDSRGSKM
	1			ŀ		TIDVPQAKSTNVVITSYMTNRG
				ŀ		FFEPEGSKGSITAAVMAKGLSV
			ľ			ASGNSTPERRRATANENVOPRA
	1			ŀ		IRDAEKAGRLPHPDMEIRGRVE
						ORVGYTIEOINHMRDVFGTRLR
				į		
						RAEDVFPPVIGVAAHKGGVYK
				I		TSVSVHLAQDLALKGLRVLLV
				į .		EGNDPQGTASMYHGWVPDLHI
		l		l		HAEDTLLPFYLGEKDDVTYAIK
		l		1		PTCWPGLDIIPSCLALHRIETEL
						MRKFDEGNLPTDPHLMLRLAIE
		l				TVAHDYDVIVIDSAPNLGIGTIN
		l		1		VVCAADVLIVPTPAEQLDIS\SS
		L_	l			RQFFD\ILRDLLKNVDLKGFEPD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24604	54972	A	24742	li	3899	MVDSLIAPVGVMARGNAITLPV
		1				RATNVKFTLEELRGDSVEKTSR
		l				VWSEKKDRGGQEAEVSGEGSS
		1		İ		QTKSLQKRQHSNGSDFTARGF
i		l		1	l	HTGQALVRSKGTYWNPTGLGL
		1		i		SHGTEDPNLIGEELDAGEWDK
		1			i	NTRKELAVLNVRRDFADFGTTI
						KQDFRLLGQTSVDRLLQLSQG
		1				QAVKGNQLLPVSLVKRKTTLA
		l				PNTQTASPRALADSLMQLARQ
		1				VSRLESGQFWVFEGGLRVLVR
						ERVTTPKGT\ASMYQGW\VPD
24605	54973	Α	24743	268	2617	RMFRMKLMETL\SQCINAGHE
						MTKAIAIAQFNDDSPEARKITR
		l				RWRIGEAADLVGVSSQAIRDAE
		l		1		KAGRLPHPDMEISGR\VKHGVG
		1				YTIEQIYL\TRDVFGTRLPRAED\
		l		1		VFPPVIGVAAHKGGVYKTSVSV
		l				HLAQDLALKGLRVLLVEGNDP
		1		ł	1	QGTASMYHGWVPDLHIHAEDT
		l		}		LLPFYLGEKDDVTYAIKPTCWP
		1		1		G\LDIIPSCLALHRIETELMGKFD
		1		ł		EGKLPTDPHLMLRLAIETVAHD
		l			İ	YDVIVIDSAPNLGIGTINVVCAA
		1		1	i	DVLIVPTPAELFDYTSALQFFD
		l			i i	MLRDLLKTVDLKGFEPDVRILL
		l				TKYSNSNGSQSPWMEEQIRDA
		1				WGSMVLKNVVRETDEVGKGQI
		ĺ				RMRTVFEQAIDQRSSTDTSLSTP
		l		İ		AAPMVDSLIARVGVMARGNAI
		1				TLPVCGRDVKFTLEVLRGDSVE
		1				KTSRVWSGNERDQELLTEDAL
		l				DDLIPSFLLTGQQTPAFGRRVSG VIEIADGSRRRKAAALTESDYR
		ı				VLVGELDDEQMAALSRLGNDY
						RPTSAYERGQRYASRLQNEFAG
		ŀ				NISALADAENISRKIITRCINTAK
		į.				LPKSVVALFSHPGELSARSGDA
		1				LQKAFTDKEELLKQQASNLHE
		1				QKKAGVIFEAEEVITLLTSVLKT
			l			SSASRTSLSSRHQFAPGATVLY
		1	l			KGDKMALNLDRSRVPAYIIRSY
						IRCGRKGFASAGVGGCRGWLN
		1	l			YAASEQIVLRVHHMRCEIPHRC
		Ц	<u> </u>	L		THIS EQUALITY THINK CEIF THE

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, =possible nucleotide insertion)
1				sequence		
21/0/	14.004	<u> </u>	2.011		laca.	Lamparin and arrival and arrival
24606	54974	A	24744	1	2624	MTPQKRGYLCKAGARNLDVLL
						EGCEIFLLIPMGMRSESGVSDA
		l		ĺ		DTVSAPRKKHSLEQGIFRAQVE
l	i					ASKPSSVPACIVVGNVSGYQFP
	1	1				PGTSYGPDSESELGYREKFMSF
	1				i	VGTMNEAGNPPFSANYSKAKK
	1					PKPRMFSLIERMSPSPRVGSQSV
Ì	1	l				QSSCFRDIPFEQDQMFPHPSLVL
	i .					RSKEQQPLLTQSIGVNSARKAM
l	1					AKRRRHRRRRRVSGVLPIA\VG
		l				VPS*SVHLPKVLSCSGASWI*QS
	1					CISRLGRLSPTRLMNVA\GNDP
	1				1	QGTASMYHGWVQILHIHAEDT
	1				1	LL/PFY/LGEKDDVTYAIKPTCW
						PGLDIIPSCLALHRIETELMGKF
						DEGKLPTDPHLMLRLAIETVAH
						DYDVIVIDSAPNLGIGTINVVCA
						ADVLIVPTPAELFDYTSALQFFD
1			İ		İ	MLRDLLKNVDLKGFEPDVRILL
	1					TKYSNSNGSQSPWMEEQIRDA
	1				l	WASMV*K\NNVRNANEVGKDT
						LKGFYSLKERPLGNHFLGPNNR
1						PFGKIMKHKTPAFGRRVSGVIEI
	ł					ADGSRRRKAAALTESDYRVLV
ł						GELDDEOMAALSRLGNDYRPT
			İ			SAYERGORYASRLONEFAGNIS
						ALADAENISRKIITRCINTAKLP
			İ		İ	KSVVALFSHPGELSARSGDALO
					İ	KAFTDKEELLKQQASNLHEQK
	1					KAGGFCRFRNHHOTGFSPAGA
						NORGPLAATLSGPGGEGQSAV
l	1					ARLTGEKKNHPGAQYANRLSP
24607	54975	A	24745	1	385	MWOAISRLLSEOLGEGEIELRN
24007	3.773	ľ	247.45		303	ELPGGEVHAAWHLRYAGHDFF
						VKCDERELLPGFTAEADOLELL
						SRSKTVTVPK\AFILGOOIARLH
	1			1		OWSDHAVLKIVTTGVL*GAYV
						GAPSIWKCPERITLPGYHO
24608	64076		24246		1200	GATSIWACTERITETGTHQ
24608	54976	Α	24746	I	1209	

	n of first   codon for last amino acid   *-Stop codon, /-possible nucleotide
	for peptide of peptide sequence deletion, \=possible nucleotide insertion)
	ce
24609 54977 A 24747 I	857 MHACRSELLGEGEIELRNELPG
	GEVHAAWHLRYAGHDFFVKC
	DERELLPGFTAEADQLELLSRS
	KTVNRALKVWA\VGADRELTV
	FLV\MDYLPPRPLDAHSAFILGQ
1 1 1 1	QIARLHQWSDQPQFGLDFDNA
	LSTTPQPNTWQRRWSTFFAEQR
	IGWQLELAAEKGIAFGNIDAIVE
	HIQQRLASHQPQPSLLHGDLWS
	GNCALGPDGPYIFDPACYWGD
	RECDLAMLPLHTEQPPQIYDGY
	QSVSPLPADFLERQPVYQLYTL
	LNRARLFGGQHLVIAQQSLDRL
24610 54978 A 24748 1	2094
24611 54979 A 24749 1	1209 MVREDLYTYYSCNTSREQQQL
	ENPMESPLCSKEINQGGVFMLA
	GKASDTLLAGGTMNNLGGEDS
	DTIVENGSIYRLGTDGLQLYSS
	GKTQNLSVNVGGRAEVHAGTL
	ENAVIQGGTVILLSPTSADENFV
	VEEDRAPVELTGSVALLDGAS
	MIIGYGAELQQSTITVQQGAPP
	VKLRFALYGRPGFTKCGWMLG
	YKPAHDKTLLRITRGHDFACYQ
	RTTQLARQRGLKVCSHLIVGLP
	GEGQAECLQTLERVVETGVDGI
	KLHPLHIVKGSIMAKAWEAGR
	LNGIELEDYTLTAGEMIRHTPPE
	VIYHRISASARRPTLLAPLWCE
	NRWTGMVELDRYLNEHGVQG
	SALGRPWLPPTENSLMKQIRLL
	AQYYVDLMMKLGLVRFSMLL
	A\WPSSFLPLWYKWR
24612 54980 A 24750 200	310
24613 54981 A 24751 I	4398 MCIPVPPIATGDRHFIAVAHIHQ
	NSRRSPVDSDESSTRSAVAAHP
1 1 1 1	ATRDFNVRALYTVTSSVSPTKP
1 1 1 1	PLPATFRQGRYRPAEPCVGSIG
	VIPQSSCVLANGSTGAQSAFGDI
	IRAGPPSAGLVPVAQATVIETFL
	RYQTINERDFWAARNRLLKQP
	YGSRILRFTEAYAIAERAAQSV
	LRISLADAFNVDGPRPAEDSIFR
	LLRMPGSAVQRPDRRHNRRCQ
	YRPAMAFPAGSKANKQRQYNG
	GRQFYRKRICWL

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24614	54000	<u> </u>	0.4750	lose	10160	Indiana in the control of the contro
24614	54982	Α	24752	939	2169	RPASPPARDGARWSTGLHSSYS
			l	I		AMRCRNASTCAEDSQLS/DPLA
1	1	1	l	1		R/PSVASGPYRVTSWKLGQNIV
1	1			l		YCRVKDYWPATLTVNRGRWN
	1	1	1	I		FDTIRSDYYLDDNVAFEAFKAG
1		1	l	l		AFDLRMENDAK\NWATRYT/G
l			l	l		DRRVREAITLAFDFEWMNKAL
	1		l	1		FYNAWSRTNSYFQNTEYAARN
	1	1	l	1		SPPPPEL\VLLPPIKKVLPSEVFP\
		1	l	[		QIYQPPVSKGDGYDRDNLLKA
		1	l	1		DKLLNEAGWVLKGOORVNAT
1	1		l			TGOPLSFELLLPASSNSOWVLPF
1			l	1		OHSLORLGINMDIRKVDNSOIT
1	1		1	l		NRMRSRDYDMMPRVWRAMP
i			l	1	1	WPSSDLQISWSSEYINSTYNAP
1			l	1		GVOSPVIDSLINOIIAAOGNKEK
1			l	1		FLPLGRALDRVLTWNYYMLPM
1			l	1		WYMAEDRLAWWDKFSOPAVR
		1	l	I	l	PIYSLGIDTWWYDVNKTAKLPS
		1	l	l		
24615	54983	l.	24753	12	450	ASKQGE
24615 24616	54983	A	24753	2	203	DI DDA ADVI BROCOVE A BUTTO
24016	24984	^\	24/34	ľ	203	PLPDAARYLRRQCQKPARVHDI
1			1	İ		FAAMHTAHRSRPDRPSLPDDAF
1			İ	I		SSLRL*FFQPEHYPRQYQHRHL
1			l	I		CS*ERYQHQALSRTRFRSG*PTP
1			l	I		SVPETSTGSRYFCGNAHSAPKP
1		1	l	I		PRPPITTGRRVFFTTPLILPTRAL
		L.			1212	PASISTPASL
24617	54985	A	24755	1016	1219	
24618	54986	Α	24756	1695	2021	PDTFSMLPATRFLPPLQFPDLQH
		1	l	I		PEAAQYAHWLPASGCFLFLPPP
l		1	l	I		GSGTVFLLPYPSPRLCRSTSETP
1	1	1	l	i	[	LPAITR*HFPVTDRVQK*ITRRR
		_				KPRHKPFYPDDLQRDAR
24619	54987	A	24757	1671	1911	
24620	54988	Α	24758	513	1104	CWRNCARCERNLVFRCQYGIY
I	1		İ	1		WCDNAANRSCRTKRDQPRLVE
l	l	1	Ì	1		W*KSACSHHR*LH\PCGHCRQF
			1	1		MNELNSGLDLRIHLPGREAHAL
l		1	1	1		RDYLPDAFGPKDLEIKTLLMDE
			l	t		QDHGYALTGDALSQAAIAAAN
			Ì	1		RSHMPYSKSPSGVALECKDGRI\
l				I		LVAATLKTPH/INPTQICGQPWS
	I	1	l	l		MHRRALTSKFGAHGDRRTSAG
			1			FRRN
2462I	54989	Α	24759	131	759	
24622	54990	A	24760	662	889	LPIKCRAARGVPARCLRWTRW
	1	1	l	1	[	ALRRILPPLRNRSRAASRWRAS
			1	1		PGARK*WMPSLQAVWAAPMR
	1		1	1		VTRLPAWLRWKC
	L		L	L		

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24623	54991	I <sub>A</sub>	24761	1	1518	MQRRDGDIALIYRSKIGPRTSIT
	.,,,,	1		ľ		FTARRANPVQRIAARILLRDHLI
					1	CRMSCTAARHANTFDLIQGSG
		1				ADNFAAIYGGANDRITRADAA
					1	VAGAGNWHRFGISNGKLSPRSI
	ŀ					TRTSSPARAMTKMPYNPOASG
		1				GSNLAVSNPELDKLIAARVAAL
						RAANPDASASVPVELVTASASY
		1				PRSLMRCNRILSPGSARGQMIIT
						ALFIYAGNPIACVAALEVLKVF
		l				EQENLLQKANDLGQKLKDGLL
1						AISFWRAKWLKIFVVCGAEIFV
						EYVLKNKVIWLLCFANIFLYVV
						RIGIDQWSTVYAFQELKLSKAV
						AIQGFTLFEAGALVGTLLWGW
						LSDLANGRRGLVACIALALIIAT
						LVIPFHMVFHPNEQYAYCVNEL
						NSSVDVWELKDPHGNIECVQT
						LDMMPENFSDTRWAADIHITPD
						GR\HLYACDRTASLITVFSVSED
				1		GSVLSKEGFQPTETQPRGFNVD
		1				HSGKYLIAAGQKSHHISVYEIV
		1				GEQGLLHEKGRYAVGQGP\MW
24624	54992	Α	24762	3	486	ACRRALKD\AGVEADEVLEVV
	-					MVGGSTRVPLVRERVGEFFGRF
	ł	Į				PLTSIDPDKVVAIGAAIQADILV
		1				GNKPDSEMLLLDVIPLSLGLET
				1	ŀ	MGGLVEKVIPRNTTIPVARAOD
						FTTFKDGQTAMSAGGAHIRVTF
				1		OVDADGLLSVTAMEKSTGVEA
						SIOVKPSYG
24625	54993	В	24763	1	2469	5127111515
24626	54994	A	24764	1255	1761	ESFOVRTHGTGEPVNKTRTSOA
						VSHHNOSCOVDOCVPCAVIAG
						NVFPRHNVQGQH*RNCQQTNR
	1	l	1			SSINDFTKLSNTRPISVHSLGIKO
		1	1	I		SRPDRHAKASPVVTAVKACEO
		1				VIAAVNQIADDHQPDRTKQRN
						AIVVADDLPDLFPVHFFGVDHQ
		1				QHNHRDKKQPGEDLLCC
24627	54995	A	24765	1	3141	QUINTED KKQI GEDELECC
24628	54996	B	24766	1	3969	
24028	24990	l <sub>B</sub>	Z4/00	11	3707	

SEQ ID NO:	SEQ ID NO: of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
24629	54997		24767	643	2082	GAHAMDKHESTTPAEKNLEVI- LALIGIWYNNFFDKNDALVMV DDFPRRSGLSWKIVVVPHEYW VGGSTRVPLVRERVGEFFGRPY VGGSTRVPLVRERVGEFFGRPY UTSIDPDKVVAIGAAIQADILVG NKPDSEMLLLDVIPLSLGLETM GGLVEK VIPRNTTIPVARAQDF TTFKDGQTAMSIHVMQGEREL VQDCRSLARFAICVVFRRYRLA GAHIBVTFGVDADGLLSVTM EKSTGVEASIQVKPSYGLTDSEI ASMIKDSMSYAEQDVKARMLA SCKPGQQEAKLALKTFHWQQA IADKRVIGAGITGVTAGTDHRA DVTEVASDFRVQTTNADSALF HVRSAQQHIHQLLHFTTHLLCQ LAGLIDHVVFQQIATNPADQVCV AVGFITTGKDLCHFHGGFTHA EELHKAGVEAGKVTGQAKVEG MRVQAFVLQONGADHLRTFW HLNTHRVFHRRGVGGAVGKA ADPAHTVREEGHFVITHTGFRQ FFHAAMDVEV
24630	54998	Α	24768	1	502	

SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	or pepude sequence	desentin, (-possible nucleotide insertion)
24631	54999	IA	24769	li	2345	MFMIGALVLALVMTLITFMVL
		1				RRIVIRPLOHAAORIEKIASGDI
		1	Ì			TMNDEPAGRNEIGRLSRHLOG
	i	1			1	MQHSLGMTVGTVRQGAEEIY
	i					GTSEISAGNADLSSRTEEQAAA
	l	1			1	EQTAASMEQLTATVKQNADN
						HHASKLAQEASIKASEGGQTV
		1				GVVKTMGAMSTSSKKISEITG
		1				HOOGIRTPVTAVKGRCPGPLE
ı						GDTDTAYYALRDIFALTPNRK
				1	i	LAIPVSTDNPGKPCKDPSLSKI
					VSNRVPQRVPCYDSPRSSSVN	
						NRLPGKDFHDDERSMGRSGS
	ľ				VLALAYPPKIALSDADSVTVN	
	1			l	AGWQGEISREQFNELIAPLVK	
	1				TLLACRRALKD\AGVEADEVL	
	1				VVMVGGSTRVPLVRERVGEF	
				i	GRPPLTSIDPDKVVAIGAAIQA	
						ILVGNKPDSEMLLLDVIPLSLO
					ETMGGLVEKVIPRNTTIPVAR	
					ODFTTFKDGQTAMSIHVMQG	
						RELVODCRSLARFACVVFRRY
					l	LAGPVDLFLRPWEVDISRRTS
						DSPLPVQVLEASPKGHYTQLV
				i		QPLGWYNEPLTVVMHGDDAI
		l				ORGERLFVGLQHARLYNGDE
						ASRDPGFLMARFVTCRPDKTF
				1		LRIRQHHVWIEIVSTLEQTIGN
				1		PLVKLORMGPDNGSEVWLKL
						GNNPAGSVKDRAALSMIVEA
				1		KRGEIKPGDVLIEATSGNTGIA
						AMIAALKSYRMKLLMPDNMS
24632	55000	A	24770	313	676	DCOPRSSAFTKPDATTAGHYL
24032	33000	1.	21770	3.5	10,0	GSGGRMTQLAIGKPASLGAH
				ì		REGGENFTFFSLNADGEKL/C
				1		DANGO/EHRYDLPGHSGDIWI
						G/YLPDARPALRMVSRH/GP/W
						PAGGMLTPAVVMILPRK
24633	55001	A	24771	1760	2053	FRVHGKNAFSH*IKPAAMLLP
24033	33001	Ι.		1.700	2005	SPVTRSVKPTQCGSAPSKRPN
						TLLPSITLMPPLPVTDLKLGCI
						PCSSDCFSFITFSISCATRLSVN
			1			LPAAGO
24634	55002	A	24772	296	732	
24635	55003	Α	24773	606	695	
24636	55004	Α	24774	1520	1737	PVHGLCGTRRDAGS\PAIYPFF
		1	1			LML/RFWLR/TCTVPGWPLDD
		1	1			SLAGEAFSAFTTDAAVWSLIS.
		1	1			TAMLAVQAG
24637	55005	A	24775	1	1049	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleutide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24638	55006	Α	24776	248	933	RTTMRAVSRPKYCSRERWL/HY
						DFTVARFDENASCGTFAATSAV
		l				VLIFSHCLRLLCRVVVLVTRVN
		1				FQFTEHSTTQRAFWQHAFNRDF
		1				NHTLRTASNHLFKGRLFDTTDV
				*		AGVVIVHFVSTLVAGYSNFVSV
		Į.		1		QNDDVITGIYVRSVFRFVLTAQ
						ATSQFSSQTAQSFTGRVNNIPV
ŀ				l		AFYGFWFSCAKYYRHGARWCS
l		1		i .		NGRKIDQRHTHCFFCPCIRTDFA
		<u> </u>				VEIGKEEFIT
24639	55007	Α	24777	219	3441	DCQPRSSAFTKPDATTAGHYLA
						GHSGDIWHGYLPDARPGLRYG YRVHGPWOPAEGHRFNPAK\LL
						IDPCARQIDGEFKDNPLLHAGH
						NEPDYRDNAAIAPKCVVVVDH
						YDWEDDAPPRTPWGSTIIYEAH
		1				VKGLTYLHPEIPVEIRGTYKAL
	1					GHPVMINYLKOLGITALELLPV
						AQFASEPRLQRMGLSNYWGYN
						PVAMFALHPAYACSPETALDEF
					1	RDAIKALHKAGIEVILDIVLNHS
	1	1				AELDLDGPLFSLRGI
24640	55008	Α	24778	454	586	
24641	55009	В	24779	130	1557	
24642	55010	В	24780	92	2808	
24643	55011	Α	24781	2	1051	WRLRPITPLWRWQKIFFPDA/R
				l		YGIRFRNLETGNWYPELLDNVE
		1			1	PSFVWANDSWIFYYVRKHPIFI
		1		i	1	DLTTEELAASSYHESWVLEDRII
		1		l	i	KDGSYNIDQGVGVRAISGEKTG
		1	İ	l	1	FAYADQISLLALEQSAQAARTI
	į.	1				VRDSGDGKVQTLGAVEHSPLY TSGRSGWQSMSREEKLDILRRV
		1			1	DKVAREADKRVQEVTASLSGV
		1		l	1	YELILVAATDGTLAADVRPLGK
		1				VLLVGQSPNAELSARAKQIAM
			1	I	1	GVDGANEVYNEIRQGQPIGLGE
1				I	1	ASNDTWITTKVRSOLLTSDLVK
		1	l	l		SSNVKVTTENGEVFLMGLVTE
1			1			REAKAAADIASRVSGVKRVNR
				l	1	TLFLGYAVMFSELILAPVTPSNS
24644	55012	В	24782	1	2079	
	1	1				L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24645	55013	A	24783	1	3214	MGAEKQLIPDGCGVSYIPSSGP
						LDKWRALLFIQPDYRADPVYR
		1				QHTITDLRILYDYTENFVLPLSH
	İ					DEVVHGKKSILDRMPGDAWOK
		l				FANLRAYYGWMWAFPGKKLL
						FMGNEFAQGREWNHDASLDW
						HLLEGGDNWHHGVQRLVRDL
				1		NLTYRHHKAMHELDFDPYGFE
						WLVVDDKERSVLIFVRRDKEG
1	j					NEIIVASNFTPVPRHDYRFGINQ
						PGKWREILNTDSMHYHGSNAG
		l	1			NGGTVHSDEIASHGRQHSLSL
24646	66014	١.	24704	1	1079	
24646	55014	Α	24784	11	1079	MKQIKELQRLLGKKTWKMNSS
		i		1	\	KKPLNMDGPKVDSARALIGRG
				1		WGTHKFYRCDCIKPTIKTNTSS
				i		RGNEKNPDGSHNNIHNSWFRI.
						LTSQNMCKVPESPAILVDVGQS
1						AETVQSVLTVKVEHPILRIAVA
						GYACQRQSCLLAMRHPQYAIN
1						SSKVVKPCSTARQPFQKAYAYP
						PVVRAFPAINVGISGNKLTNDR
						RYGRTSNKAWGSGDGHTLSEC
						GWAPLAAGDNVGKVSYQTLG
						YYQRILGYIFYPIAW/VMGVPSS
		1		ŀ		EALQVGSIMA/TKLVSNEFVAM
	1				1	MDLQK/IASTLSPRAEGIISVFL/
				i		VSFANFSSIGIIAAAAECRDWFG
	1	1				ILAAQTLAVRAALRVVQAERD
						CVLSMEQHQCARGRQR
24647	55015	Α	24785	121	258	LTEPRHYCRSIQFFGLTNMGQN
						CYQLS*E*FIGTLNHIRRIPQPLS
24648	55016	Α	24786	1	470	WGSGDGHTLSECGWAPLAAG
l						DNVGKVSYQTLGYYQRILGYIF
	1					YPIAW/VMGVPSSEALQVGSIM
1				1		A/TKLVSNEFVAMMDLQK/IAS
	1					TLSPRAEGIISVFL/VSFANFSSIG
ì	İ					IIAAAAECRDWFGILAAQTLAV
				l		RAALRVVQAERDCVLSMEQHQ
						CARGRQR
24649	55017	Α	24787	1324	1539	GWCGCEVPFKITDGLACLLQSP
				1		QGHQTFCFT*HNLGLQPFWIPM
l	1			l	1	CLCSVNVFKTRLILTQVEEGCR
1		1	1		1	AVSMTQ
24650	55018	A	24788	71	403	RTTFIFDLSSGWPFILWQVLSPN
				1		*RCLQVGLFAQIPTGRMGCLHR
l	1	1				FLTCRMGVCTDSSPAGWAVTLI
				1		RMSPIFPASSKSTLSAALLNTSC
1	1	1				LHSRDLEPPGAFRSGGPVLL

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24651	55019	A	24789	309	1653	SVLMDESDIYRNNRERFFCVFL
2.051	330.7	1	24707	507	1,055	LVGVPARGACLGGGGGGCGLCV
						RYLRSAGWGCGRRFPCVGDN
		1		i		WSAILAHIGKPEELDTSARNAG
						ALTRREIRDAATLLRLGLAYG
						PGGMSLREVTAWAQLHDVATL
	l .	1				SDVALLKRLPKCRHWFGILAG
					1	QTLAHIRVLPVIIRAIGFLLSKV
		1			i	NGMGKLESFNAVSSLILGOSEN
						FIAYKDILGKISRNRMYTMAAT
				1		AMSTVSMSIVGAYMTMLEPKY
						VVAALVLNMFSTFIVLSLINPYR
				1		VDASEENIQMSNLFEGQSFFEM
						LGEYILAGFKVAIIVAAMLIGFI
		1				ALIAALNALFATVTGWFGYSIS
	1	1				FOGILGYIFYPIAWVMGVPSSE
	1	1				ALOVGSIMATKLVSNEFVAMM
	ŀ	1				DLQKIASTLSPCAEGIISVLLDSF
	l .					ANFSSIGIIARAVKGLNEEOGNE
						GSRFGLKLVYRSTLVS\VLSASI
			l			AALVLSDHT
24652	55020	Α	24790	754	957	
24653	55021	В	24791	75	3707	
24654	55022	В	24792	75	264	
24655	55023	В	24793	344	461	
24656	55024	Α	24794	1	2203	
24657	55025	Α	24795	20	198	
24658	55026	Α	24796	1239	1409	RGPPTPFFHVWEWQQRPLSVW
	ı	1				EADHV*RRDEGACPRMVARAR
						NCRPKLLELRAESQ
24659	55027	Α	24797	1325	1564	
24660	55028	Α	24798	323	694	TGYARQKPVPALGWWTNVSAS
	ŀ					TAPPIILPSITGSRLAVIKWLTVS
	1	1				AGKLSALLCASCQKGGGAKWR
	1	1	1			MAMANGITNKLAIQCSPPHSTI
	l	l				EKFTSQSQHVLA*GVSAVRSM
		l				VSSG*GRRPLPALG
24661	55029	Α	24799	4708	4878	
24662	55030	A	24800	20	199	
24663	55031	A	24801	743	1186	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
24664	55032	A	24802	1394	2651	RLMTCRHEGSLGDDPGINGQL WDVNRIDVTAHEGTWERWTV ARDERQAFHIEGWMFQIRNVNG AMPPPDBGWKDTVWVDGQV LLVYFGQSWAHPPFYNGVO LLSWPQYWAACEGPAPFLDMS REEMDQLGWDSCDIILVTGDA YVDHPSFGMAICGRMLEAQGF RVGIIAQPDWSSKDDPMRLGKP NLFGVTAGNMDSMINSYTAD RRLRHDDAYTPDNVAGKRPDR ATLVYTQRCKEAWKDVPVILG GIEASILRRTAHYDYWSDTVRRS VLVDSKADMLMFGNGERFLVE VLVDSKADMLMFGNGERFLVE VLVDSKADMLMFGNGERFLVE VLVDSKADMLPGVSTRLDTTPGKI DPIPHPYGEDLPCADNKPVAPK KQEAKAVTVQPPRREWEKTY VLLPSFEKVKGDKVLVAHASRI LHHEINPAVPAH

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	tocation of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24665	55033	A	24803	11	2126	MOEKQVLAAYVQPSSEGOSRS
				ľ		RRARRVSOCHOHSAAAASLAR
		1		1		TAASATADSAHPPCPRSAARAG
		1				ATMHVKKYLLKGLHRLOKGPO
						YTYKELLVWYCDNTNTHGPKR
		1				IICEGPKKKAMWFLLTLLFAAL
		1				VCWOWGIFIRTYLSWEVSVSLS
	1	1				VGFKTMDFPAVTICNASPFKYS
	1					KIKHLLKDLDELMEAVLERILA
		1		l		PELSHANATRNLSFSIVNPTP\L
	ŀ				ŀ	
	1					VLIDERNPHHPMVLDLFGDNH
		1		ł		NGLTSSSASEKICNAHGCKMA
	ĺ				l	MRLCSLNRTQCTFRNFTSATQA
				l		LTEWYILQATNIFAQVPQQELV
	1					EMSYPGEQMILACLFGAEPCNY
	l					RNFTSIFYPHYGNCYIFNWGMT
						EKALPSANPGTEFGLKLILDIGQ
			ļ			EDYVPFLASTAGVRLMLHEQR
	1	l			l	SYPFIRDEGIYPMSGTETSIGVL
					ŀ	VDKLQRMGEPYSPCTVNGSEV
					ł	PVQNFYSDYNTTYSIQACLRSC
		1		l		FQDHMIRNCNCGHYLYPLPRG
		1				EKYCNNRDFPDWAHCYSDLQ
	1	ľ				MSVAQRETCIGMCKESCNDTQ
					1	YKMTISMADWPSEASEDWIFH
		1				VLSQERDQSTNITLSRKGIVKLN
						IFFQEFNYRTIEESAANNIVWLL
					İ	SNLGGQFGFWMGGSVLCLIEFG
i		1				EIIIDFVWITIIKLVALAKSLRQR
						RAQASYAGPPPTVAELVEAHT
		1				NFGFQP\DTAPRSPNIGP\YPGEQ
ĺ						ALPNPG/TPAPPNYDSWRLQPL
24666	55034	Α	24804	905	1051	
24667	55035	A	24805	1	1257	
24668	55036	Α	24806	1	3116	MPIITLPDGSQRSFDHPVSVAEV
1	1					aqsigaglakatlagkvdgrli
	ì	1				ITPKDEEGLEIIRHSCAHLVGHA
l		1				VKQLYPTAKMVIGPVIEEGFYY
	İ					DIFFERPFTPEDMAAIQQRMRE
ł						LIDKDYDVIKKMTPRAEVIELF
		1				KLQAAPDRRHAGREGHGLYFH
		1				EEYVDMCRGPHVPNTRFLKAF
						QLTKISGAYWRGDSKNEQLQRI
		1	l	l		YGTAWADKKOLAAYIQRIEEA
		l		l		EKRDHRRIGKOLDLFHLOEEAP
1	1	1	l	I		GMVFWHPNGWSVYO
24669	55037	A	24807	1924	2790	
24670	55038	A	24808	1	1185	
	1	1		1	1	<u></u>

	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24671	55039	Α	24809	823	5990	MARPVPLWSSWGLRTSYLPKP
						LSVNPSRNDGSA/FAGTHPLGV
						TRGTLAGPAFVRLSLVFLLRRV
						LAGSSLLPLLMG*QK/PEVLLPD
						GASEHDYSLRPSDVKRLQNAD
						LVVWVGPEMEAFMQETGKQIT
						RSEVSPLCRRVAFNKFNRDPQP
						RYDWGRLTVLYSGSSLSGGRY
						VVIIRECHCQLSKPLRLEQNEIR
						SLLPEASEPIDQAAQEDEAIPQD
				ŀ		ELDDKIAGEAGVHEYVVSTGD
						TLSSILNQYGIDMGD
	55040	Α	24810	2305	2550	
24673	55041	A	24811	665	844	ISFNNEVISYRLSGKNQ*LNLG*
				1		EIWLESGAFKKALSPQKHPGLE
1						PSVCTPTPTLVPDR
24674	55042	Α	24812	1	2031	
24675	55043	Α	24813	106	912	HFETVIDQRDFHPVFSHKGIRAT
						PEGNEEKGQRVADVTEQCGRC
ĺ						RCQPPAATLTQAVKNVHVEDL
						PQRVGHETGGGDTGDKQVEVG
						ECAESHTLDALGLRCPEPVMM
						VRKTVRNMQPGETLLIIADDPA
			ļ			TTRDIPGFCTFMEHELVAKETD
l		1				GLPYRYLIRKGG**GLIGFDAAF
		l		l		SPHPNPLPRGARGPIALNVAIGL
		l		l		PYLLRNNLNAFAVTSTVAPVSA
		1		l		STASHNPVIQRGDEEDPFQPQR
			1	l		NSDVLADIGVSGACQFNHLHQ
						AAQVVMG

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hođ	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24676	55044	Λ	24814	1	1495	MOKLTLTYAETRRLYGKEVYH
24070	33044	^	24614	l'	1493	RPSRFIGELPEECVEEVRLRATV
				ŀ		SRPVSHORMGTPMVENDSGYK
					İ	
					1	LGQRVRHAKFGEGTIVNMEGS GIAALCHCRVLIATAALMDPDD
						AVELSVTTMMFALCNTRNPRV
						AWDTAPCVPATTAASMAKRAP
	ĺ			l		DMSQSAAPEAGSQKPPRLSCGE
						SLHPLPATKRAYNYCRPVGRIR
						HLCRIRQSMPDATLSRLIRPTTV
					İ	ADPPDKALAPHPAVFTRGDSKF
			i		i	LSHKPARSPAIRYLLASVWGPV
			ļ			GMMAMMLAMTGFVVATRKLR
					İ	RRFGFKSCKNGVLYRISSSSITT
						SPASPIATCRPVLPCWMRMDPM
		i		l		LDMMGMQMLMEKYGDQAMA
				ĺ		GMDHSQMMGHMFLGHKVIRA
		ŀ				NHVGDWGTQFGMLFRIAVETF
		ŀ				KEDWEAVWDQLDDLNLEGKIV
						A*GRDPAAFHIDNGAFTKLSVA
						YALAELVAAVVLDHRRTHPLM
						ADRAAYRGAQAHLFHTLFRQL
						ADKARRAMVNLFTIOTAGFRV
						GQRQFLH
24677	55045	Α	24815	3	707	GCTLGPVKSFSLRVAWLSWPQ
		ĺ				YFYIIERACSPCCGPLAPGEAPH
		l				VNLFHSTHSENKKQPHNSPYHN
		ĺ				DIQPTLNYLPTNQKKQTQQEQS
		l				HNITKQGSQLHDVTQVPYQAY
		l				RSAIVVGLIRRDSVASGIDCRM
		İ		l		RRERLIRPTGRASDNTEFTGTO
		İ		l		NMONITHSWFVOVMIKATTDA
		İ				WLKGWA*AQRRQPDATPG*RR
		İ				YRTISRQFPATSVLYPAQPAHA
						FTGKYTVYCHRLGQILP
24678	55046	A	24816	2	1340	
	55047	A	24817	1	2457	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24680	55048	Α	24818	41	1053	QRNQQAHLSF/QHSRDIYDNQV
						HLVRNCNLEMPDQEFIVLYGPS
						DCGKSTTLRMIAGLEEISGGDL
						LIDGKRMNDVPAKARNIAMVF
				l		QNYALYPHMTVYDNMAFGLK
ĺ						MQKIAKEVIDERVNWAAQILG
						LREYLKRKPGALSGGQRQRVA
						LGRAIVREAGVFLMDEPLSNLD
						AKLRVQMRAEISKLHQKLNTT
				l		MIYVTHDQTEAMTMATRIVIM
						KDGIVQQVGAPKTVYNQPANM
						FVSGFIGSPAMNFIRGTIDGDKF
						VTETLKLTIPEEKLAVLKTQEV
	l					CPDHTLDALGLRCPEPV/HDGA
						QNRAQYAAWRNVADYRRRSG
	1					HYPRYSWVLYLYGTRTGC
24681	55049	Α	24819	3	131	
24682	55050	Α	24820	247	492	
24683	55051	Α	24821	2	241	YFFQKSSKTVIGGRRLCSVFRY
						QFSIVLATC*GTFFPSR*STILS*
1						VTQSATSSGREGRSSSRSLNGRF
						MFSIASMMSW
24684	55052	Α	24822	1	1143	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24695	55053	_	24823	242	2151	FSROHVVKMKHCCKNVVILMP
24685	33033	A	24823	242	2131	EPVAEPALNGLRUNLRIVSIVM
				1	1	
	ŀ	1				NFASYLTIGLPLAVLPGYVHDV
						MGFSAFWAGLVISLQYFATLLS
		1				RPHAGRYADSLGPKKIVVFGLC
		İ				GCFLSGLGYLTAGLTAVCLSSA
				į		VILCRGVQLHPVSDLRIPRGEK
				j		AGRNRSVDGCCEKAMSVIIVG
		1				GGMAGATLALAISRLSHGALPV
		l				HLIEATAPESHAHPGFDGRAIAI
		l				AAGTCQQLARIGVWQSLADCA
						TAITTVHVVELHNVGQRLFA\L
		İ				LRKAPGVTLHCPDRVANVART
						QSHVEVTLESGETLTGRVLVAA
						DGTHSALATACGVDWQQEPYE
		ļ				QLAVIANVATSVAHEGRAFERF
						TQHGPLAMLPMSDGRCSLVWC
ĺ		ı	i		1	HPLERREEVLSWSDEKFCRELQ
		ŀ				SAFGWRLGKITHAGKRSAYPL
		ŀ				ALTHAARSITHRTVLIQSERLNE
						KALEKRTLTVWDNSFLIYRQSD
						VSEIRLASLFASFSIRKSKQQAR
						KHTNRRSKDKEKRTROKRKTT
		1	İ			SRORRRRORMVRVGDEQIAGC
						HCLYSTGSPNRQLREAGIELSDI
						VRGNEKARERMKAQYSIAGMT
						SGVVVGTDHAAEAITGFFTKYO
		1				DGGTDINPLYRLNKROGKOLL
		ŀ	1			AALACPEHLYKKAPTADLEDD
24686	55054	A	24824	2	91	THIS TO SHE THE RESTREET
24687	55055	В	24825	1	2346	
24688	55056	Ā	24826	I	1713	
24689	55057	A	24827	i	918	
24690	55058	A	24828	415	816	
24691	55059	A	24829	72	296	FCSATFGRPSDOYONGE*LRWF
_,,,,				l -		GLGSFACOSPAHENPOWKFVL
		l		1		ARRGFARGTAEAHPSQYRHWC
		1	1			KIHRLNPGLR
24692	55060	A	24830	1	620	
24072	22000	1,	2-7050	<u></u>	1	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24693	55061	A	24831	1625	2460	GVVNPRQGRVLSMLPAMLLYL
		1				LFFLIOTSLKSNGGKGKLDPTL
İ		l				WMWTVNLIYLALAIVLNLWDT
		l				VPVRRLRASFSRKGARIPFVGC
		l				RETCELPQIELVKMMLGRELDT
						HALORAGRTLLSDKPVAAFKN
		ŀ				YGKKGTIAPFDLEVRPGEIVGL
						AGLLGSGRTETAEVIFGIKPADS
						GTALIKGKPONLRSPHOASVLG
						IGFCPEDRKTDGIIAAASVRENII
	1					LALQAQRG\CYVPFPAKNSKRL
]	İ					PNALSASLAFAHLQLNNRLNFS
						PAAISKKCCFYVGY
24694	55062	A	24832	1	2034	
24695	55063	Α	24833	3839	3970	
24696	55064	В	24834	694	765	
24697	55065	Α	24835	1778	1982	Many I and Doc Lavior
24698	55066	Α	24836	1	268	MTCRLLTRLPGQAGVGKRVSG
		l				VPDELSPLFSVGSRYLQGGVGL
		l				VSPTSGANVGLPVISTNNLVKE
		ļ		510	210	CR\DGKWKMTEKGCLNMFHFK
24699	55067 55068	A	24837	217	713	A PTROPOUNTABRO A MOCKANA
24700	22068	Α	24838	217	1910	AFTFQESVMAFSQAVSGLNAA ATNLDVIGNNIANSATYGFKSG
l		l				TASFADMFAGSKVGLGVKVAG
		1				ITODFTDGTTTNTGRGLDVAIS
		1				ONGFFRLVDSNGSVFYSRNGOF
		l				KLDENRNLVNMQGLQLTGYPA
						TGTPPTIQQGANPTNISIPNTLM
1		1				AAKTTTTASMOINLNSSDPLPT
		1				VTPFSASNADSYNKKGSVTVFD
1		1				SOGNAHDMSVYFVKTGDNNW
		1				QVYTQDSSDPNSIAKTATTLEF
1	1					NANGTLVDGAM/ANNIATGAIN
	1	l				/GLSFLNSMOONTGANNIVATT
1		l				QNGYKPGDLVSYQINDDGTVV
		1				GNYSNEQTQLLGQIVLANFAN
1		ı				NEGLASEGDNV\WSATOSSGVA
						LLGTAGTGNFGTLTN/GSIESGI
						AFLVNVPLNPKLKRVNVAGAR
						WHPYGWPAFAERACLIEPEGD
						RRTHHRPNNQRTYSRKTQRQG
		1				GHKTRQDNWEQKGDGGPRPEP
1		1				TDPHOHDANRPTVATKKRRKS
1	1	l			1	TOSORNHRNPKGTHPTEEHGT
						AGTTKPPDTPOTDNWTHKGSL
		1		1		REGKANRKRNPLRGAEVAGGG
						KORAKAEROTORGERREDVDE
		1				GEEDRSKKTEK
24701	55069	A	24839	500	653	OLEDIOR IER
24/01	122002	<u> </u>	64037	1200	000	1

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24702	55070	Α	24840	445	849	GSPGTAGTEVAVVLKIGGVHD
		l		1		KVIGHYRCSTTNTGRVLDVAI/S
	i i	l		ł	1	QNGFFRLVDSNGSVFY/SRNGQ
		l		1		FKLDENRNPATGTPPT/IQQGAN
	1	1		1		PTNISIPNTLMQRKPTAGQIVLA
	1	l		1		NFANHEGLASEATTSGLRRNLL
	1	l	1	ł		AWRCM
24703	55071	Α	2484 I	I	453	MKQMDTRGKVINCAFAVSAAF
						ALGDHLGFAAANMNAMIFPMI
	1	İ		ı		VGKLIGGVTAIGVAMMLVPRY
	1					EFIKREISWQSPVFFTPVDKQGG
		ļ				LKEAELKTLILEQYHAAGIEPES
		i		1		VDSGAIIITGESAKTRNAR*TGR
		l				FKRSGTENL\KLEQYHAAGIEPE
		l				SVDSGAIIITGESAKTRNARPTV
ł				1		MALSQSLGDFVVASAGPHLE
24704	55072	Α	24842	370	670	YSSNIMLRVLSRKALILVPSSSP
	1	l		i		VKARKPAMLARRGWRSLSRW
	1	l	İ			AILSLPGPGR*TGRFKRSGTENL
		1				\KLEQYHAAGIEPESVDSGAIIIT
	1	ļ			-	GESAKTRNARPAGMALSOSLG
		1				DFVVARAGPHLESVNAGYRTRI
		ŀ				RNHGHSWFPGEIGIRSQFPHTLR
				1		TGSINGKA WGA
24705	55073	Α	24843	I	1623	
24706	55074	В	24844	1	4986	
24707	55075	В	24845	65	726	
24708	55076	Α	24846	4107	4460	FMSTCGYGGGLSRFPARCLSYQ
		1		1		PLRSWRETVAASG*RRTGSARA
		1	Į.	1		NCFCFSGLTRDFSIWRPETK*SA
				1	1	QTFVVGTWRCGGMGR*IAAVL
		1		1		SRYSTVESGVSSTHHRLPLQPDI
		_				PSGRRL
24709	55077	A	24847	624	895	PLVPAYKQSQRQKPHDYLNRC
		1		1		RKSL*QNSTTLHAKNSQ*IRY*
	1	1	İ	1		WD/SISE**ELSMTNPQPISY*MG
ļ.	1			1	1	KNWKHSL*KLAQDRDALSHRS
						YST
24710	55078	Α	24848	1434	1594	
24711	55079	Α	24849	1294	1488	PAGKQTQQQRQQFANDGRGEI
			1	1		WRKLIKPNPRRQKS*CSTDPRQ
				ļ		KSTLISQREAVIRRFSEAGNFH
24712	55080	Α	24850	595	879	RRCSTTNIIKKIQQDKKGNRKA
		1	1	1		VHRSRFVHGRPITLLFFQLSGRI
1	1	I		1		QSHRLPGRAALFAGIPAACDQS
1		1	1			PSLRQPISSEWSDGR*HRRIFRS*
l				1		SEEF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24713	55081	Α	24851	1009	1478	IYSLSVSVWAGATVMESPVWM
						PIASKFSIEQTMMQLSFLSRTTSI
						SYSFOPISDSSISNSLVGERSRPR
						AQISSNSSRL*AIPPPLPPMVKD
						GRIMHGKPTSAATASASSIVCAI
						PERAVSR PIFFIATSKRRRSSALS
						IASAVAPIMVTPNSSNTP
24714	55082	Α	24852	48	209	GLFQVGYAENCRDNNHSFSLH
						SVVIGSSSERVVAKK*PDADHF
						SASFVPVILK
24715	55083	A	24853	1358	3194	PTASFAATLAIGKPVAFDASAE
					\	ERDTRGFISITIRRPFFGFTANVT
						RLETERGGICSRSVPWEVVSKI
1						AWAEAPDPPGVTILGLKTQHAT
1						/VSERVTSRFTRSHYRQFDLDQ
		1				AFSAKIFDRYLNLLDYSHKRKT
ł						ELGDEAAFSAKLDVFYDLYNL
İ		1				AQKRRFERYQYALSVLEKPMD
l						FTGNDTYNLDRSKAPWPKNEA
					ļ.	ELNALWDNVFSLAMTAFAREI
	1					DPHTNYLSPRNTEQFNTEMSLS
1						LEGIGAVLQMDDDYTVINSMV
		1				AGGPAAKSKAISVGDKIVGVG
						QTGKPMVDVIGWRLDDVVALI
						KGPKGSKVRLEILPAGKGTKTR
						TVTLTRERIRLEDRAVKMSVKT
1						VGKEKVGVLDIPGFYVGLTDD
		1				VKVQLQKLEKQNVSSVIIDLRS
						NGGGALTEAVSLSGLFIPAGPIV
		l				QVRDNNGKVREDSDTDGQVFY
		1		1		KGPLVVLVDRFSASASEIFARD
				1		VVVGLCICLSSLDVWLCGLFCR
		1		i		CSVDAERTKRQGKKGEESRKR
						RRKGYELSYLLFGWSAVVLLF
		1		l	1	VSDAEQHRASRHGGNACQQHP
				1		DVRHDEADGYPRQSHQLRLRR
			1	1		FRCFRPGRPLRLRRCQHERHDL
2.54	55001	-	0.1051		CON	PDDCRQVDRRRNGDWRGDDA
24716	55084	A	24854	100 852	671 1335	YFCFWTYPLLFPVCMDRKAGK
24/1/	22082	l <sup>A</sup>	24833	032	1333	HG\APAGDLYVOVOFNSHPIFE
						REGNTLYCEVPINFAMAALGGE
1			l	1		IEVPTLDGRVKLKVPGETQTGK LFRMRGKGVKSVRGGAQGDLL
1		1	1	1		
1				1		CRVVVETPVGLNERQKQLLQE
1		l		1		LQESFGGPTGEHNSPRSKSFFD
24710	55006	<del>  -</del>	24056	326	471	GVKKFFDDLTR PLOTHPAPQQRGHPIYQHGQTV
24718	55086	A	24856	320	4/1	
				1		S*SCRRRGWSSISRPVIHHADAQ
	1				L	LMP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nueleotide insertion)
1				sequence		
24719	55087	Α	24857	1095	1283	SCRRRGWSSISRPVIHHADAQL
						MP*PQIVYQHLKPPGIYRQQDR
						L*IPD*RPVLTIQDVRGP
24720	55088	Α	24858	1	1159	
24721	55089	Α	24859	1744	3019	KISPRRPQET/CFQKSTNIAREKT
		1				LEQEFSVQLFEKIGRRMCLTRE
		1				GKKLLPHIYELTRVMDTLREAA
1						KKESDPDGELRVVSGETLLSYR
1						MPQVLQRFRQRAPKVRLSLQSL
l						NCYVIRDALLNDEADVGVFYR
1						VGNDDALNRRELGEQSLVLVA
						SPOIADVDFTEPGRHNACSFIIN
		1				EPOCVFROIFESTLRORRITVEN
						TIELISIESIKRCVAANIGVSYLP
						RFAVAKELECGELIELPFGEOSO
1	1			ŀ		TITAMCAHHAGKAVSPAMHTFI
						HALYSCRMRRERLIRATRSCOF
l	1					NILHEPRRADKRSASGSLRLOE
	1					FNYODKPCMEIRIRTYEKTPIR
						MDKGLTNFGSRWILPELAHKE
	1	1				KDEETOORRKSKRDSRREETDT
						KKKTRDKATKREKDKEIEEMA
						SISITSRCEDKLENFSSMKYYTEI
24722	55090	IA	24860	321	575	SYRRYVFPAO*NRHLOFAVKPP
		1				APVIVHPTLVDSEHHHSLHDKR
	1					ROHRPHHSVAHHGSRNSSATA
						TINALLGRVAONAATRGTR
24723	55091	A	24861	935	1637	POPPPPLRREGAGLEKELGGRR
		1		1		VRVKGSGCOPWICGKVPVFIPV
	1					ITEOESFOELI/RRTTTACESLGK
	1				}	EYEILMIDDGSSDNSAHMLVEA
	1			l		SOAENSHIVSILLNRNYGOHSAI
	1					MAGFSHVTGDLIITLDADLONP
	1					PEEIPRLVAKADEGYDVVGTVR
				l	1	QNRQDSWFRKTASKMINRLIQR
			1			TTGKAMGDYGCM/LRAYRRHI
		1		l		VDAMLHCHERSTFIPILANIFAR
						RAIEIPVHHAEHS
24724	55092	A	24862	1020	1229	KAILII VIIIALII3
24/24	33092	ΙΛ.	24002	1020	1227	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequenc <b>e</b>		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24725	55093	Α	24863	98	1242	MDKFRVQGPTKLQGEVTISGA
						KNAALPNLFAALLAEEPVEIQN
						VPKLKDVDTSMKLLSQLGAKV
l						ERNGSVHIDARDVNVFCAPYD
				ì		LVKTMRASIWALGPLVARFGQ
						GQVSLPGGCTIGAHIVMDKVSV
						GATVTIMCAAILTEGATIIEVFY
		1.01				FLPLAIGKFNELYPNIKVRIL\EQ
1						GTNNCM\ESVLCN\ESDFG\INM\
						NNVTNSSI\DFTPL\VORRPFVL\
						ACRRDHPLAKKOLVEWOELVG
						YKMIGVRSSSGNRLLIEOOLAD
				i		KPWKLDWFYEVRHLSTSLGLV
1						EAGLGISALPGLAMPHAPYSSII
1						GIPLVEPVIRRTLGIIRRKDAVLS
						PAAERFFTLLSDFCPGVPSEDNI
1						FESPASOOHEYIGSROCFLMPSE
1	İ					ттотмну
24726	55094	A	24864	1	833	MAELGKRSSVAVSWIGKVKTT
						AQMVALAWLLWRPPIWVEYA
1			ŀ			GIALFFVAAVLTLWSMLQYLTL
						RVOICLISDRFGVIFSKRSKVVK
-						NIVDSSRQEYLEEFYARYNVELI
İ			ŀ			RAPEGFFYLRPRSTTLIPRSVLS
						ELDMMVGKILCYLYLSPERLA
						NEGIFTQQELYDELLTLADEAK
			ļ			LLKLVNNRSTGSDVDRQKLQE
						KVRSSLNRLRRLGMVWFMGH
						DSSKFRITESVFRFGADVRAGD
						DPREAQRRLIRDGD/AMPIENHL
						QLNDETEENOPDSGEEE
24727	55095	Α	24865	819	1428	SPRGISRGGCRCQPISGDG\RIFA
1			İ	1		GILHGLDNELPLQEEVEGNGLE
				1		QEGLPFPIRQSDALDLCFSDILV
			l	1		SPNMYIDDGMKRDWPVMKQC
			ŀ	1		ALQRRWRILPDHYGTEPAEKRP
				1		GFAPHYCFSYALLVHMMAQQC
			ĺ			DLEVGDFVWTGGDTHLYSNH
1			1			MDQTHLQLSREPRPLPKLIIKRK
			1			PESIFDYRFEDFEIEGYDPHPGIK
24728	55096	A	24866	2	1445	
24729	55097	Α	24867	I	1785	
				l		

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
}	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
		<u> </u>				
24730	55098	Α	24868	3	654	VRFFKGRGSSWHMV\SQWDYV
						ADRFGTADLLPFTISDMDFATA
1		l				PCIJEALNQRLMHGVFGYSRWK
1		ŀ				NDEFLAAIAHWFSTQHYTAIDS
1	1	ŀ	1			QTVVYGPSVIYMVSELIRQWSE
1	i					TGEGVVIHTPAYDAFYKAIEGN
		ŀ				QRTVMPVALEKQADGWFCDM
1		1			1	GKLEAVLAKPECKIMLLCSPQN
1						PTGKVWTCDELEIMADLCERH
		l				GVRVISDEIHMDMVWGEOPHIS
1		1			1	LE
24731	55099	A	24869	955	1278	TLTPDFL*QGHFFRFAGIAYQIV
						KOTTVGTTVEITLRRYVVDGNR
		ı				IPPRODROGDAFFGFATHTOOW
Į.						HQVFKRQRDIQIVTANTATTVT
		l				QQAGFTIETRTPLRPHQQQ
24732	55100	A	24870	<del> </del>	1707	QQAGITIETKITEKITQQQ
24732	55100	Ā	24871	i	3615	
24734	55101	A	24872	i -	1931	MLLLREHTDTRHDHPRTPTRAT
24/34	33102	Γ.	24072	1'	1991	RRRRHTEKKRRKKKRPATHVL
						MTATLIPVSRLLATDQPQLFHE
I	1	l l				SASKPAPHLVSSLGCHCGDASC
1	1	ļ				SGRAVADAMOFKTVFPVFVAA
	ļ	ı				
1		l				AMNPEHMAESGHRITRPEFPDY
		1			1	RELFRESDIKSAVVDSICQCNTP
1		l				FNYLFRCFELQCLSRHGHSAYG
		ł				VMQRRHSPMQETRIASLPLQRY
1		l				RWHEDSVRNRWFSVMVGPSVR
						VNEWFSAYAMAGMAYSRVST
						FSGDYLRQPLVSGFHEA
24735	55103	Α	24873	1281	2234	ISTNSILRIFSGFRKLMEV/TRLR
		1				DTPILTFMNKLDR/DIRDPMELL
		1				DEVENELK/IGCAPITWPIGCGK
		l			1	LFK/GVYHLYKDETYLIQEVRIV
					į	KGLNNP/DLDAAVGEDLAQQL
	ļ	1				RDE/LELVKGASNEFDKELF/LA
	1	l				GEITPVFFGTALGNF/GVDHML
						DG\FMAGDRSHVEEAY/PGDIL
1	1	1	1		I	G\QGEMMKFTGIPNF/APELFRR
		1				IRLKDPLKQK/QLLKGLVQLSEE
l		l			1	GA VQV/FRPISNNDLIVGA VGV
I	1	1			1	LOFDVVVARLKSEYNVEAVYE
1	1	1	1		1	SVNVATARWVECADAKKFEEF
		1			1	KRKNESQLALDGGDNLAYIATS
1					1	MVNLRLAQERYPGRQFHQTRE
		ഥ_		L		I TILLLA QUALITURQI AQIAE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24736	55104	A	24874	2	760	AKFEEKFLAVPAEALVYTMKG
						DQKYFPVYANDGKLLPNFIFVA
						NIESKDPQQI/DRIQALAGWIAE
						Q\IGADVNHATRAGLLSKCDLM
						TNMVFEFTDTQGVMGMHYAR
						HDGEAEDVAVALNEQYQPRFA
						GDDLPSNPVACALAIADKMDT
				l		LAGIFGIGQHPKGDKDPFALRR
						AALGVLRIIVEKNLNLDLQTLT
						EEAVRLYGDKLTNANVVDDVI
		1				DFMLGRFRAWYQDEGYTVDTI
l				-		QAVLARRPTRPADFDDWHA
24737	55105	A	24875	2	391	
24738	55106	A	24876	2	1785	WLLYRAHVKGE/STEALLPNM
						VATSLAKLPIPKLMRWGATYV
					İ	HFVRPVHTVTLLLGDKVIPATIL
		ł			ŀ	GIQSDRVIRGHRFMGEPEFTIDN
			ŀ			ADQYPEILRDSGKVIADYEERK
						AKIKADAEEAARKIGGNADLSE
		l	ŀ			TLLEEVASLVEWPVVL/TAKF/E
		1				EKF/LAISRTALVPYSADNMYQ
1	l	l				LVNDVQSYPQFLPGCTGSRILES
İ						TPGQMTAAVDVSKAGISKTFTT
į						RNQLTSNQSILMNLVDGPFKKL
1		1	l			IGGWKFTPLSQEACRIEFHLDFE
		1	Ì		}	FTNKLIELAFGRVFKELAANMV
İ		1	Ì		!	QAFTVRAKEVYSASMRYIYVIV
			İ		1	YISYRPPNLLDSHIIGFSSITTHC
						AVTSHHYNSCDMTMTIHSYVT
						PYISVRVSLTQTYAPSPSRNLRI
						TDLTIYRAISSEKSIDDTRHIHTI
						ESRCRVCGAHDSRDAERLDRF
		l	l			AQTADEIRIADRGFSSRPECIRS
		1				LAFGEADYIVRVHWRGLRWLT
1		1	1	I	l	AEGMRFDMMGFLRGLDCALIS
1		l	l	I	l	KTRLLSENRRKGRVVQAETLE
						AAGHVLLLTSLPEDEYSAEQVA
1		1	l			DCYRLRWQIELAFKRLKSLLHL
		1				DALRAKEPELAKVGIFANLLAA
		١		ļ		FLIDDIIQPSLDFPPRSAGSEKKN
24739	55107	A_	24877	1	2022	
24740	55108	A	24878	2344	2523	
24741	55109	Α	24879	82	732	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24742	55110	A	24880	828	2184	SGCILPPESLRLWASVARRPTP NOPROGERIGISPAGSALALA CGKRTVLFASLCTRTGGSQLGE PALVLLADQMLALDDQYTFLQ RIPRSPYGLAFOPVPHLHYLING MRLLDIAPIAFRAMSLAFPVNY LDAVRTGSICSNCNQRSNDSAM GISMNYSTLMRVRAIWVYAAY MERVLDNLLNNALRYCHSTVE TSLLLSGNRATLIVEDDGPGIAP ENREHIFEPFVRLDPSRDRSTGG CGLGLAIVHSIARGNWATSDHR SLTGTQPYARIVVFLVLIFAFR CYDLTGLYSFVFRVVVQNAFPG CPLGIGDVHYYAVAYGVFD LSSRTGTTVFFDDLNTPDFDGC CPLGGTGVHYPYAVAYGVFD RAMAYGERERFQLYRRGRY VEFNLPSELAATVYQSDPNFAT GCFRLYTSCNTFNMHKAATML
24743	55111	A	24881	679	1628	VRAEFSQGYOHQV PRADARKAYDTICLAFGCDACF IEITFTRLPEVRIHHLQSPASALS SCNHLLIRITGFNADTIGHHLP VNRRVYTVLRDMRHHGDIVFG VRRGVEHYAAMDPGIVKEIM EVRLLFLAVFVGNHHSRNDSLP VQFVVHTNGDTYTFPGNNIRRD IGFKWRIAALMLHHFLIIDPHFA VMSDRIETQHDTLACPHFRYKD KAPVYRWYHGYKALSKEIL VYQRLYQIFOHAEYQTGTNDA EISTKLCLFSSSLLLLSSSSLOHSI PPNACL
24744	55112	A	24882	1	1515	TIMES
24745	55113	Α	24883	1954	2859	
24746	55114	A	24884	121	393	SLARWIICNTSEELAANIKRLGD VTVRLNAFHAHGVYGEAQSM GERHAGRR*AVG*CVKGARGE PVDISGAQL/RGCGVNALSGLR FGTDL

SEQ ID	SEQ ID NO:					Amino acid sequence (X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24747	55115	Α	24885	1	3706	MDLGANGWQTFRYVVLPNLSS
		1				ALLAGGMLAFALSFDEIIVTTFT
	ŀ	1		l		AEQVDAAVRAADAAFAEWGQ
				ŀ	l	TTPKVRAECLLKLADVIEENGO
						VFAELESSNNTAFARASSNGDL
					1	PTKADLQAQLDSLNKQKDLSA
				1		ODKLVOODLTDTLATLDKIDRI
		İ				KEETVQLRQKVAEAPEKMRQA
	l					TAALTALSDVDNDEETRKILST
İ			1			LSLRQLETRVAQALDDLQNAQ
				1		NDLASYNSQLVSLQTQPERVQ
						NAMYNASQQLQQIRSRLDG
24748	55116	Α	24886	2842	5034	NVRLSPAMRCRWRRGSPMPAM
				F		FEVGVKTRIIORSREVILMADHS
				1		KFDAVEPHAVATLSCIKTIISDS
	i	ł		1		GLPETIAORYORAGSSLPEAOP
		l		1		DREIEKRGPAIAQAFDAEGKPS
		Į.	1	ŀ		KASEGWARGCGITVDQAERLT
1		1				TDKGEWLLYRAHVKGESTEAL
		ŀ				LPNMVATSLAKLPIPKLMRWG
				İ		ASDVHFV\WPVHTVTLL\LGDK
		1		1		VIPATILGIOSDRVIRGHRFMGE
	ł					PEFTIDNADQYPEILRERGKVIA
						DYEERKAKIKADAEEAARKIGG
						NADLSESLLEEVASLVEWPVVL
		1		1		TAKFEEKFLAVPAEALVYTMK
1		1		l .		GDOKYFPVYANDGKLLPNFIFV
		ı		l		ANIESKOPOOIISGNEKVVRPRL
		1		1		ADAEFFFNTDRKKRLEDNLPRL
		1				OTVLFQQQLGTLRDKTDRIQAL
				i		AGWIAEQSGTDAGDQTGYSDE
				1		RWVPDAHSEAPSPVSDMLSAL
1						LLLTLVLAGMVRMAARLLMA
		1				KPPOAVNRGDIGWLTTSPMVIL
		1	1			LVMMLAMGTHIPOPVIRIPGGR
1		1				FHYSPHOGRTDLPAQRSTWHD
		1		i		FCLOAPHLFRRNTVNVNSSSNR
1		1				GEAILAALKTOFPGAVLDEERO
	1	1		1		TPEQVTITVKINLLPDVVQYLY
1						YOHDGWLPVLFGNDERTLNGH
1	i	1		1		YAVYYALSMEGAEKCWIVVK
ł	1			I		ALVDADSREFPSVTPRVPAAV
1	1	1		1		WGEREIRDMYGLIPVGLPDORR
				1		LVLPDDWPEDMHPLRKDAMD
24749	55117	A	24887	49	531	
24750	55118	Α	24888	1619	1968	
24751	55119	Α	24889	1	553	
24752	55120	Α	24890	744	970	LAVISEASNQKRGDPVDHAD*I
1		1				AVANMLLNQFQQSYTPMLHDL
	1	1	1			IVRYDGDIHQQKSFGVQLPGKL
		L				RIVKLIQPVE

	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
24753   55121   A   24891   52   455	NO:		hod				
24753   55121		sequence	1	09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
24754   55122		1			sequence		
24754   55122	24753	55121	A	24891	52	455	
FHSEDVYRHPVARIVNAYEA WEEAPQKTMTPANQHAGGLV QCDKMLQRSREVIELSEQN, AQMRHVRGADMAMIFQEPMT SLNPPFTVGEQLAESIRLHQNA: REEAMVEAKRALDQVRIPEAC TILISRYPPQLSGGMRQRVMIA MALSCRPAVLIADEPTTALDVY IQAQILQLIKVLQKEMSMGVIF THDMGVVAEIDARVLVMYQG EAVETGTVEQIFHAPQHPYTRA LLAAVPQLGAMKGLDYPRFFF LISLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPPLRSGLLNR: TREVHAVEKVSPDLWGETLS VGESGSKSTTGRALLRLVESC GGEIIFNQQRIDTLSPGKLQALE RDIQFFQDPV3ASLDPRGTIGDS IEPLRVHGLLPGKDAAARVAW LLERYGLLPEHAWRYPHEFSG QRQRICIARALALNFVIIADE/ VVSALDVSIRGQIINLLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVENPOP PYTRKILLAEPPVAEPSQRPQ VLLSDLPSNIHLRGEAVVAL KPGAQIGRIPQSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRILVPVVTPESIVP PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSTPTAILIS PGRWPAAGSECVGRGHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAQGVGH IIVPATEAENFARVLALAENNYQ PLYAALGLHRGMLEKHSDVSL GQAERFVQLGYKIGVGGTTTYP ASKTRDVAKLPLASLLETIDA PMPLNGFQGQPNRFEQAAR FAVLCELRREPADEIAQAVLN TYTLVNNP	24754				2988	3614	PVSVLTQKRLSPATSHRSTCRV
WERAEQKTMTPANGHAGGLV QCDKMILQRRSREVIELSEQN. AQMRHVRGADMAMIFGEPMT SLNPVFTVGEQLAESIRLHQNA: REEAMVEAKRINLDQVRIPEAC TILSRYPHOLSGGMRQRVMIA MALSCRPAVLIADPTTALDVT IQAQILQLIKVLQKEMSMOVIF THDMGVVAEIADRVLVMYQG EAVETGTVEGIFHAPQHPYTRA: LLAAVPQLGAMKGLDYPRFFE LISLEIPAKQAPPIEQKTVVDG PVLRVRNLVTRPPLRSGLLNRX TREVHAVEKVSPDLWPGFTLS VGESGSKSTTGRALLELVESS GGEIFINGQRIDTLSPGKLQALF RDIOFIFODPYASLDPROTIGOS IEPLRVHGLLPGHAWRYPHEPSG QRQRICIARALAINPKVIIADE VSALDVSIRGQINNLLDLQRDI GIAVLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVFENPQI PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHRIRGEAVVAL KPGAQIGRPQSWT RAVINGRESS ALRIEVRGGRCHKTIRRVSVG KKVIGLKFRRILVPVVTPESIVIF PAPVANDTLVAEVSDAPQANDE PTFRNEDLA*FAVLSTPTAILIS PGRWPAAGSECVIKGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAGVGR IVPATEAENFARVVAVGEIG DLFGDDPQFERQQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERRYQLGYKIGVGGTTTYP ASKTRDVAKLPLSLLELTED PDMPLNGFQGQPNREQAARN FAVLCELRREPADEIAQAVLNN TYTLVNNP		ŀ	l			ļ.	LNOAYVTPSKCWPDVEEISFNF
QCDKMILQRRSEEVIELSEQN. AQMRHVRGADMAMIFQEPMT SLNPVFTVGEQIAESIRLHQNA: REEAMVEAKRMLDQVRIPEAG TILSRYPHOLSGGMGRQKVMIA MALSCRPAVLIADEPTTALDVI [QAQILQLIKVLQKEMSMGVIF] THDMGVVAEIADRVLVMYQG EAVETGTVEQIFHAPQHPYTR- LLSLEHPAKQAPPIEQKTVVDG PVLRYRNLVTRPFLRSGLLNR. TEEVHAVEKVSPDLWPGETLS VGESGGSKSTTGRALLRLVESG GGEIIFNQRIDTLSPGKLQALE RDIQFIFQDPYASLDPRGTIGDS IEPLRYHGLLEGKDAAARVAW LLERVGLLPEHAWRYPHEFSG- QRQRICIARALALNPKVIJADE- VSALDVSIRGQINILLDLQRDI GJAVLFISHDMAVVERISHRVA VMYLQQIVEIGPRAVFENDG- PYTRKLLAEDPVAEPSRQRPQ VLLSDDLPSNIHLR.GEEAVVAL KPGAQJGRPQSWT  24755 \$5123 A 24893 134 \$95 IRTGRIESYKGDISRYKFVSAR ALRNEVRGGKCHKTTRRVSVG KKVIJGLKFRILVPVVTPESIVIF PAPVANDTLVAEVSDAPQANS PTFNNEDLA*PAVLSTPTALLS PGRWGPAAGSECGVRGAHAH ELALRAFSCCFSSNAISIPN PTFNNEDLA*PAVLSTPTALLS PGRWGPAAGSECGVRGAHAH ELALRAFSCCFSSNAISIPN PLYAALGLHFGMLEKHSDVSL EQLQQALERRPAKVJAVCEGE DLFGDDPQFERQQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERRVQLGYKIGVGGTTTYPR ASKTRDVAKLIPLASLLETIAD PDMPLNGFQGQPNRPEQARVEN TYTLVNVP		l				i	FHSEDVVRHPVVARIVNAYEA
AQMRHVRGADMAMIFQEPNT SLNPVFTVGQIAESIRLHQNA: REEAMVEAKRMLDQVRIPEAG TILSRYPHQLSGGMRQRVMIA MALSCRPAVLJAEPTTALDV- IQAQILQLIKVLQKEMSMGVIF THDMGVVAEIADRVLVMYQG EAVETGTVEQIFHAPQHPYTRS LLAAVPQLGAMKGLDYPRFF LISLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPPLRSGLINR TREVHAVEKVSFDLWPGETLS VGESGSKSTTGRALLRLVESC GGEIIFNGQRIDTLSPGKLQALF RDIQFFGDPYSALDPROTIGDS IEPLRVHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEFSG QRQRICIARALALNPEVILADE VSALDVSIRGQIINLLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVENPOP PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT IRTGRNESYKGDISTRYKEVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSTPTAILIS PGRWPAAGSECVGRAHAH ELALRAFSCCCSSNAISIPN 1444 TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLVACHGEI DLFGDPPQFERQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTTTYP ASKTRDVAKLPLASLLETTDA PDMPLNGFQGGPNREQAARV AFAVLCELRREPADEIAQAVLN	1	l	1				WEEAEOKTMTPANOHAGGLV
SLINPYFTVGEQIAESIRI, HQNA: REEAMVEAKRMLDQVRIPEAC TILSRYPHQLSGGMRQRVMIA MALSCRPAVLIADEPITALDVI [QAQILQLIKVLQKEMSMGVIF THDMGVVAEIADRVLVMYQG EAVETGTVEQIFHAPQHPYTER LLLAAVPQLQAMKGLDYPRFF LLSLEHPAKQAPPIEQKTVVDG PVLRVRILVTRPFLRSGLLINR TEEVHAVEKVSFDLWPGFTLS VGESGSKSTTGALLALLVES GGEIIFNGQRIDTLSPGKLQALF RDIOFIFGDPYASLDPRTGTDS IEPLRYHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEFSG QRQRICIARALANPKVIJADE VSALDVSIRGQIINLLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVFENYQI PYTRKLLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEAVVAV KPGAQIGRPQSWT  24755 55123 A 24893 134 595 IRTGRNESVKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIJGLKFRHLVPVVTPESIVIF PAPVANDITUAVESDAPQAND PTFNNEDLA*FAVLSIPTALILS PGRWPAAGSECVGRGHAH ELALRAFSCCCFSSNAISIPN PTFNNEDLA*FAVLSIPTALILS PGRWPAAGSECVGRGHAH ELALRAFSCCCFSSNAISIPN LAGGGGGGCVGCGHAH ELALRAFSCCCFSSNAISIPN LAGGGGGLGGGGGGGGGCGGGGGGGGGGGGGGGGGGGGG							QCDKMLLQRRSREVIELSEQNA
REEAMVEAKRILDOVRIPEAC TILSRYPHQLSGGMRQRVMIA MALSCRPAVLIADEPTTALDVI IQAQILQLIKVLQKEMSMGVIF THDMGVVAELBURVLMYQG EAVETGTVEQIFHAPQHPYTR- LLAAVPQLGAMKGLDYPREFP LISLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPLRSGLLNR\ TREVHAVEKVSPLWGETLS\ GGEIIFNCQRIDTLSPGKLQALF RDIOFIFQDPYASLDPROTIGDS IEPLRYHGLLPGKDAARAVAW LLERYGLLPEHAWRYPHEFSG QRQRICIARALALNFXVIIADE/ VSALDVSIRGQIINLLLDLQRDI GJAYLFISHDMAVVERSHRYAV VMYLGQIVEIGPRRAVENPOP PYTRKILAEDPVAEPSQRPQ VLLSDLPSNIHLRGEAVVAL KNGAQIGRYQSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRILVPVVTPESIVP PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSIPTAILIS PGRWPAAGSECVGRGHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAQVGH IIVPATEAENFARVLALAENNY PLYAALGLHRGMLEKHSDVSL EQLQALERRPARVVAVCEGI DLFGDDPQFERQQWLLDEQLI VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFGSGLQ QAERRYQLGYKIGVGGTTTYP ASKTRDVAKLPLSLSLLETDA POMPLNGFQGGPNRFEQAAR FAVLCELRREPADEIAQAVLN							AQMRHVRGADMAMIFQEPMT
TILSRYPHOLSGGMRQRVMIA MALSCRPAVLIADEPITALDVI [QAQILQLIKVLQKEMSMOVIP THDMGVVAEIADRVILVMYQG EAVETGTVEGIFHAPQHPYTRA LLAAVPQLGAMKGLDYPRIFE LISLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPPLRSGLLNRX TREVHAVEKVSPDLWPGFILS VGESGGKSTTGRALLELVESS GGEIFINGQRIDTLSPGKLQALF RDIOGFFODPVASLDPROTIGDS [IEPLRVHGLLPEHAWRYPHEPSG- QRQRICLARALANPEVILADE- VSALDVSIRGQINNLLDLQRDI GIAVLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVFENPQI PYTRKILLAEDPVAEPSRQRQ VLLSDDLPSNIHLRGEAVVAL KPGAQIGRPQSWT RTGRNESVKGDISTRYFEVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRILVPVVTPESIVIF PAPVANDTLVAEVSDAPQANDE PTFRNEDLA*FAVLSTPTAILIS PGRWPAAGSECVIKGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAQAGVG IIVPATEAENFARVVAVGEIG DLFGDDPQFERQQWLLDEQLI VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERRYQLGYKIGVGGTTTYP ASKTRDVAKLJEASLLETIBA PDMPLNGFQGQPNRPQAARN FAVLCELRREPADEIAQAVLN			1				SLNPVFTVGEQIAESIRLHQNAS
MALSCRAVLADEPÍTALDVI QAQILQLÍKVLQKEMSMGVIF THDMOVVAEIDARVLVMYOG EAVETGTVEQIFHAPQHPYTR- LLAAVPQLGAMKGIDVPRRFP LISLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPLRSGLINR\ TREVHAVEKVSPDL WPGETLS VGESGSGKSTTGRALLALVES\ GGEIFNOGROITS-FOKLQALE\ LLERVGLLPEHAWRYPHESSG\ QRQRICIARALALNPKVILDES\ QRQRICIARALALNPKVILDES\ QGAVLISHDMAVVERISHRVA\ VSALDVSIRGQIINLLDLQRDI GIA'LFISHDMAVVERISHRVA\ VWMLGQIVEIGPRAVFENPO\ PYTRKILAEDPVAEPSQRPQ\ VLLSDLPSNIHLRGEEAVVAL KPGAQIGR'PQSWT ALRINEVRGGRCHHTIRRVSVG KKVIGLKFRILDYVVTTESIN'P PAPVANDTLVAEVSDAPQANE PTFNEDLA*FAVLSTPTAILIS\ PORWOPAAGSECCVRGAHAH\ ELALRAFSCCCFSSNAISIPN 1444 1544 1555 155124 155124 165124 165125 165126 1651267 16512		1	l		1	i	REEAMVEAKRMLDQVRIPEAQ
IQAQILQLIKVLQKEMSMGVIF THDMGVVABIADRVLVMYQG EAVETGTVEQIFHAPQHPYTRA LLAAVPQLGAMKGLDYPRFFI LISLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPPLRSGLINR TREVHAVEKVSFDLWPGETLS VGESGSKSTTGRALIALIVES GGEIIFNGQRIDTLSPGKLQALF RDIQFFGDPYSALDPROTIGS IEPLRVHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEFSG QRQRICIARALALNPKVIIADE VSALDVSIRGQIINLLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVENIOP PYTRKILLAEDPVAEPSRQRD VVLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT IRTGRNESVKGDISTRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSTPTAILIS PGRWPAAGSECVGRGHAH ELALRAFSCCCSSNAISIPN TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLALAENVQ PLYAALGLHPGMLEKHSDVSL EQLQQALERRPARVVAVGEIG DLFGDPPQFERQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTTTYP ASKTRDVAKLPLASLLETDA PDMPLNGFQGGPNREQAARV FAVLCELRREPADEIAQAVLN							TILSRYPHQLSGGMRQRVMIA
THIDMOVAEIADRYLVMYOG EAVETGTVEQIFHA PQHPYTRA LLAAVPQLGAMKGLDYPRETF LISLEHPAKQAPPIEQKTVVDG PVLRVRILVTRPFLRSGLLRN TEEVHAVEKVSPLLWPGETLS VGESGSKSTTGTALLRLLVSE GGEIIFNGQRIDTLSPGKLQALF RDIOFIFQDPYASLDPROTIGDS IEPLRYHGLLPGKDAARAVAW LLERVGLLPEHAWRYPHEFSG QRORICIARALANPEVIJADE VSALDVSIRGQIINLLLDLQRDI GJA'VLISHDMAVVERISHRVA VMYLGQIVEIGPRAAVFENPOJ PYTRKLLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEAVVAL KPGAQIGRPOSWT  IRTGRYSKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDITLVAEVSDAPQAND PTFNNEDLA*PAVLSIPTAILIS PORMPAAGSECVYGAHAH ELALRAFSCCFSSNAISIPN LATATION PHYNAEDLA*PAVLSIPTAILIS PORMPAAGSECVYGAHAH ELALRAFSCCGFSSNAISIPN LATATION PLYAALGLHFOMLEKHSDVSL GOLQALERRPAKVJAVGEG DLFGDDPQFERQQWLLDEQLI VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIGVGGTTTYPR ASKTRDVAKLPLASLLETIA PDMPLNGFQGPNREQAARN FAVLCELRREPADEIAQAVLNI TYTLVNVP		1					MALSCRPAVLIADEPTTALDVT
EAVETGTVEOIFHAPQHPYTEA LLAAVPQLGAMKGLDYPRRFF LLSLEHPAKQAPPIEQKTVVDG PVLRVRNLVTRPPLRSGLLNR TREVHAVEKVSPLWGETLS VGESGSGKSTTGRALLRLVESG GGEIIFNOGRIDTLSPGKLQALF RDIOFIFODPYASLDPROTTIGDS IEPLRVHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEFSG QRQRICIARALALNPKVIIADE/ VSALDVSIRGQIINLLLDLQRDI GJAYLFISHDMAVVERSHRVA VMYLGQIVEIGPRRAVENPOP PYTRKILAEDPVAEPSQRPQ VLLSDLPSNIHLRGEAVVAL KNGAQIGRPQSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRILVPVVTPESIVP PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSIPTAILIS PGRWGPAAGSECVGRGHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLGARAQAOVGP IIVPATEAENFARVLALAENNQ PLYAALGLHRGMLEKHSDVSL EOLQQALERRPAKVVAVGEIG DLFGDPPQFERQQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFGSGLQ QAERRVQLGYKIGVGGTTTYP ASKTRDVIKKJELASLLETIDA PDMPLNGFQGGPNRFEQAARW FAVLCELRREPADEIAQAVLNN TYTLVNNP							IQAQILQLIKVLQKEMSMGVIFI
LLA AVPQL GAMKGL DV PREPE LISLEHPAKQAPPIEQKTVVDG PPURVRNLVTRPPLRSGLINKY TREVHA VEKYSPDL WPGETLS VGESGSKSTTGRALLEL VESS GGEIFNGQRIDTLSPGKLQALF RDIOFFODPY ASL DPROTIGOS IEPLRVHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEPSG QRQRICLARALANPEVIJADE VSALDVSIRGQINNLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRRAVFENPQI PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHRIRGEAVVAI KPGAQIGRPQSWT RTGRNESVKGDISTRYFEVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRILVPVVTPESIVIF PAPVANDTLVAEVSDAPQANDE PTFRNEDLA*FAVLSTPTAILIS PGRWPAAGSECVIKGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAGVGR IIVPATEAENFARVLALAENYQ PLYAALGLHFGMLEKHSDVSL GOLQALERRPAKVVAVGEIG DLFGDDPQFERQQWLLDEQLII VVKRYELEPVILFSRKTHDKLAM HLKRHDLPRTGAKVAVGEIG QAERTVQLGYKIGVGGTTTYP ASKTRDVAKLPLSLLETLB PDMPLNGFQGQPNRPQAARV FAVLCELRREPADEIAQAVLNI TYTLVNVP			1				THDMGVVAEIADRVLVMYQG
LISLEHPÄÄQAPPIEQKTVVDG PVLRVRNLVTRFPLRSGLINR\ TREVHAVEKVSPDLWPGETLS VGESGSGKSTTGRALLALVESG GGEIENGQRIDLSPGKTLSS VGESGSGKSTTGRALLALVESG GGEIENGQRIDLSPGKTLGSE RDIOFIFODPYASLDPROTIGDS IEPLRVHGLLPGKDAAARVAW LLEEWGLLPEHAWRYPHEFSG QRQRICIARALALNPKVIIADE VSALDVSIRGQINLLLDLQRDI GJAYLFISHDMAVVERISHRVA VMYLGQIVEIGPRAAVENPO! PYTRKILLAEDPVAPENSQRPQ VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHHTIRRVSVG KKVIGLKFRILVPVVTTESIVIP PAPVANDTLVAEVSDAPQAND PTFNNEDLA†FAVLSTPTAILIS PORWGPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN 1444 TDAPGDEEASLQRAAQAGVG IIVPATEAENFARVLALAENYQ PLYAALGLHRGMLEKHSDVSL EQLQQALERRPAKVVAVCEIG DLFGDPPOFERQQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERRVOLGYKIGVGGTITYPR ASKTRDVIAKLPLSSLLEITDA PDMPLNGFQGPORPREQA AR FAVLCELRREPADEIAQAVLNN TYTLVNNP	1		1				EAVETGTVEOIFHAPOHPYTRA
PVLRVRILVTRPURSGLLNR TREVHA VEKVSFÜLWGETLS VGESGSKSTTGRALLRILVSEK GGEIIPNGQRIDTLSPGKLQALE RDIOFFGDPV3ALDPROTIGDS IEPLRVHGLLPGKDAARAVAW LLERVGLLPEHA WRYPHEFSG QRQRICIARALALNPEVIIADE VSALDVSIRGQIINLLLDLQRDI GIA VLFISHDMA VVERISHRVA VMYLGQIVEIGPRRA VERNFOR PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT IRTGRNESVKGDISTRVKFVSAR ALRNEVRGGRCHKTIRRVSVG KK VIGLKFRHLVPVVTPESIVIF PAPVANDTLVAEVSDAPQANE PTFNNEDLA*PAVLSTPTAILIS PGRWPAAGSECVGRGHAH ELALRAFSCCCSSNAISIPN TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLALAENVQ PLYAALGLHPGMLEKHSDVSL EQLQQALERRPARVVAVGEGE DLFGDPPGFRQOWLLDEQLI VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLETIDA PDMPLNGFQGGPNRFEQAARV FAVLCELREPADEIAQAVLN			1			l	LLAAVPQLGAMKGLDYPRRFP
TREVHAVEKVSPOLWPGETLS VGESGSKSTTGRALLRLVESC GGEIIFNOGRIDTLSPGKLQALE RDIOFIFODPYASLDPROTIGDS IEPLRYHGLLERGKDAARAVAW LLERVGLLPEHAWRYPHEFSG QRORICLARALALNPKVIJADE VSALDVSIRGQIINLLLDLQRDI GJAVLFISHDMAVVERISHRVA VMYLQQIVEIGPRAVFENYGL PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEGAVVAL KPGAQIGRPQSWT  24755 55123 A 24893 134 595 IRTGRNESYKGDISRYKFVSAR ALRNEVRGGKCHKTIRRVSVG KKVIGLKFRILVPVVTPESIVIF PAPVANDITLVAEVSDAPQAND PTFRNEDLA*PAVLSIPTAILIS PGRWGPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN LALRAFSCCCFSSNAISIPN PLYAALGLHFGMLEKHSDVSL GOLQALERRPAKVJAVGEG DLFGDDPGFRQQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIGVGGTTTYPR ASKTRDVAKLPLASLLLETIAD PDMPLNGFQGPNRPQARAVN FAVLCELRREPADEIAQAVLNI TYTLVNVP		1					LISLEHPAKQAPPIEQKTVVDGI
VOESGSGKSTTGRALLALVESG GGEIIFNGQRIDTLSPGKLQALF RDIOFIFODPYASLDPROTIGDS IEPLRYHGLLPGKDAARRVAW LLERVGLLPEHAWRYPHEFSG QRQRICIARALALNPKVIJADE/ VSALDVSIRGQIINLLIDLQRDI GJA'LFISHDMAVVERISHRVA VMYLGQJVEIGPRRAVERISHRVA VMYLGQJVEIGPRRAVERISHRVA VMYLGQJVEIGPRRAVERISHRVA VMYLGQJVEIGPRRAVERISHRVA VMYLGQJVEIGPRRAVERISHRVA VMYLGQJVEIGPRRAVENOPI PYTRKILLAEDPVAEPSQRPQ VLLSDDLPSNIHLRGEEAVVAL KRGAQJGRPQSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGKCHKTIRRVSVG KKVGLKFRILLPVVTTPESIVIP PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSTPTAILIS PGRWGPAAGSECVTGAIHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLORAAQAGVGK IIVPATEAENFARVVAVGEIG DLFGDDPQFERQQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERRVQLGYKIGVGGTTTYPR ASKTRDVIAKLPLASLLETIDA PDMPLNGFQGGPNRPEQAARW PAVLCELRREPADEIAQAVLNN TYTTLVNNP			1				PVLRVRNLVTRFPLRSGLLNRV
GGEIIFNGQRIDTLSPGKLQALF RDIQFIFQDPYASLDPRQTIGDS IEPLRVHGLLPGKDAAARVAW LLERVGLLPEHAWRYPHEFSG QRQRICIARBALAINPEVIIADE VSALDVSIRGQIINLLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLQQIVEIGPRAAVFENPGI PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEGAVVAL KFGAQIGRPQSWT IRTGRNESVKGDISR YKEFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDITLVAEVSDAPQANDE PTFRNEDLA*FAVLSIPTAILIS PGRWPAAGSCOVGGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAGVGR IIVPATEAENFARVLALAENVY PLYAALGLHFGMLEKHSDVSL GOLQQALERRPAKVVAVGEIG DLFGDDPQFERQQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLLETIA PDMPLNGFQGQPNRPQAARVA FAVLCELRREPADEIAQAVLNI TYTLVNVP	ŀ						TREVHAVEKVSFDLWPGETLSI
ROJOFIFODPY ASL DPROTIGOS IEPLRVHGLLPGK DAAARVAW LLERVGLLPEHAWRYPHEPSG QRQRICIARALALNPKVIIADE VSALDVSIRGQINILLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLQQIVEIGPRAAVENPOP PYTRKILLAEDPVAEPSQRPQ VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPPOSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGKCHHTIRRVSVG KKVIGLKFRILLPVVTTESIVIP PAPVANDTLVAEVSDAPQAND PTFNNEDLA*FAVLSTPTAILIS PORWOPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN 1444 TDAPGDEEASLQRAQAGVGVG IIVPATEAENFARVLALAENYQ PLYAALGLHGMLEKHSDVSL EQLQQALERRPAKVVAVCGIG DLFGDPPOFERQQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIRGVGGTTTYPR ASKTRDVIKALPLASLLETDA PDMPLNGFQGPORPREQA AR FAVLCELRREPADEIAQAVLNN TYTLVNNP			1				VGESGSGKSTTGRALLRLVESQ
IEPLR VHÖLLPGKDAAARVAW LLERVÖLLPEHA WRYPHEFSG QRQRICIARALALNPKVIIADE- VSALDVSIRGQIINLLLDLQRDI GIAVLFISHDMAVVERISHRVA VMYLGGIVEIGPRRAVEENPOP PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT IRTGRNESVKGDISR VKEVVSAR ALRNEVRGGRCHKTIRRVSVG KK VIGLKFRHLVPVVTPESIVIF PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSITTAILIS PGRWGPAAGSECVIRGAHAH ELALRAFSCCCSSNAISIEN TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLALAENVQ PLYAALGLHPGMLEKHSDVSL EQLQQALERRPARVVAVGEGE DLFGDPPOFERQOWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLEETDA PDMPLNGFQGGPNRFEQAARV FAVLCELREPADEIAQAVLN TYTLVNNP							GGEIIFNGQRIDTLSPGKLQALR
LLERVGLIPEHAWRYPHEFSG QRQRICIARALALNPKVIIADE QRQRICIARALALNPKVIIADE VSALDVSIRGQINLLLDLQRDI GIAVLISHDMAVVERISHRVA VMYLGOVEIGPRAVPENPO PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT LKTGRNESVKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTESIVIE PAPVANDTLVAEVSDAPQAND PIFFANEDLA*PAVLSTPTALLIS PGRWGPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIFN 1444 TDAPGDEEASLQRAAQAGVG IIVPATEAENFARVLALAENVQ PLYAALGLHPGMLEKHSDVSL EGOLQQALERRPAKVVAVGEIG DLFGDDPOFERQOWLLDEQLII VKKYELPVILLARSRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIGVGGTTTYP ASKTRDVIKALPLASLLETDA PDMPLNGFQGQPNRFEQAAR FAVLCELRREPADEIAQAVLN TYTLVNVP			1				RDIQFIFQDPYASLDPRQTIGDS
QRQRICIARALALNPKVIJADE/ VSALDVSIRGQIINLLIDLQRDI GIAYLFISHDMAVVERISHRVA VMYLGGIVEIGPRRAVERISHRVA VMYLGGIVEIGPRRAVERINOP PYTRKILLAEDPVAEPSQRPQ VLLSDDLPSNIHLRGEEAVVAL KRGAQIGRYQSWT IRTGRNESYKGDISRYKFVSAR ALRNEVRGGKCHKTIRRVSVG KKVGLKFRILVPVVTPESIVE PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSIPTAILIS PGRWGPAAGSECVRGAHAFI ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQARAQAGVG PLYAALGLHRGMLEKHSDVSL EQLQQALERRPAKVVAVGEIG DLFGDPPQFERQQWLLDEQLI VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFGSGL QAERFVQLGYKIGVGGTTTYPR ASKTRDVIAKLPLASLLETIDA PDMPLNGFQGGPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNNP	1		1				IEPLRVHGLLPGKDAAARVAW
VSALDVSIRGQINLLLDLQRDI GIAYLFISHDMAVVERISHRVA VMYLQQIVEIGPRAVFENPGI PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEAVVAU KFGAQIGRPQSWT  24755 55123 A 24893 134 595 IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIE PAPVANDITLVAEVSDAPQANDE PTFRNEDLA*PAVLSIPTAILIS PGRWPAAGSECVIKGAHAH ELALRAFSCCCFSSNAISIPN  708 1444 TDAPGDEEASLQRAQAGVGR IIVPATEAENFARVLALAENVY PLYAALGLHRGMLEKHSDVSL GOLQQALERRPAKVVAVGGIG DLFGDDPQFERQQWLLDEQLII VVKRYELPVILHSRKTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLLETIDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNI TYTLVNVP	1						LLERVGLLPEHAWRYPHEFSGC
GIAVLFISHDMAVVERISHRVA	1	1	1				QRQRICIARALALNPKVIIADEA
VMYLGOJVEIGPRRAVERNOH PYTRKILAEDPVAEPSRQPQ VULSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT RTGRNESYKGDISRYKEFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSITTAILIS PGRWGPAAGSECVIRGAHAH ELALRAFSCCCSSNAISIPN TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLACHSDVSL EQLQALERRPARVVAVGEIG DLFGDPPOFERQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERTVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLEETDA PDMPLNGFQGGPNREQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP					1		VSALDVSIRGQIINLLLDLQRDF
PYTRKILLAEDPVAEPSRQRPQ VLLSDDLPSNIHLRGEAVVAL KFGAQIGR:PQSWT 24755 55123 A 24893 134 595 IRTGRESVKGDISR:VKFVSAR ALRNEVRGGRCH:TIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDTUVAEVSDAPQAND PTFNNEDLA*PAVLSTPTAILISI PGRWGPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAAQAGVGW IIVPATEAENPARVLALAENVQ PLYAALGI-HPGMLEKHSDVSL EQLQQALERRPAKVVAVGEIG DLFGDDPQFERQWLLDEQLII VKKYELPVILLSKRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIRGVGTTTYPF ASKTRDVIAKLPLASLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP							GIAYLFISHDMAVVERISHRVA
VLLSDDLPSNIHLRGEEAVVAL KPGAQIGRPQSWT 24755 55123 A 24893 134 595 IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRILLPVVVTPESIVIP PAPVANDTLVAEVSDAPQANE PTFNIEDLA*FAVLSTPTAILLS PGRWGPAAGSECCVRGAHAH ELALRAFSCCCFSSNAISIPN 10444 TDAPDEEASLGAAQAGVG PLYAALGLHRGMLEKHSDVSL EQLQQALERRPAKVVAVCEIG DLFGDPPQFERQQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFGSLQ QAERVQLGYKIRGVGTTTYPR ASKTRDVIAKLPLASLLEETDA PDMPLNGFQGGPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNNP	1					1	VMYLGQIVEIGPRRAVFENPQH
24755 55123 A 24893 134 595 IRTGRNESYKGDISRYKFVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIE PAPVANDTLVASVSDAPOAND PTFNNEDLA*FAVLSIPTAILIS PGRWGPAAGSECVGKGHAH ELALRAFSCCCFSSNAISIPN 11444 TDAPGDEEASLQRAQAGVGR IIVPATEAENFARVLALAENVQ PLYAALGLHRGMLEKHSDVSL EQLQALERRPAKVVAVGEIG DLFGDDPQFERQQWLLDEQLII VVKRYELPVILHSRKTHDKLAM HLKRHDLPRTGVVGFSGSLQ QAERTVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLLETDA PDMPLNGFQGPNRFQAARVA FAVLCELRREPADEIAQAVLNN TYTLVNVP							PYTRK\LLAEDPVAEPSRQRPQF
24755 55123 A 24893 134 595 IRTORNESVKGDISRYKEVSAR ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTESIVIE PAPVANDTLVAEVSDAPQAND PTFNNEDLA*PAVLSTPTALLISL PGRWGPAAGSECGVRGAHAHI ELALRAFSCCCFSSNAISIPN TOACH PAPVANDTLVAEVSDAPQAND PLYAALGALPROMALALAENVQ PLYAALGALPROMALAENVQ PLYAALGALPROMALALAENVQ PLYAALGALPROMALALAENVQ PLYAALGALPROMALAENVAVCEGE DLFGDDPOFERQOWLLDEQLII VKKYELPVILARSTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIGVGGTTTYPR ASKTRDVIKALPLASILLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNYTYTLVNVP	i		1				VLLSDDLPSNIHLRGEEAVVAL
ALRNEVRGGRCHKTIRRVSVG KKVIGLKFRHLVPVVTPESIVIF PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSIPTAILIS PORWGPAAGSECOVRGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLALAENVQ PLYAALGLHFGMLEKHSDVSL EQLQQALERRPAKVVAVGEIG DLFGDPOFERQOWLL DEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLEETDA PDMPLNGFQGPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP							KPGAQIGR\PQSWT
KKVIGLKFRHLVPVVTPESIVIE PAPVANDTUVAEVSDAPQANE PTFNNEDLA*FAVLSTPTALLISE PORWOPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAAQAGVGR IIVPATEAENFARVLALAENYQ PLYAALGLHPGMLEKHSDVSL EQLQQALERRPAKVVAVGEIG DLFGDDPGFERQQWLLDEQLII VKKYPLEPVILBSRTHDKLAM HLKRIDLPRTGVVYGFSGSLQ QAERFVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLN TYTLVNVP	24755	55123	Α	24893	134	595	IRTGRNESYKGDISRYKFVSAR
PAPVANDTLVAEVSDAPQANE PTFNNEDLA*FAVLSTPTAILIS PGRWGPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN 24756 55124 A 24894 708 1444 TDAPGDEEASLQRAAQAGVG PL-YAALGLHRGMLEKHSDVSL EQLQQALERRPAKVVAVCGEG DLFGDPPQFERQQWLLDEQLII VKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYQFGSGLQ QAERRVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASLLEETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNNP			1	1			ALRNEVRGGRCHKTIRRVSVG
PIFRNEDLA*FAVLSIPITÄLIS PGRWGPAAGSECGVRGAHAH ELALRAFSCCCFSSNAISIPN TDAPGDEEASLQRAQAGVG IIVPATEAENFARVLALGENYO PL.YAALGLHFGMLEKHSDVSL EQLQALERPRAVVAVGEIG DLFGDDPGFERQQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVGFGSGLQ QAERVQLGYKIGVGGTITYPR ASKTRDVAKLPLASILLETDA PDMPLNGFQGPNRFEQAARV FAVLCELRREPADEIAQAVLNI TYTLVNVP	1		l	1		1	
PGRWGPAAGSECGVRGAHAHI ELALRAFSCCGSSNAISIPN 24756 55124 A 24894 708 1444 TDAPGDEEASLQRAAQAGVG PLYAALGLHPGMLEKHSDVSL EQLQQALERRPAKVVAVGEIG DLFGDDPQFERQQWLLDEQLII VKKYFLEPVILHSRFTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNY							PAPVANDTLVAEVSDAPQAND
24756 55124 A 24894 708 1444 TDAFGDEEASLQRAAQAGVGH IIVPATEAENIFARVINALAENIVQ PLYAALGLHFGMLEKHSDVSL EQLQQALERRPARVVAVGEIG DLFGDDPOFERQOWLLD EQLII VVKRYELPVILHSRRTHDKLAM HILKRHDLPRTGVVYGFSGSLQ QAERRVQLGYKIGVGGTITYPR ASKTRDVAKLPLASLLEETDA PDMPLNGFQGQPNRPEQAARV FAVLCELREPADEIAQAVLNN TYTLENNP						1	
24756 55124 A 24894 708 1444 TDAPGDEEASLQRAAQAGVGHIVPATEAENFARVLALAENYQPLYAALGLHRGMLEKHSDVSL EQLQQALERPAKVVAVOEIG DLFGDDPGERQQWLLDEQLII VVKRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERFVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNY							PGRWGPAAGSECGVRGAHAHF
IIIVPATEAENFAR VLALA ENYQ PL YAALGHPGMLEKHSDVSL EQLQQALERRPAKVVAVCEIG DLFGDDPOFERQOWLLDEQLII VKK YEL PVILHSR THDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERRVQLGYKIGVGGTTTYPR ASKTRDVIAKLPLASLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP							
PLYAALGLHPOMLEKHSDVSL EQLQQALERPAKVVAVGEIG DLFGDPPQFERQQWLLDEQLI V\KRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERFVQLGVKIGVGTTTYPP ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGPPNRPEQAARV FAVLCELRREPADEIAQAVLNN TYTLVNVP	24756	55124	Α	24894	708	1444	
EQLQQALERPAKVVAVGEIG DLFGDDPGERQQWLLDEQLII VKKPYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFSGSLQ QAERFVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASILLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLNY							
DLFGDDPQFERQQWLLDEQLII V\kryelpvilhsrrthdklam Hilkrhddprtgovygfsolg Qaerfvolgykigvggtitypb Asktrddvaklplasllletid pdmplngfqggpnrbeqaarv Favicelrepadeiaqavlnn tytlvnyp					l .		
V\KRYELPVILHSRRTHDKLAM HLKRHDLPRTGVVYGFGSSLQ QAERFVQLGVKIGVGGTTTYPB ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGPNRPEQAARV FAVLCELRREPADEIAQAVLN TYTLVNVP			1				
HLKRHDLPRTGVVYGFSGSLQ QAERFVOLGVKIGVGGTITYPR ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGQPNRPEQAARV FAVLCELRREPADEIAQAVLN TYTLVNVP	1		1				
QAERFVQLGYKIGVGGTITYPR ASKTRDVIAKLPLASLLLETDA PDMPLNGFQQPNRPEQAARV FAVLCELRREPADEIAQAVLNY TYTLVNVP			1		1		V\KRYELPVILHSRRTHDKLAM
ASKTRDVIAKLPLASLLLETDA PDMPLNGFQGPNRPEQAARV FAVLCELRREPADEIAQAVLN TYTLVNVP			1		l		HLKRHDLPRTGVVYGFSGSLQ
PDMPLNGFQGQPNRPEQA A RV FA VLCELRREPA DEI AQA VLNN TYTL VNVP			1				QAERFVQLGYKIGVGGTITYPR
FAVLCELRREPADEIAQAVLNN TYTLVNVP	1		1				ASKTRDVIAKLPLASLLLETDA
TYTLVNVP				1			PDMPLNGFQGQPNRPEQAARV
	1		1				FAVLCELRREPADEIAQAVLNN
24757 55125 A 24895 1460 1777							TYTLVNVP
	24757	55125	Α	24895	1460	1777	

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24758	55126	A	24896	381	482	IPGPQSPQSSPDLGWLQC*NP*R LLWKAPRSDK
24759	55127	Α	24897	977	1144	
24760	55128	A	24898	2	280	CTFALRDEYPRMLNVDNKGLR DHIELQPLAV/DASYPGGDFRK NA VYVPMW*SAHCEPEGRFAE TGSRRYGEDFASTAPGFRRAAT RKRVRRKR
24761	55129	В	24899	1	1665	
24762	55130	Α	24900	296	495	
24763	55131	Α	24901	1	5352	
24764	55132	A	24902	187	280	AVDTGLADIIRD\EPNMVARLP LSFTASLSIS
24765	55133	A	24903	1775	1981	HIWQNSLIVLFRGCRSAHAKVH RWKN*LPLNLAPLLPRSGSSAPI RPPPSAQARQPMKSTYGVDRR HS
24766	55134	Α	24904	760	1473	
24767	55135	A	24905		2124	IMNRMSGYYWQLFAESGETCR ARELEQCLEDFYDQRKESVRW HLDLHTAIRGSLHPQFGVLPQR DIPWDEKFLTWLGAAGLEALV FHQEFGGTFHESARHFGALV FHQEFGGTFHESARHFGALV FMGERGFHFHSARHFGALV FMGERGFHFHSARHFGALV FMFEKGTLLAQDGEERTTVTH DVEVAKNATHEIKTOFEKEKLA QDRIKRNQ/LDANIQRLNYSLDI ANAAGIKEPYYSNDGIERKLEI EKAYTDVAELMGELRNIQVL EQLITKAHVNDVNFTPFKYQLSP SLPVKKDGPGKALIVILSALIGG MLVGRVCIKRNADSPEVFSGFS DPNVVLIAAVFIIGDGLVRTGV VLIAMVFILGDGLVRTGV VLIAMVFILGDGLVRTGV VLYLGILVMLVAGNSEIKML VLLMLTVAGLGFMSSTGVVA FIPPVLSVARMRQTSPSRLMM PLSFAGLISGMMTLVATPPNLV VNSELLBGGVHGFSFFSVTPIGL UVLVLGILVMLVMFFMLKGDT QTPQREGWTRTFRDLIREYRL TGRARRLAIRPGSPMIGQRLDD LKIRRYGANNIGVER WREFF RVYNVNGVSEFRARDVSLIAM SAADVDLRQFCSERLLEPDGIA RSADIPESELIGESVREIGERTRY GLNYVGUTRTGVARAAD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24768	55136	A	24906	834	1993	EEIEVARI.RDQKSAEGGIQNRE YWPGRSGHR*SPHAPIIGTQFLQ ALFQTWDQFVFALSACGRRHP TDGRRQNPAVSGHSVAARQPA HSQTDEASG
24769	55137	Α	24907	3519	5161	
24770	55138	A	24908	374	1891	KWKLKRPDSNIDHRRVPNLET WFSRHDKTRPTSKNPSDYQAG DIVSWRLDNGLAHIGVVSDGFA
						RDGTPLVIHNIGAGAQEEDVLF NWRMRQCQHNQHNTATFNGP RILAEOPPGKEYAANGNGOLYP
						MSSLNIKQGSDAHFPDYPLASP SNNEIDLLNLISVLWRAKKTVM
						AVVFAFACAGLLISFILPQKWTS AAVVTPPEPVQWQELEKSFTKL RVLDLDIKIDRTEAFNLFIKKFO
						SVSLLEEYLRSSPYVMDQLKEA KIDELDLHRAIVALSEKMKAVD
						DNASKKKDEPSLYTSWTLSFTA PTSEEAQTVLSGYIDYISTLVVK ESLENVRNKLEIKTQFEKEKLA
						QDRIKTKNQLDANIQRI.NYSLD IANAAGIKKPVYSNGQAVKDD
				\ -		PDFSISLGADGIERKLEIEKAVT DVAELNGELRNRQYLV\EPITK AHVNDVNFTPFKYQLSPSLPVK
						KDGPGKAIIVILSALIGGMVAC GGVLLRYAMASRKQDAMMAD
24771	55139	A	24909	1111	1895	PLVNFSNSSHPVSNPSIQLSSITL PLVENESRARA\VKDQMDAIDH QTGVRPLVFYSIVLPEIRAIILQS
						EGFCQDIVQALVAPLQQEMKL DPTPIAHRTHGLNPNNLNKYDA
		ļ				RIAAIDYTLAHDDGISLRNLDQ AQVILLGVSRCGKTPTSLYLAM
						QFGIRAANYPFIADDMDNLVLP ASLKPLQHKLFGLTIDPERLAAI REERRENSRYASLRQCRMEVA
						EVEALYRKNQIPWINSTNYSVE EIATKILDIMGLSRRMY
24772	55140	Α	24910	77	434	EKKRGREDKPGTMATFPPATSA PQQPPGPEDEDSSLDESDLYSL AHSYLGPLIMPMPTSPLTPALV
						TGGGGRKGRTKREAAANTNRP SPGGHR/ERKLVTKLQNSERKK RGARRLRQSWR
24773	55141	A	24911	31	295	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
				sequence		
24774	55142	A	24912	75	426	EKKRGREDKPGTMATFPPATSA
24,,,4	55142	ľ.	24712	1,3	420	PO\OPPGPGGRDSQPWMDLDLL
						/YSLAHSYLG\GGGRKGHTKRE
	1	1				TAANTOPPOPLAGHERKTVDP
						KLONSERKKRGARALROELEM
						RRRPWTLTPSO
24775	55143	A	24913	1	1107	and Highley
24776	55144	Α	24914	1	1468	
24777	55145	Α	24915	I	2463	
24778	55146	Α	24916	1	603	
24779	55147	Α	24917	118	1087	IRSKKMTTQTVSGRRYFTKAW
						LMEOKSLIALLVLIAIVSTLSPN
		l				FFTINNLFNILQQTSVNAIMAVG
1		1				MTLVILTSGIDLS/VAASIVGIEV
						NALVAVAAALALGAAIGAVTG
						VIVAKGRVQAFIATLVMMLLL
						RGVTMVYTNGSPVNTGFTENA
						DLFGWFGIGRPLGVPTPVWIMG
l						IVFLAAWYMLHHTRLGRYIYA
						LGGNEAATRFSGINVNKIKIIVY
						SLCGQLASLAGIIKVARLSSAQ
						HTAGTGYELDAIAAVVLADDR
				ĺ		OSGGDFAGGAGROOKAVITTT
İ						GHLEYEHEKTGYPGFRCCAKR
		1				HRQCECDGKRHHRAGGLHA
24780	55148	A	24918	1	1286	MHEREPGLRAALAGOLEFRVG
						LGLGVWTLRLMELLRORLELV
		1				VYTASDGQEYEMVSRLNWVN
						YLVLEDVHIILPDQMRGITGCY
						ATHPHERRLHAGTVHRONIVN
İ						NPPDCVPRDAGEAEVAPDPSLA
						SLQLQTPELPGLISCHNSIQVSN
						EARLFELLICOWRDFRKRVIAA
		1				KSMQGRELEGGQRGQDKATNP
						FRVLALKGSGDPDPHGAGRQG
						SDLLLHPVSDAQVLQHFFQRRA
	l			1		LLSSPWDYHDVVGLCAQEPCG
1	1	1	1	1	1	YIMELFIIKHQCSLAQTAGSLAP
		l		1		EQKKELEMTVRYYISSADLTAE
l		1				KFATAIRN/HWHVENKLHWRL
l	1					DV*RQFDKHCSTADSTRILASF
l		1				VRHVNAALDVRVVFASGSETT
l						HGDGARRYLRCVDVDWRRRT
	1					AVAQADKSARACHFHYAGYH
					1	HHEHFADPVSVGAKYHTVFST
		_		L	L	PHILLIADI VOVOAKIIII VESI

## WO 01/075067

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
24781	55149	Α	24919	417	861	AKGPCPDRNHSSDDKDVIAIDG
24761	33143	n	24515	1117	1001	KTLRHSYDKSRR\RGAIHVISAF
	1					STMHSLVIGQIKTDEKSNEITAI
		İ				PELLNMLDIKGKIITTDAMGCO
l	1	l	ŀ			KDIAEKIOKOGVIFSLCPASIIDD
						KKVTDLAVAVQGTLKTGSGGI
						LPPGGALKKISEKL
24782	55150	A	24920	3	1767	HISIIPDYR*AWKVEHKLSGILL
24/62	133130	^	24920	ľ	11707	LTIFAVISGAESWKDIEDFGKTH
						LDFWKOYGDFENGIPVHDTIAR
ŀ	l		İ			VVSCISPAKFHE\CFINWMRDCH
ŀ						SSNDKDVIAIDGKTLRHSYDKS
					l	RRRGAIHVISAFSTMHSLVIGOI
						KTDKKSNEITAIPELLNMLDIKG
	ŀ				ŀ	KIITTDAMGCQKDIAEKIQKQG
					ľ	GDYLFAVKORNGAVENRAKTO
į .						TRIAFGDHFFRROVSORIRLFCH
1						RLATOFAARLRMFIATGOPMN
	1		1			GLRLLLFIVNKOAALLVNKLDA
						QMAAFQQLPGRGRQATVRRE
						MDLCAFAERMGLPVSRPGDIOE
	1	i				FHAGCRTKFDAGAFRDKHHVA
Ì	1				ł	CFGDHGLAFVANMOLPFOHHV
İ						DFVVVQGPREECVLPLHKTGG
	1					HAAAVVSGHKISQAHAMRLCA
ŀ			i			VETTKLDATGINHFDAAFAGHR
ŀ	1	l				FESSVDCACSATVSFITFPSVCD
ł		l			l	RFGNWLRSGRCSHAARKNEITL
	1	l				TNTRRSLRPKRNTERHDMQTR
		1			l	ATVIAAGEKLLPYAETLMSTW
}	i		İ			OAARKEVAHTSRHNEFSIGASA
1	1		1			SLWDMVMTSAGAVVTTVVVA
					İ	VRPSSFYILCSHKKKRTLHTKR
			1		ĺ	EKTVDRRKEYETRAKRSETDT

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence	1	
24783	55151	A	24921	110	1282	SNTPYLKENKMELKKLMGHISI
24/03	122121	^	24921	1110	1202	IPDYRQAWKMEHKLSDILLLTI
		1				CAVISGAEGWEDIODFGETHLD
		l l				FLKQYGDFENGIPVHDTIARVV
		l		l	İ	SCISPAKFHECFINWMRDCHSS
		l				DDKDVIAIDGKTLRHSYDKST/
		1			l	RRRGAIH\VNNAFSTMHSLVIG
		l			ł	OIKTDKKSNEITAIPELLNMLDI
		1				,
						KGKIITTDAMGCQKDIAEKIQK OGGDYLFAVKGNOGRLNKAFE
		l		ĺ	}	
ł		1				EKFPLKELNNPEHDSYAMSEKS
		l				HGREEIRLHIVCDVPDELIDFTF
		1				EWKGLKKLCVAVSFRSHAEQK
						KEPEMTVRYYISSA\DLTAEKFA
		1				TAIRNHWHVENKLHWRLDVV
		l				MNEDDCKIRRGNAAELFSGIRH
		1				IAINILTNDKVFKAGLRRKMRK
		_				AAMDRNYLASVLAGSGLS
24784	55152	В	24922	258	507	
24785	55153	Α	24923	1	3060	MTEIEENMLLPISGQELPIRWLA
		l			l	QHGSEKPVTHVSRDGLQALHIA
		l			i	RAEELPAVTALAVSHKTSLLDP
		1				LEIRELHKLVRDTDKVFPNPGN
		l				SNLGLITAFFEAYLNADYTDRG
		l				LLTKEWMKGNRVSHITRTASG
l		1				ANACGGNLTDRGDSFVHDLTS
		1			l	MARYVATGVLARSMGLVIYSFI
		1				QHTLTLEEYREITAFLFREFTHA
		1				AAARYTGEQETLPLSPQWILRQ
		l			ŀ	CKEVASLCDGDTFSGEQLNLM
						LQQREWREGFLAER
24786	55154	В	24924	56	967	
24787	55155	В	24925	1	1776	
24788	55156	A	24926	1	864	
24789	55157	Α	24927	424	513	
24790	55158	IA.	24928	1	5049	l i
24791 24792	55159	В	24929 24930	1	939 1837	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24793	55161	A	24931	I	2249	MLPDIARFLPRLANDQIEEFTW YVNHFTYSNAIKIFCYQMFLAS TQARASGAPLQRLFRAIGGNA WERPFRMVFCSAAFSEESSPFR
						ETNYEPQLFLGFATDYRFAGW TLRDVEMGYNHDSNGRSDPTS RSWNRLYTRLMAENGNWLVE VKPWYVVGNTDDNPDITKYM GYYQLKIGYHLGDAVLSAKGQ YNWNTGYGGAELGLSYPITKH
						YNWNTGYGGAELGLSYPITKH VRLYTQVYSGYGESLIDYNFNQ TRVGVGAIGVNVAQAEVLNLE SGAKQVLQETFGYQQFRPGQE EIIDTVLSGRDCLVVMPTGGGK SLCYOIPALLLNGLTVVVSPI.NS
						LKEKSANPFEFTFAAFAHAFHW VIQAIGMINTPADGSTHKQART SWLPYSSLPVLSVSTQDEKAKK KMRFMQRSKDSLAKWLSAILP
						VVIVGLVGLFAVTVIRDYGRAS EADRQALLEKGNVLIRALESGS RVGMGMRMHHVQQQALLEEM AGQPGVLWFAVTDAQGIIILHS DPDKVGRALYSPDEMQKLKPE
						ENSRWRLLGKTETTPALEVYRL FQPMSAPWRHGMHNMPRCNG KAVPQVDAQQAIFIAVDASDLV ATQSGEKRNTLIILYALATVLL
						ASVLSFFWYRRYLRSRQLLQDE MKRKEKLVALGHLAA/GVAHE IRNPLSSIKGLAKYFAERAPAGG EAHQLAQHVQIRRFHAHHPAS

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24794	55162	A	24932	261	2115	TLVFCWHAKLLSHGVFMDIISV
						ALKRHSTKAFDASKKLTPEQAE
						QIKTLLQYSPSSTNSQPWHFIVA
					1	STEEGKARVAKSAAGNYVFNE
			l			RKMLDASHVVVFCAKTAMDD
					i	VWLKLVVDQEDADGRFATPEA
			ŀ			KAANDKGRKFFADMHRKDLH
					l	DDAEWMAKQVYLNVGNFLLG
			i			VAALGLDAVPIEGFDAAILDAE
	İ					FGLKEKGYTSLVVVPVEDLAGI
		1	İ			EIDHTTSMVMIFGIIFLTAVVVH
						IILHWVVLRTFEKRAIASSRLWL
						QIITQNKLFHRLAFTLQGIIVNIQ
					i	AVFWLQKGTEAADILTTCAQL
						WIMMYALLSVFSLLDVILILGQ\
						KFPA\AFQLPLKG\IFQGIKLMGP
						ILVGILMISLLIGQSPAILISGLGA
						MAAVLMLVFKDPILGL\VAGIQ
1						LSANDMLKLGDWLEMPKYGA
				ŀ		DGAVIDIGLPTVKVRNWDNTIT
						TIPTWSLVSDSFKNWSGMSASG
						GRRIKRSISIDVTSIRFLDEDEM
					1	QRLNKAHLLKPYLTSRHQEINE
						WNRQQGSRESVI\NLRRMP\NIG
					i	\TFCAYLNK\YLGTH\PRIRKDM
						TLMVRQLAPGDNGLPFEIYAFT
1	ľ				1	NTVVWLEYESIQADIFDHIFAIV
i						EEFGLRLHQSPTGNDIRSLAGA
						FKQ
24795	55163	Α	24933	1	757	
24796	55164	A	24934	8	343	
24797	55165	A	24935	I423	1761	A CONTROL OF THE CONT
24798	55166	A	24936	1	851	MKGDTKVINYLNKLLGNELVA
			ŀ			INQYFLHARMFKNWGLKRLND
			İ			VEYHESIDEMKHADRYIERILFL
			i			EGLPNLQDLGKLNIGEDVEEML
		ļ	ŀ			RSDLALELDGAKNLREAIGYAD
						SVHDYVSRDMMIEILRDEEGHI
						DWLETELDLIQKMGLQNYLQA
	l		l			QIREEGKSIYQEQTTAMKRPDY
		1				RTLQALDAVIRERGF/EARGTK
1		l	l	l		AVHYTISRLTAH*ATGKYVRAA
1			l	l		AVGAYRTAAPDGTRAKTAGTA
1		1	l	l		APGGVAGRRVAGR*TNRFDSA
						AAFTGGQRRQSGDVVASCTGS
	L		L	L	l	CVG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2.4700	100160	<u> </u>	0.1000	11645	2009	I PVFIOFVEGMCGTANEPACLLV
24799	55167	Α	24937	1645	2009	
						NQSPAIYFPGKIAAIWQNPRHV
						ESGSM*TL/IDSD*VSPTECLSPR
		l				HHYMPFEEAARGYEIFEKREEE
1						CRKVILVPGAQSAEAAQKAVS
		<u> </u>				GLVNAMPGGTI
24800	55168	A	24938	1	3936	
24801	55169	Α	24939	1	2240	MRSPMTRNSRNGKHDYKPPPR
		1				KRRQPPHDHTAPNSTPARNQRO
		1				RPHRPNRQAGQREQRANNPTP
			1			NTPSPPPTNDPAEPHQTRHDSR
						QPHNTPPAYAELVAAALLTTDT
						NVTRRRLRYMQPDTKLCHSAG
	1					KSIYQEQTTAMKRPDYRTLQAL
						DAVIRERGFERAAQKLCITQSA
		1				VSQRIKQLENMFGQPLLVEDET
1		1				RTQERLRRGEVVGAVSIQHQAL
		l				PSCLVDKLGALDYLFVSSKPFA
1		l		ļ		EKYFPNGVTRSALLKAPVVAFD
		1				HLDDMHQAFLQQNFDLPPGSV
		l				PCHIVNSSEAFVQLARQGTTCC
1		l				MIPHLQIEKELASGELIDLTPGL
l	i	1		İ		FORRMLYWHRFAPESRMMRK
	1	1				VTDALLDYGHKADDIILRITAT
		1				AICGSDLHLYRGKIPOVKHGDI
		l				FGHEFMGEVVETGKDVKNLQK
1						GDRVVIPFVIACGDCFFCRLQQ
1	1	1				YAACENTNAGKGAALNKKOIP
						APAALFGYSHLYGGVPGGQAE
		1				YVRVPKGNVGPFKVPPLLSDD
1		l				KALFLSDILPTAWQAAKNAQIQ
	1	1				QGSSVAVYGAGPVGLLTIACAR
	1					LLGAEOIFVVDHHPYRLHFAAD
1		1				RYGAIPINFDEDSDPAQSIIEQTA
1			ł			GHRGVDAVID\AVGFEAKGSTT
1		1				ETVLTNLKLEGSSGKALRQCIA
1		1				AVKRCGIVSVPGVYAGFIHGFL
1		1				
1	ŀ	l				FGDAFDKGLSFKMGQTHVHA
		<u>_</u>				WLGELLPLIEKGLLKPEEIVTHY
24802	55170	Α	24940	687	792	TPTLTRPLRHPVAYRATLK*NR
				L		PAKVSQLCCTNA
24803	55171	Α	24941	3	510	AGDMVWLCVRTQISY*IPRTHP
		1			1	AVGIPRERPLRGADTPQRGASH
1		1			1	RIRGEGKRK*KRWALLCCPGCN
1	1	1				I*RHFCHHN*ERYFW\IYWVEST
1	1	1			1	GAVKHLQNTGHWLNAGALPV
1	1	1			1	RRPRKSVTGSIARQ\VSVPISAR
1				1		ALLACPCGQCAGYATQFVMKS
		1				ITORFNVACRTRMYAVG
24804	55172	l <sub>A</sub>	24942	189	563	
£4004	100172	l''	2772	1.07		L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24805	55173	Α	24943	1224	1772	GSPSVSLATSSCSIKVQNPGISR
						VVAGSSAIISNVSPGCILRTVLR
		ŀ				TIITGSGQRRPSASSVWSGHTSC
		l				VFRTANFSSGMVNLSVSVTNLS
	Į.					PSIVPRIKFIAGDPINPETNIFAG
1	i .			l		WL/VNGFRRTYLLNNPVFHNH
l	I	1		i		NPRRHGHRFGLIVGHVDHGGV
				l		QFLMQLADLCAHLHAQLGIKV
24806	55174	Α	24944	1541	3675	LEHKRKISMRRNWMHSHTRY
	i i					WRFLDFPTLRGGRWMR*SGEK
	1	ı				LNPISTPLRANCLALAQRATRL
						APMSFTWGMPTSQPDCAVPGR
		1				RALPPELLCLQRSSQSRFAGTAI
			1	1		T
24807	55175	В	24945	1	1497	
24808	55176	Α	24946	650	739	
24809	55177	Α	24947	4447	4804	RQNDRYSGRERHEITPLCW*IPR
						IAWALWLRSLRRGPQEKSLHN
						RVARTISWPYQARHPCRTLLGG
		1				HGFFLHIVLSQLPCLSYPLSSFA
						GLLARSSMFLKLAARFLCCRRS
						YAASPLSI
24810	55178	Α	24948	1	3774	
24811	55179	Α	24949	431	949	NYAIYHQNHGVNISPGLGKTHN
l	1					YRQQHCGITYYWRDLMPANK
				1		NYKQRWITPGSASFYRSSHKAL
				1		IRLLATRLPAFPWGRRSAWRWP
		1				VRY*IRVPSSGSYHLEISMRWVI
		1			1	FPQPKALTPSNLHWKTA*LWS*
					1	KTLSFVCWIATVLPARFWKLTD
						PWLAILPCANIYWQASAPD
24812	55180	Α	24950	337	648	

SEQ 1D	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
		<u> </u>				
24813	55181	A	24951	1	1430	MFTYPHSKFRVNRFVGQVLLIE
					i	FSILLDGGRTGLGHSLSVWCISG
İ			ĺ			DCSSFLQGKPTSLPLRKPSAIICS
ł	ŀ					DSLSGSADLLRNHNFVCTAADT
İ						FTTDITPEAGDARLIGIAQTVRH
						LEDPMRAWKSIHKSCEILDPIHR
l					l	APVKENTHPARKINISDPAAGA
						VARIRYEGVLSVCRASASAYVS
l	l	1	ŀ			RSRTITVACWYVSNTGVTGATI
	1	l				GVKRQHRHARLFSGDGAPGFG
İ						TGKRDIRQLRRLVRIQIQRTFFA
						AVLHVPTPWSRAIDAAALLTVI
		l				DVKVLTACACQACRTLALRVA
	ŀ				1	QVIDRCSNPGDIMSSVARRYWF
l						ISRWSAKRDCAVSYDQDPGQA
						ORSCRSCLVAVDRGLWLSAYC
l						RSLMTQTLLPDDVPRILPNASSP
i						SRLRCL\HIWVITACWICANSSG
		1				FIARNL/GLCGWEKRLVKDLTRI
1		1				ODTGRAKEILGATATLEFR\R*T
1		l l				PTLTRPLRHPVAYRATLK*NRP
1		ı				AKVSOLCCTNA
24814	55182	В	24952	1	1295	ARVSQUEETIVA
24815	55183	A	24953	3151	3207	LQWLID*WCL**TFDLRFA
24816	55184	A	24953	2740	3917	NGRSVWAVKLELFRVKPLDIPO
24810	33164	l <sup>A</sup>	24934	2740	3917	QRVGQQHVLLKAFNRRLAMQF
		l				
		l				IQLIATDVTEILPLHVVEDGTDS
		l				LYCLALSHLRCGRLSLRWRREL
1		ı				PRGLGVNVSWCYPFKAQGQCA
1		1				AEITDKAGQREIFGFARVKENA
1		1				GYVIYECYQPDDGDKLIRELPF
1		1				SSLIFARQWFVVGELLQHLPPE
1		1				DRITPIVGMLQGVVEKGGELRV
l		1				EVADTNESKELLKFCRKFTVPL
1		1				RAALRDAGVLANYETPKRPVV
		1				HVFFIAPGCCYTGYSYSNNNSP
		1				FYMGIPRLKFPADAPSRSTLKLE
1	1	1	1			EAFHVFIPADEWDERLANGMW
						AVDLGACPGGWTFQLVKRNM
		1				WVYSVDHGSMVQ/SLWITTGT
						CWGTRFHSARGOKFPEVLOGS
						QTLPAATDPPGMQWLASGVLE
24817	55185	A	24955	1	519	
24818	55186	A	24956	510	731	
27010	55.00	<u></u>	1-1,550	1	1	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24819	55187	Α	24957	ī	1055	MRLCPEKTTKAKRVKAVLAWS
		1				KEEPWLSEWSEEVLEMGYKKL
ĺ	ŀ					GDFSTAGAILETEIRPSPASAFTL
		1				DSQPPESNNLSEAKYAPNNIESI
		1				AKYFAPKSPMFSESPSGTALDS
1	l					FNRNERRRWPLWPNKSGFGSD
		1			1	LTLSKIGISSPDIALERLYEQAR
						KLSGKFRALSELDESARSGVLK
ĺ	1	1			}	VLCAFAYQDYSRSAASTRKCD
		1	l			CCDGGGFTEAQVFTNKVSYPW
ŀ	l	1				GKPPYWSKMSRAVRPSDWESW
			l			TQAREVVRVKCKPCNGKGVIS
						NSCRCHGKGKVLAKHESDRRG
		1	l			VPVMKACDRCGGRGYARLKFS
		1	İ			SV\MRALILLRRLKKTAAYEQL
	1	l				QPLFEELVAECHKQESMADSIL
						SKVTR
24820	55188	Α	24958	361	725	
24821	55189	Α	24959	1100	1738	WQRSTLPLLFESAMQTGVNAG
		1				NPVAW*KSAGYGHIKLYDAKN
	1	l				RL\LVQSTALWASQLVQYLSTF
	ł	1	ŀ			FRKNLKRPSEFVTLADEIEHVN
						AYLQIEKARFQSRLQVNIAIPQE
	İ					LSQQQLPAFTLQPIVENAIKHGT
						SQLLDTGRVAISARREGQHLML
	ł					EIEDNAGLYQPVTNASGLGMN
					i	LVDKRLRERFGDDYGISVACEP
		Ļ.				DSYTRITLRLPWRDEA
24822	55190	A	24960	1	2043	WINDLAND FINANCIA DI LI SOCI
24823	55191	Α	24961	2164	2487	KLKRIARHNFHGIRDLHLFQQV
1		1	İ	1		NRFSSGFPTTYWLMMADHVHH
		l		1		LKTYSTCRIEGGHRFLKDHRHS
		l		1		CAAPLTKLFFPRVKNIFSQQGN
	L	Щ.	L	L	l	LPPMYAITARR*QTHNQHCGD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24824	55192	A	24962	128	2574	QVVVVMAMVAKVVIDIVVVV
24024	33192	^	24702	120	2374	GVEMIRVKVVAIVVEVVVVEV
						VVVMVAWWW****WW*/DMG
						EARWWWEYGVWEVEPEIILNA
ł			l			POOYLLAGIGDTLAKWYEAVV
1		1				LAPQPETLPLTVRLGINNAQAIR
		1			ł	DVLLNSSEQALSDQQNQQLTQS
						FCDVVDAIIAGGGMVGGLGDR
						FTRVAAAHAVHNGLTVLPQTE
						KFLHGTKVAYGILVQSALLGQ
1						DDVLAQLTGAYQRFHLPTTLA
			Į.			ELEVDINNQAEIDKVIAHTLRPV
			1			ESIHYLPVTLTPDTLRAAFKKYS
						QSCFVIRLGGDFIHQLAENHIVI
						FVNNHNGTRCQTFQWAISNCH
			1			TVSLQKFSVRKFLSDLFAIGGR
				l		RGVRPPTEAPGHQKSDNQAHV
						SVSFDGLDLVFFVVNQWAGVV
		l				FCFDLFSRKRGRFSVWRNKGFG
				l		RYCQRLANFRDRQAFQLLNQIH
						FTRCKQVDNGGTEFKATHFLAF
						QQCHRTVVFPGRPAIKTRVERL
						DRYRNRMEKSNGQANLRVHG
						GTWEKLVLQLDSAGMVNRVSS
						VGAPLREPIPTEGKGAKEDTWG
						NLSSNDPLLEAFGGQFGIAISMH
						QTLATRGGKRNARPTTRPRFHR
						GTNPRGIAPHIGTANARYSTGH
		-				CPVALPFGLRGPPLARENVATA
	l					TKGHESASRETEVVAVAKLTSR
		l				VLLICDATHALPIQVLRNDIRVI
		l				AAGNGCTDDLOLEHLPANTDIR
24825	55193	A	24963	117	335	PGLAPATRRSTPGRFNADAGAD
1		ľ.	[	l		*RRAAGTGAGRAKRRGVGIHR
			1			CLADPFLADCRNAGLRGAALC
1						GTAAASGK
			i	L		UIAAASUK

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon fur last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24826	55194	IA	24964	208	1903	YLAIKTERCLHDEFTDEOLSRA
24620	33134	^	24904	208	1903	VWIYGKRAIAAAQTKLPPAFGL
				į.		
				Ì		PGAKHILFRGHCSESDVQQLAA
		1		ŀ		ESGDDRSVVIGVGGGALLDTA
1						KALARRLGLPFVAVPTIAATCA
l				ŀ		AWTPLSVWYNDAGQALHYEIF
ı				1		DDANFMVLVDPEIILNAPQQYL
		İ		1		LAGIGDTLAKWYEAVVLAPQP
						ETLPLTVRLGINNAQAIRDVLL
						NSSEQALSDQQNQQLTQSFCDV
				1		GDAIIAGGGMVWGLGDRFTRV
						EAAHAGPNGLTGLPQTEKFLH
			ĺ	1		GTKVAYGILV\QSALLGQDDVL
l				1		AQLTGAYQRFHLPTTLAELEVD
I		1				INNQAEIDKVIAHTLRPVESIHY
		ı				LPVTLTPDTLRAAFKKLIQGLIS
						AEQLAQALAEQNGVAWESIDA
		1				WQIPSSLIAEMPASVALHYAVL
		1				PLRLENDELIVGSEDGIDPVSLA
		1		1		ALTRKVGRKVRYVIVLRGQIVT
		1				GLRHWYARRRGHDPRAMLYN
		1				AVQHQWLTEQQAGEIWRQYVP
		1				HQFLFAEILTTLGHINRSAINVL
		1				LLRHERSSLPLGKFLVTEGVISO
		1	Ì	1		ETLDRVLTIQRELOVSMOSLLL
		1				KAGLNTEQVAQLESENEGE
24827	55195	В	24965	31	205	
24828	55196	В	24966	69	402	
24829	55197	В	24967	1	721	
24830	55198	A	24968	1	1703	
24831	55199	A	24969	2853	2889	LIIGLDLPAVSAIFQRALRFTHV
				1		GIADGGAYVVQR/HRPDEPRRR
0.1000		ļ.	21050	207	400	CCSE
24832	55200	A A	24970	297 1179	2148	CQVLRPRTKRLNVLFLHRMQH
24833	55201	A	24971	1179	2148	
				1	i	QWRQRELVHNMCFVIACAKRK
				1		RAPFVQAAEEV\RPGQHDDEFP
						LAIWQTGSGTQSNMNMNEVLA
						NRASELLGGVRGMERKVHPND
			1			DVNKSQSSNDVFPTAMHVAAL
		1				LALRKQLIPQLKTLTQTLNEKS
						RAFADIVKIGRTHLQDATPLTL
l		1	1			GQEISGWPASRSGTGSWRYSGG
l		1				YWTKYPSGVCASRSKMNWYST
l		1		I		RASDGGHASDAVRTAQAADRE
l		1			1	LRAPVRDELNASITSKTRLAEST
		1		1		SLAEWVKASPHDDDKPILLPGE
ı		1		1		WEVNTRRERQKQGIPLDAGSW
1		1		1		QAICDAARQIGMPEETLQAFCQ
l		1			1	Q
	·	_			1	L'

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24834	55202	I <sub>A</sub>	24972	166	365	NPFSNSPWETYPVAFTIPLALFM
2-105-1	55252	ľ.		1.00	505	GIYLRYLRPGRIGEVSVIGLV/SP
						DFRHYLWRLGGRKSDLGTVL
24835	55203	A	24973	83	362	KPPCFLOASVTCWLRLPFASMII
	50200	· ·	2.075	00		LPPCACS*ST*ESIRPAVVGPREP
ł						EGITFRRFGRTRVVNRMIFDVL
						RHLFTVIHPLFQFGVTYITTDDN
24836	55204	A	24974	584	853	
24837	55205	A	24975	1	3017	MSODPFOEREAEKYANPIPSRE
						FILEHLTKREKPASRDELAVEL
		l				HIEGEEOLEGYAPVLAPESGILI
1						MRPTLTMPALTKFVDGTGPVW
		l				TGNLFPFLFITIACGAVSGFHALI
		1				SSGTTPKMLANEGQACFIGYGG
		1				MLMESFVAIMALVSACIIDPGV
l		1				YFAMNSPMAVLAPAGTADVV
						ASAAQVVSSWGFSITPDTLNQI
l						ASEVGEQSIISRAGGAPTLAVG
		1				MAYILHGALGGMMDVAFWYH
l		ŀ				FAILFEALFILTAVD
24838	55206	Α	24976	3	206	EPDFLPL**RRNHEQNYRDGKC
						TGSYRSLRTGR*SGQYDHHLRS
						DPGKSENGRSTGRRRCTGTSVA
						G
24839	55207	Α	24977	3	982	GDAEPFVFLPR\RKDHEYSLDH
						YQHRFYLRSNRHGKNFGLYRT
						RMRDEQQWEELIPPRENIMLEG
						FTLFTDWLVVEERQRGLTSLRQ
1		1				INRKTREVIGIAFDDPAYVTWIA
						YNPEPETARLRYGYSSMTTPDT
						LFELDMDTGERRVLKQTEVPGF
		1				YAANYRSEHLWIVARDGVEVP
		1			İ	VSLVYHRKHFRKGHNPLLVYG
				1		YGSYGASIDADFSFSRLSLLDR
		1				GFVYAIVHVRGGGCKINLVVD
		1		1		NGKIVRAEAAQGKTNQGTLCL
l		1				KGYYGWDFINDTQILTPRLKTP
		İ		1		MIRRQRGGKLEPVSWDEALNY
l						VAERLSAIKEKYGPDAIQTTGSS

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	1	09/540,217	sequence	or pepude sequence	deletion, v-possible aucleotide insertion)
		1		sequence		
24840	55208	IA	24978	1339	3640	SPLSTAGISICGPLLIITDVDLGT
		1				TVAGIKGMIATGEGTTEWNSV
		1				MVAMLLTLIPPVVIVLVMORA
	1	1				VRGLVDMRNKMAGLKLQAVT
		1				KSWDGKTQVIKPLTLDVADGE
	1	1				FIVMVGPSGCGKSTLLRMVAG
		1				LERVTEGDIWINEORVSELRLIC
		1			1	YMSRKMGGGKNRREPHIDVKE
		1				GIFGLSITPEFSEPLAEDFLSRRC
		İ				YGIRFRNLETGNWYPELLDNV
		1				PSFVWANDSWIFYYVRKHPVT
	1					LLPYQVWRHAIGTPASQDKLIY
						EEKDDTYYVSLHKTTSKHYVV
						HLASATTSEVRLLDAEMADAE
		l				PFVFLPRRKDHEYSLDHYOHRI
	1	1				YLRSNRHGKNFGLYRTRMRDE
	1	1				QQWEELIPPRENIMLEGFTLFTI
						WLVVEERQRGLTSLRQINRKT
	1					EVIGIAFDDPAYVTWIAYNPEP
						TARLRYGYSSMTTPDTLFDLDI
	1					DTGERRVFKPPE/V/PGFYAA/SY
						RREPRW/IVSADGVKYSFV\APR
	1					OHFRRDAPVLSFLLFSDRAPFR
						NNGPRVVLLLGYYHPELLGVT
		1				YSOLSVHEARPKPLPIPHSRHRI
						VPTRNEMAQEKERPAGSQSLFF
	l	1				GLMLIEILSNYPNGCPLAHLSEI
		1				AGLNKSTVHRLLQGLQSCGYV
		1				TTAPAAGSYRLTTKFIAVGQKA
		1				LSSLNIIHIAAPHLEALNIATGET
	ŀ	1				INFSSREDDHAILIYKLEPTTGM
						LRTRAYIGOHMPLYCSAMGKI
21211	55000	١.	24070	1	240	LKTRATIOQHMFLTCSAMOKT
24841	55209 55210	A	24979	839	248 1625	PDAFILTTKPAGAIPTSTSITRPI
24842	33210	I <sup>A</sup>	24980	839	1025	
		1			1	FCPSFAPCENATPAAET/HQRNT
		1				RPEWRFTFAFFLFAIFRNAVNT
		1			1	VTMSIRKGIGVHHNAANLVPW
				İ	1	MTKFFQRFGIAFQSRGAVFHQF
						HHAGYAGQRGKTALAEQRLVI
					1	GFGINKQMRAVPLIGEVYQFSG
						*CQRQSFTADGFTDSNAFNNIS
		1				GNSTARDKLFIAGYGNRYFHC
						GVNAQIIFMQELGDFRHFVIF/A
						QKGNEYHGDTRISPGRFRRGH
	ļ	١.				PLGALRLAASVERSGNGHRA
24843	55211	Α	24981	2538	2864	GSSLINSKVMP/SF*QQNRKFAY
	1	1				KRAGVATDEFHAESFVRGRAP
		1				MKRKL*LFMQLGGDVIQPFDGI
		1				IAGNTVYRCQQLAVGDAVGKI
	L	-				LHNRYAFRQQSTVIQQQCRHLF
24844	55212	A	24982	1	1281	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	ł			sequence		
24845	55213	Α	24983	1	2180	METLNLYADLRSVTGEALLLL
						DEPGVGVDPISRRELWQMVHE
		l				LAGEGMLILWSTSYLDEAEQCI
						DVLLMNEGELLYOGEPKALTO
		l				TMAGRSFLMTSPHEGNRKLLO
		l				RALKLPQVSDGMIQGKSNIVGI
						KDTIDSVGHLRTMINTVKSVRP
	i	1			ł	SFSVFCGYDDHLLNTMLLGGD
		1			1	GAITASANFAPELSVGIYRAWR
						EGDLATAATLNKKLLQLPAIYA
	1	1				LETPFVSLIKYSMOCVGLPVET
		1				YCLPPILEASEEAKDKNRPLVD
	1	1			l	LEHAALQVGKGIIPPPLREYGAS
						EVRSVTRAFNHMAAGVKQLAD
		l				DRTLLMAGVSHDLRTPLTRIRL
	1	1				ATEMMSEODGYLAESINKDIEE
		l		1		CNAIIEQFIDYLRTGQEMPMEM
						ADLNAVLGEVIAAESGYEREIE
				İ		TALYPGSIEVKMHPLSIKRAVA
	t e	l		l		NMVVNAARYGNGWIKVSSGTI
						PNRAWFQVEDDGPGIAPEORK
						HLFQPFVRGDSARTISGTGLGL
				1		AIVORIGDNHNGMLELGTSERG
l						GLSIRAWLPVPGTRAOGTTKE
						GAREDAVEFFAKLGFVNQGEIT
						TPTTTPIRHFLMIKPVATLDDIL
				i		HRGDWCAQLQQAWYEHIPLSE
		1				KMGVRIQQYTGQKFITTMPETO
						NONPHHTLFAGSLFSLATLTGW
						GLIWLMLRERHLGGTIILADAH
		1				RYSKPISGKPHAVADLGALSGD
				1		LDRLARGRKARVQMQVEIFGD
24846	55214	Α	24984	875	1150	
24847	55215	A	24985	1507	1974	
24848	55216	Α	24986	1	1006	
24849	55217	A	24987	1491	1703	RECRYATNGKNNGCCRSAGSD
				ĺ		FSSRLRYVR*PFIYTQ*SCGIGH
		1			l	CPGTDIRAKIRRTARFIKNYGTY
		1				CPS
24850	55218	Α	24988	I	1758	
24851	55219	Α	24989	1773	2165	PSRGVEVNSGWNWQATNRRVI
		1				RNFDDLDQLIIPGTARNAQTCIF
		1		1	1	NFVTVTMTLNNCRRIVQLANQ/
	1				1	DYRQPTGTAVAETHGTAEIALL
				1	1	ATNFNVA VFIAPLGNQRHNRVI
1		1		1	I	TVWHKFRRVGVLHVGNMASVI
		1		l	1	N
24852	55220	Α	24990	1	141	SPGKIRPVIAAAMKQIKEFMSP
						DSDFFRYMKTPTSATR*YNDCG
		1	1	I		TGQ

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24853	55221	A	24991	1430	1933	PHVCMGSLTMPDSACMAPFPPS
				l		AVRRWNSSFPPTFSAHTSSPCA
Į.						CYPRCYRTVKGVL**HHR*W/V
						LISTPGRGAYAASKYALEAWSD
İ						ALRMELRHSGIKVSLIEPGPIRT
		1		l		RFTDNVNQTQSDKPVENPGIAA
		1				RFTLGPEAVVDKVRHAFISEKP
	}			1		KMRYPVTHGDLWR
24854	55222	A	24992	1318	4265	LAIVALFLDLQNHIFSKGFWPS
		ŀ				DKFYAAKVEEQNQRHQRYHGT
		l				SYNLEPDIKSSPGGLRDIHTLO
		l				WVARRHFGATSLDEMVGFGFL
						TSAERAELNECLHILWRIRFAL
					l .	HLVVSRYDNRLLCVHPTLLTTL
		[				DIHGEAQIWRREVSSRYGQYPK
Į.		ı		l		AQAAQPDQLMSDYFFRVSLAM
		1				QNKTLLFSLDDTLVNNALQTLN
		l				KTRPAMVDVIPTDGIVPLYINPQ
		1			1	GIAKLLRNETLTSLPKNLEPVFY
		ŀ				NAAQTLLMPKLDAL
24855	55223	Α	24993	I	454	MGFDDTRDRALFEDSAMSQQP
		l				TVPDRLRWLLQTFKYQKNIRI*
				l		STPRKKPMRHSIWNIWGSRRC
		i				WSNPKRTFMSISVRGNMAAIM
		l				SFHTSAVMRSHCSILTTIKSRW
		1				ATLNTLILR
24856	55224	Α	24994	65	330	
24857	55225	В	24995	1	1998	
24858	55226	Α	24996	1175	1877	QQVPQKGPGRAKRHLHAAGW
						HWHQRDRCPEEKNVRQ*RRYR
						AVRFIII
24859	55227	В	24997	I	3117	
24860	55228	A	24998	1888	2412	ARFKHVGDGTVTHRLFRRAAQ
		1				IVRVV*RAVSHRQHFTGVDIHQ
		1		ļ		HGATRFSLVKGHRIVQFAINQR
1		1	1		1	LQAFINTQRQVVRSLAVSRRNI
1						FNYATIAVFTHNALTRLPGKPFI
1	1	1	1		1	ETLLNALNPLTEHAARDLEDSP
1		1	1	1		VRITAYIEDVDALAQAGADIIAI
						DGTDRPRPVPVETLLARIHH
2486 I	55229	A_	24999	I	2457	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	-			sequence		
		L				
24862	55230	Α	25000	1	3019	MAALRQSFWSQLFDRVHIGLD
		1				FFDASINRIAAWVIGTRNMKKA
		1				LLRALLEPTAELRNWKRRAITL
		ĺ	1			RVWHCWKSRNRCRGRRSGKCI
						ANVTIROODHOIETVFINORLH
				i		ERMFPPFVLFAERLSGDEDLGL
						KAPILEALNDLGYEKPSPIQAEC
			İ			IPHLLNGRDVLGMAQTGSGKT
				ľ		AAFSLPLLONLDPELKAPOILVL
					i	APTRELAVOVAEAMTDFSKHM
1						
	ļ		1			RGVNVVALYGGQRYDVQLRA
						LRQGPQIVVGTPGRLLD
24863	55231	A	25001	60	545	PSPFTAGASMAVERSTG\HEGE
1			ļ			LVLETLVIDGDENT/CAGTRRSL
						RANA*CLFHPFRAGAEKLAEEV
						WFCRYPHCGCEQNTTTEEQRR
			l	l		TEWMVTESLADFLDPHDPGKT
				l		VEGYPAPKRARNRNRAEDHRQ
l		l		1		RLRHRTRKKQTHGQRRRHRPE
1	-		l	ŀ		PAQRQPQTGTTD
24864	55232	A	25002	1410	1575	<u>````</u>
24865	55233	A	25003	200	691	
24866	55234	A	25004	1336	2028	
24867	55235	A	25005	1	345	
24868	55236	A	25006	671	1204	RTSDKLPFCRRSRMENLARFLS
24000	33230	ľ.	23000	l***	1201	TTLKQLRQQRGWSLSRLAEAT
l	1					GVSKAMLGQIERNESSPTVATL
				1		WKIATGLNVPFSTFISPPOSAT/P
						SLFPYDPQLCFEHLAIQMASGAI SESTPHEKGVIEHVVVIDGQLD
1				l	`	
						LCVDGEWHTLNCGEGVRFAAD
1				1		VTHIYRNGGEQTVHFHSLIHYP
		_				RS
24869	55237	Α_	25007	2251	2466	
24870	55238	A	25008	181	626	WQNFDTCGGDMLDKLDAALR
1					1	FQQEALNLRAQRQEVLAANIA
1				ŀ		NADTPGYQARDIDFASELKKV
i						MQRGRDATSVVALTMTSTQHI
ł						PAQALTPSTAELQYRI\PANPSL
[						DGNTVDMDRERTQFADNSLQY
				l		QMSLSALSGQIKGMMNVLQSG
						N I
24871	55239	Α	25009	57	278	
24872	55240	A	25010	171	532	KPVOFAIADGNNOPLALLNIHL
	1	Γ.			I	PVMMLAIAHGPLLPAFPPELLV
			l	ŀ		LFDDS/PLSSRVLLINAFSGGSDT
		l		ŀ		AMRRAGKGAPAFLLPELPIITV
		1	l	l		VSPFLPOSSPRRKPIMSKRIPSAV
			l	l	I	
		ļ		l		NQRNPRQ
24873	55241	Α	25011	I	648	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		•
24874	55242	A	25012	158	514	VLOLIKAVWTORTOKPSWLHP
24074	33242	ľ	23012	130	511	VDSAPGLOMELPASPVPCTCTP
						OPLGGRWDWALWSRGWRLLR
	1	1				RLGPHRSPRRS*GSGLWPWPAQ
		1		l		KGAPIVORWAKGLLKCHOSGS
		l				PGRGGAESERGL
24875	55243	A	25013	1	693	
24876	55244	A	25014	119	304	DRRRCAHKITVIPKRMTIAGIRL
						PPOTVNI*LGNFLRALIASTAGI
		l				MTAQMVAHSPAPPIP
24877	55245	Α	25015	361	540	
24878	55246	A	25016	191	446	AKRRLGVYDADCCSIDKTQSLS
	į .					ACTTRNCGAYSKCLCGKYAKP
						VGGIPQPLQESHVR*CCNVMEL
l	1					SPCSDFT**HPPGAVSQPQT
24879	55247	Α	25017	1	2259	
24880	55248	Α	25018	1	1170	
24881	55249	Α	25019	3	1240	
24882	55250	Α	25020	1	1259	MAGPRYPVSVQGAALVQIKRL
	l	l				QTFAFSVRWSDGSDTFVRRSW
						DEFRQLKKTLKETFPVEAGLLR
l	ŀ					RSDRVLPKLLGQASLDAPLLGR
						VGRTSRGLARLQLLETYSRRLL
		ı				ATAERVARSPTITGFFAPQPLDL
		1				EPALPPGSRVILPTPEEQPLSRA
	1					AGRLSIHSLEAQSLRCLQPFCTQ
			1			DTRDRPFQAQAQESLDVLLRHP
					i .	SGWWLVENEDRQTAWFPAPYL
		1				EEAAPGQGREGGPSLGSSGPQF
1						CASRAYESSRADELSVPAGARV
						RVLETSDRGWWLCRYAGAGPE
			1		0.0	ELDTSARNAGALTRRREIRDAA
l				1		TLLRLGLAYGPGGMSLREVTA
		1				WAQLHDVATLSDVALLKRLRN
				1		AADWFGILAAQTLAVRAAVTG
l				1		CTSGK/QIASCRWNSNQCARGR
l				1		QR*MATTYGI*SSYLSVH*F*AN
l	1	i i		1		RQQRR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24883	55251	Α	25021	803	2061	AKPAARGGILAAPVRDTLFLYF
						RLKKNQRQEGFINTYPWPKKP
						GIFYMCVPIKGANAQDVAAFC
						VTARGRQNCLWESIARGPALIN
						NRGAARGRCNDRVVEVDHGFA
		1				VLTFNFQGVSPGEFTQTVDHFD
						FAAFRHTSQTTGQLIDHFLFPGT
						NLVDIGFRFAEDDTVFSQRFGF
						FDNFCYVQQCFRRDTADVQAN
		l				TAKGVVTFYDYGFQTYWVKV
						LDPGSEVVAEAGDGASAIDLAH
i i		İ				RLDIDVILLDLNMKGMSGLDTL
						NALRRDGVTAQIIILTVSDASSD
		İ				VFALIDAGAAGYLLKDSDPEVL
						LEAIRAGAKGSKVFSERVNQYL
						REREMFG AEEDPFSVLTEREL\D
					ľ	VLHELAQGLSNKQIASVLNISE
						QTVKVHIRNLLRKLNVRSRVA
						ATILFQSAAFRSRFRRATSDNV
24884	55252	Α	25022	1	1569	
24885	55253	Α	25023	2151	2709	YLREASETARRQFTLP\VILYNF
[						RDLTGQDLTPETVTRLALQNEN
						IVGIKDTIDSVGHLRTMINTVKS
						VRPSFSVFCGYDDHLLNTMLLG
		ŀ				GDGAITASANFAPELSVGIYRA
						WREGDLATAATLNKKLLQLPA
		ŀ				IYALETPFVSLIKYSMQCVGLPV
						ETYCLPPILEASEEAKDKVHVL
		l				LTAQGILPV
24886	55254	В	25024	1	1201	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24887	55255	Ā	25025	1	2209	MIGEIRDGETAEIAIKAAOTGHI.
1						VLSTLHTNSTCETLVRLQQMG
ĺ						VARWMLSSALTLVIAQRLVRK
ĺ						LCPHCRROOGEPIHIPDNVWPSP
ĺ						LPHWQAPGCVHCYHGFYGRTA
ĺ						LFEVLPITPVIRQLISANTDVESL
ĺ						ETHARQAGMRTLFENGCLAVE
ĺ						QGLTTFEELIRVLGMPHGDGAA
ĺ					İ	MDREENELGVSCIAVPVFDIHG
ĺ						RVPYAVSISLSTSRLKQLYAGLP
ĺ						VWCDGSRFFAQKARAİKCKQW
ĺ						GYVGAKSRQRWLFYAYDRLRK
ĺ		l			i	TVVAHVFGERTMATLGRLMSL
ĺ		1				LSPFDVVIWMTDGWPLYESRL
ĺ		1				KGKLHVISKRYTORIERYNLNL
ĺ		l				ROHLARLGRKSLSFSKSVELHD
ĺ						KAAGGVPVLVRELLKAGLLHE
İ		l			İ	DVNTVAGFGLSRYTLEPWLNN
ĺ		1				GELDWREGAEKSLDSNVIASFE
ĺ						OPFSHHGGTKVLSGNLGRAVM
ĺ						KTSAVPVENQVIEAPAVVFESQ
ĺ						HDVMPAFEAGLLDRDCVVVVR
ĺ						HQGPKANGMPELHKLMPPLGV
ĺ						LLDRCFKIALVTDGRLSGASGK
ĺ	1			•		VPSAIHVTPEAYDGGLLAKVRD
ĺ		1				GDIIRVNGQTGELTLLVDEAEL
ĺ					!	AAREPHISELSAFTFGTGRGYSA
ĺ						AFGVKCPFRKRALSDPCYAMR
ĺ						EVADFLINKGVDGLFYLGTGGE
ĺ						FSQMNTAQRMALAEEAVTIVD
ĺ						GRVPVLIGVGSPSTDEAVKLAQ
ĺ						HAQAYGADGIVAINPYYWKVA
24888	55256	Α	25026	1	3395	MSELPFTIASKRIKYLGIQLTRD
ĺ						VKDLFKENYKPLLKEIKEDTNK
ĺ		1				WKYIPCSWLGRINIVKMAILAK
ĺ		1			İ	VIYRFNAIPIKLPMTFFKELEKT
ĺ		1				TLKFIWNQKGAASRSNPEPKNK
ĺ						LEDHITNSTIYRLSTKSCSVSGL
ĺ						KQTLLAESEALTSYSHRVFSAW
ĺ		1		1		DFGLCGDVHVRLRQRIILYELK
ĺ						GQVPALLLDDGTLLTEGVAIM
ĺ		1		l		QYLADSVPDRQLLAPVNSISRY
ĺ		1		1		KTIEWLNYIATELHKELKFSFH
ĺ						WSTTSHKGLGM
L						WSTTSHKGLGM

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codun, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24889	55257	Α	25027	145	681	FNGATQRIFDARGKPSTYIGSIQ
						HVNADVDQRATTLQFFIGKDTP
						AGNAAATQGAGGGNVNLSQN
						AVGHLFTQLLRIERKTMVKVV
	1	l				GQHLAQFARGIDISRACYHMA
						ARFQCHQGMFVMKTVR*ADA
						NHIRFHCQQHGLRIVPHGCIPVF
						FCQRLPLGKAAVTDSYQFQIRC
						GCSSTKH
24890	55258	A	25028	696	953	LSGLCSVRRAYPGGRSCPGVP*
			ŀ			FVGLVARRPGGG*GSCFVLLHP
						QRSGTGGCL*QPPFPGAGAGRK
						IRECIRVGRSAGHAAGGET
24891	55259	Α	25029	3	506	RGKPSTYIGSIQHVNADVDQRA
						TTLQFFIGKDTPAGNAAATQGA
						GGGNVNLSQNAVGHLFTQLLRI
						ERKTMVKVVGQHLAQFARGID
						ISRACYHMAARFQCHQGMFVM
						KTVR*ADANHIRFHCQQHGLRI
		İ				VPHGCIPVFFCQRLPLGKAAVT
						DSYQFQIRCGCSSTKH
24892	55260	Α	25030	291	560	
24893	55261	Α	25031	63	404	
24894	55262	Α	25032	660	1073	LSHECSFWLTNQLVSPRAQTVS
						GELQPAYAHGVLCRQYPSAFE
						KASETPQSSNPCPSSYTIHPTVE
						NFQTCRNQHLSKGCLINAGRA
						GPSPGTGGWGELEVAAAARLQ
					1	GAWKRHLQSSRPPGQALFASPP
						*WTGSVQ
24895	55263	A	25033	272	511	GSDTALPSAIAAPLLAAMAWLP
						PRERGTLAH/QVLEHYQLAQLP
		1				VSAL/QMPLHCPPQAIAHHQQL/
						EQQALASLQNWGVFHV
24896	55264	Α	25034	1	3300	
24897	55265	Α	25035	1117	1376	PPPIGLTYSSSASPLSLFCTVRKP
			ĺ	1	1	FSRSCW*QTNSNPISSCPELVTP
				1	1	SE*L*PRRSIRLDSLSAVRGFAS
						RIWLSSAITFPSGSLA
24898	55266	A	25036	207	427	DEHLQQRKKPLFLNYGRTEQA
				1	I	SVK*RISWVQNPERSSLC*GILA
						A*NPMSVSGL*LT*HCLSARRY

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Nucleotide Incation of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	1100	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24899	55267	A	25037	2012	2547	LKFARPKLWGIFRNRQYHHML ER\RSOAIDAPALDRGAALGAL
		1				MRLEHPNASAEAALTMLAOLS
		ļ				PAOSGEALHGLLALARHOLAC
	l	ł				OPAFIAGESSHLNOLSEADFINA
l		1				LPDLRAAMAWLPPRERGTLAH
ŀ						QVLEHYQLAQLPVSALQMPLH
1						CPPQAIAHHQQLEQQALASLQN
		ľ				WGVFHV
24900	55268	Α	25038	1	150	DKASRGRSRQQS/CAVLQPLLVI
						PRQT/WVWSGPPANSSRPGEEG
						PDC*KEN
24901	55269	Α	25039	1	150	DEASRGRNRQQS/CAVLQPLLV
						IPRQT/WVWSGPPANSSRPAEEE
		_	<u> </u>			PDC*KEN
24902	55270	A	25040	96	389	PCLSP*LYPSGVHKSTFIYGFYN
						T*PCTSQSLFWQHSC*GSITSSS
1	l .					YFYLLPEEGTGSNLCCSAASAG
						DTQANRVWSGPPANSSRPAAE
		1				GHDCWKEN
24903	55271	A	25041	1181	1364	VSLGNIKFRQTGAPLGQSFQRK
						EQSAIFAVLQPPLVIPRQI/WVW
						SGTPADSSRPAAEGPDC*KEN*
	1		l			RVNRQPTEWEKIFPIYPYDKGLI
						SRIYKELKQIYKKKIKPPHQKV
						GKGYVFSKEDIYAANRHMKKC
						SSSLAIREMQIKTTMRYHLTPA NRGIEIINCPFLDDAASCIDPTYS
ļ						SNIFPPVNLSWGLPMKPKEVKI
						KRQKKEHLLKDRDFSFQEPIMA
l						LRTVILEILMEKEMDNSQRECIK
				ŀ		DILTKHLVELSILARTFKNTOLP
						ERAIFQIKQYNSVSCGVSEWQL
						EEAQVFWAKKEOSLALSILKO
		İ				MIKKLDASCAANNPSLKLTYTE
						CLRVCGNWLAETCLENPAVIM
	1				1	OTYLEKAVEVAGNYDGESSDE
						LRNGKMKAFLSLARFSDTOYO
	1					RIENYMKSSEFENKOALLKRAK
						EEVGLLREHKIOTNRCPSGTKL
					1	PEEGTVSNLCCSAASTGDTOAN
1		1			I	RVWSGTPADSSRPAAEGPDC
	L		L	l		K V WOO I FADOOKFAAEOFDC

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleutide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodnn far last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nueleotide insertion)
				sequence		
		_				
24904	55272	Α	25042	42	963	VQEGCVRPFCCRSAGVCWRST
						PDSVCLGITSGGCRTAKTAACS
						FLWKLCPRGTPARCQVECSYTR
						CLS\SLLGGVSQAGGTRVRDPL
				1		EEEVCPLAELERCAGRSVAVFR
						ASRQEHLRLLKLTSQPPLPPGA
1						LSQGDGSFIYKPLTGVAAFLSD
			ĺ			ALPKRRNLERQSGYSTFEELCF
						QKRTWGRDAVRISDLLLGDHS
						HFGKCPISRLERAENMPVVSEL
						SAAGCSTEVNHVFVGIIWQKGK
						CSKYTAPSKSSVPVSSTRGHVHI
						TVQNPTLVPFVGKLNIDSPIGDR
						NIPVLTAGNCKTLGDLRSFPHN
24905	55273	Α	25043	98	352	
24906	55274	A	25044	3	414	PEEALCALAELERCAGRAAALF
						RAEROKRLRLLKLHPOPPLPPG
						ALSORDGS\LSISP*LGL\RLSFR
						DALPREQFYRLFTDRSDRVPEN
						SVTDVCHIESKMEPLRLGP/SNV
						SIMRPSLVCSFTTLVFISSNAOSS
						LVA
24907	55275	A	25045	2	1544	STTRGSPPOEAROYRHNOAYA
						YSIQGDGAEDDDERIVRFHTRL
						PVFMLPPTPRKTSWIVAPVLEV
						LARAIRHETEIQGIHTGTEDVPV
						SLFADDMIIYLDNLKDSSRKLL
						EVIRDFSKVSGYKINVHESVAL
						LYTNNDYAENHIKNSTPFTIGY
						VLAFVVMVIAVSCVRLLYAHN
						CTQHTSLKHKCQAWVVTTVDA
						AAFMTQATREERRIAYSAPGGY
						FFHILEVLARTIRQEKEIQGIQTG
						KEEVKVSLFADDMIIYLENLKD
		ĺ				SSRKLLEVIKEFSKVSGYKINVD
						SRGSPTDLVIYKEEIVFLIVPKA
		l				KKSKIKVLASDPLCYAATTWR
			İ			MTIIAGLPVEYNDRFIRGIAVFA
l	l			l		
	l		l			PWRKTPGIYHQSHDPLCYAATT
1	l	1	l			WRMTIIAGLPVEYNDRFIRGIA
1						VFAPWRKTPGIYHQSHGACLG
						RRSRTITVVDAQPQVMDMDPT
1	l		l			CSLFTTGQCLGEPDLLASARRL
1						QFFSHQYSIAVLMANARGNSA\
			L			LW\DNYGGLIVRADRGSLLLVG

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24908	55276	Α	25046	1	1228	MLQSNRTAASHSPSIQPAIQPAI
						<b>QPASQLSIHNLWTQFRHSTKIPV</b>
	l					EWVNGEWLNGRMPEDHHEWO
		l				CNYQNVQQFIDEGNYTSGDNH
	ŀ	ĺ				TLRDPHYVEDKGHKYLVFEAN
						TGTENGYOGEESLFNKAYYGG
		1				GTNFFRKESQKLQQSAKKRDA
						ELANGALGIIELNNDYTLKKVM
						KPLITSNTRETVDFNGKHIHVR
		l				GAKLLFPAIQOPYPPLYFGGSSD
						VAQELAAEQVDLYLTWGEPPE
		l				LVKDFIEQVRAKAAAHGRKIRF
		l		i	}	GIRLHVIVRETNDEAWQAAERL
						ISHLDDETIAKAQAAFARTDSV
				l	İ	GQQRMAALHNGKRDNLEISPN
						LWAGVGLVRGGAGTALVGDG
						PTVAARINEYAALGIDSFVLSG
						YPHLEEAYRVGELLVPLLDVAI
						P\EIPQPQPLNPQGEALRKK
24909	55277	Α	25047	1	1075	MTIKGEQAKKQLIAAALAQFGE
				l		YGMNATTREIAAOAGONIAAIT
				i		YYFGSKEDLYLACAQWIADFIG
						EQFRPHAEEAERLFAQPQPDRA
						AIRELILRACRNMIKLLTODDT
						VNLSKFISREQLSPTAAYHLVH
						EQEAEHRFAMGELPDEVLEICQ
						RLAKLTEMLRGLAELFLNDLSE
						KTGSHDIVRLHRLILQMNRALG
						MFEAQSKLWRLASLAQSSGAP
		l	İ			VTKWATREEREGQLHLWFHCV
	i	i				GIRVSDQLERLLWRSIPHIIVTS
						ATLRSLNSFSRLQEMSGLKEKA
ł						GDRFVA/SGFP/HLTTANRAKLL
						FPGCALSLPSTTKSSILPKWRPF
						SVSRWRAKNISVCWYCLPADG
						RCSAFSTM
24910	55278	A	25048	530	642	LKTLW/PAVQEPVPHRYHGATV
						FRIMQTIFIKQICRLLL*GTAGHF
			l			VCGITACHAAEAAHRLTVQPVP
						RILDQRRPAQLHSRQVTAAIRQ
			1	I		PLHRRQAVRRDAVCQPLLVVC
	l					VFRLMLPQQFPRLRVLHRLAFA
	1		1			GQAAFIVIAIVDGNTVAFAQVA
			1			DVCQPAVAIILPLLLCEFSGQVI
	1		1			MITLRPPVKAALLYQPVQRIVT
						EDAVAAVQEPVPHRYHGATVF
	1	1	I	I	I	RIMOTIFIKOICRLLL
1 4 4					1	KINQTIFIKQICKELL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24912	55280	A	25050	2	588	RWSSLTSSRYGFCRCPESADKE CLHYKSAAGKATAVGHYAG WLRTYSPHLAAHRVNFFFGINA HMDQRGFGKLMISCNBACGSA CYSNIBSYMRNDKHAVRRADSG RAEGGGPRVKSVIKAPVITEKK KPVYSTLKHWVLMLAWVTCSP LTVL\SPDGEMFDVMEKYAFSA WKWKRLRLAISQATFHALLPE KIG
24913	55281	Α	25051	912	1169	
24914	55282	В	25052	1	1665	
24915	55283	A	25053	43	302	
24916	55284	В	25054	116	1534	
24917	55285	A	25055		1017	NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGED GYQGESLFNKAYYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLIN NTRETVDFNGKHIHVRGAKLLF PAIQQPYPPLYFGGSSDVAQEL VIQVETVEGVAKAAAHGRKIRFGIRLH VIVRETNDEAWQAAERLISHLD DETIAKAQAAFARTDSVGQQR MAALHNGKRDNLEISPNL WAG RQLVRGGAGTALVGDGPTVAA RNEYAALGIDSFVLSGYPILEE AYBVGELLVPLLDVAIPEIPQP QQPLNYQGEALRKK

SEO ID	SECULO NO.	Mar	SEQ ID NO:	Nueleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nuelcotide insertion)
				sequence		
24918	55286	A	25056	1	2677	MVLNRLLTGLFFGSTPPRCHYD
21,710	55200			1		LIGADPDRTIRSVRLYWRHSLN
		l				ELISMLPKFNKELTRKLFKLQE
						MLPFLNLHMSPERMLORMDSE
						KVVTFTTALMTGLSGAMASVL
						LLVMTVVFMLFEVRHVPYKMR
		1				FALNNPQIHIAGLHRALKGVSH
						YLALKTLLSLWTGVIVWLGLEL
						MGVQFALMWAVLAFLLNYVP
		1				NIGAVISAVPPMIQVLLFNGVY
		1				ECILVGALFLVVHMVIGNILEPR
						MMGHRLGMSTMVDGVRVLKD
				1		GTDLNQTGSFYLAARPYAEKN
		l				GAFIQGVLATFSEADALTRSQR
						EOSIALLAKTMGLPAPVIASLLE
						ISOPVSNHPIRTRLTAEVAALQQ
						OTADLFYENRLVPKKVDIRQRI
						WQPTRLEGKQFMSLNMFWFLP
			1	1		THGDGHYLGTEEGSRPVDHGY
		1		1		LOQIAQAADRLGYTGVLIPTGR
						SCEDAWLVAASMIPVTOR\LKF
						LVALRPSVTSPTVAAROAATLD
		1		1	1	RLSNGRALFNLVTGSDPQELAG
		1			į .	DGVFLDHSERYEASAEFTOVW
						RRLLORETVDFNGKHIHVRGA
		1				KLLFPAIQQPYPALYFGGSSDV
						AQELAAEQVDLYLTWGEPPEL
		1		l		VKEKIEQVRAKAAAHGRKIRFO
		Ì	1	Į.		IRLHVIVRETNDEAWQAAERFV
					i	LSGYPHLEEA/YRVGELLFPLLD
		1				VAIPE/IPOPOPLNPOGEAVAND
		1	İ			LSPRRTVAASGDQLLAGAVGFS
24919	55287	A	25057	114	372	LSI KKI TAASODQEEAGA TOI S
24920	55288	Ä	25058	2270	2760	TSPIPSQIRQYSIA/VGSTGNLGL
21,720		ľ				SIGIMSARIGFKVTVHMSADAR
		ı		l		AWKKAKLRSHGVTVVEYEOD
	ŀ	1		1		YGVAVEEGRKAAQSDPNCFFID
		1	1			DENSRTLFLGYSV/AGQRLKAQ
	1	1	i	1	1	FAQQGRIVDADNPLFVYLPCGV
		1	1			GGGPGGVAFGLKLAFGDHVHC
						FFAEPTHSPCMLL
24921	55289	В	25059	1	2460	
24922	55290	Α	25060	I	993	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24923	55291	A	25061	332	1349	ILYDSDIYRFSCRSGGHIPAVIY
						HLSAKRTMENAKMNSLIAQY
	l					PLVKDLVALKETT/WGFIPATL
	l	l				HGVKGLPYVGLTEQDVQDAH\
	l					ARLSRFAPYLAKAFPGKWLPTG
	l					GIIES\ELGAL\PAMQKRL\EKEY
						QQPISGQLLLKKDSHLPISGSIK
	l	ŀ				ARGGIYEVLAHAEKLALEAGLL
	l			l		TLDDDYSKLLSPEFKQFFSQYSI
	I	l				AVGSTGNLGLSIGIMSARIGFKV
	l	!				TVHMSADARAWKKAKLRSHG
		l			1	VTVVEYEQDYGVAVEEGRKAA
						QSDPNCFFIDDENSRTLFLGYSV
					ŀ	AGQRLK\AQFAQQGRIVDADNP
						LFVYLPCGVGGGPGGVAFGLK
					1	LAFGDRVHGLQA
24924	55292	Α	25062	284	1494	RLSLPDMFPPVQQFPVSLHRAF
		1			i	YRYDKSAYYALRIAGIASRLNP
	l .					RRFSPSILTPERRCVVTLRNDIR
	į.	1				RDVLRHNQPRSTASTRQARRR
		1				MKSSCWHMPTTSKPQALSHTS
		1				NSPTTSISRPNWSYSNVCNRSRT
	1				1	MANLSGYNFAYLDEQTKRMIR
						RAILKAVAIPGYQVPFGGREMP
					1	MPYG\WGTGGIQLTAS\VIGESD
		l				VLKVIDOGADDTTNAVSIRNFF
		l				KRVTGVNTTERTDDATVIOTRH
		1				RIPETPLTEDOIIIFOVPIPEPLRFI
						EPRETETRTMHALEEYGVMOV
	İ	1				KLYEDIARFGHIATTYAYPVKV
l						NGRYVMDPSPIPKFDNPKMDM
					1	MPALOLFGAGREKRIYAVPPFT
	1	l			1	RVESLDFDDHPFTVQQWDEPC
	1					AICGSTHSYLDEVVLDDAGNR
l						MFVCSDTDY
24925	55293	A	25063	1	333	
4943	JJ273	1/1	42003	11	1222	1

3312

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24926	55294	Α	25064	1368	2451	PAHAAPGGGC/VRSLACRFLWN
		l				MRVTGKSYSTLRRVLSAIWNW
		l		l		RMMRCALTRALVAFRVR/SSVP
		l		l		LAAVLAIYARENGAGTMFEPE
		l				AAYDEDTSIMNDEEASADNET
		ı				VMSVIDGDKPDHDDDTHPDDE
		i				PPQPPRGGRPGLRGLTLRWFSV
		l		l		AAQRSDILDAVTLSLKVAALAT
		l		l		LIALVLGTLAAAALWRRDFFG
		l		l		KNAISLLLLLPIALPGIVTGLALL
		l				TAFKTINLEPGFFTIVVGHATFC
		l				VVVVFNNVIARFRRTSWSLVEA
		l				SMDLGANGWQTFRYVVLPNLS
	1	1				SALLAGGMLAFALSFDEIIVTTF
	1	1		1		TAGHERTLPLWLLNQLGRPRD
		1		ļ		VPVTNVVALLVMLVTTLPILGA
						WWLTAKATYLEKLKV
24927	55295	Α	25065	I	2072	MSEQLTDQVLVERVQKGDQKA
				i .		FNLLVVRYQHKVASLVSRYVP
				!		SGDVPDVVQEAFIKAYRELTPR
				!		RPYLLRAFYEWLLDNQLTPHL
	1	1				VVDVTLPGVQVPMEYARDGQI
				1		VLNIAPRAVGNLELANDEVRFN
				1		ARFGGIPRQVSVPLAAVLAIYA
	i	l		i		RENGAGTMFEPEAAYDEDTSI
		l				MNDEEASADNETVMSVIDGDK
						PDHDDDTHPDDEPPQPPRGGRP
	1	l				ALRVVNVIVAIIFTTKPTAMGIA
						VRFTTAKGETPAIPDVTTTTAVI
		l				GETARASVVAKCIGIIITTAVPIV
		1		l		VKPFANISPATTSVPRFFGLPAS
	1			l		SSHTLIGATIGIGLTNALLTGSSV
		1				MDALNLREVTKIFSSLIVSPIVG
		l				LVIAGGLIFLLRRYWSGTKKRD
		l				RIHRIPEDRKKKKKGKRKPPFWT
	i	ŀ				RIALIVSAAGVAFSHGANDGQK
		l				GIGLVMLVLVGIAPAGFVVNM
		l				NASGYEITRTRDAVTNFAARES
		1				EAS VIRHSNRFIETINGGRRCSR
		l	•			GITLTLHKLR\SAQPLL\AVLNR
						LEQKKPVGLRYDPQAQSLVCLP
			1	ĺ		TOTRTGWNLNGFEVGFRPCVR
				1		LMIYGRSLEAQATASLAAATG
		l	l	I		YDSHIFDLFPASASAQIDTDTAV
		1		I		ILLCHOLNRELPVLQAAREAKP
	1	1		l		FYLGALGSYRTHTLRLQKLHEL
		l				GWS\RQETTQIRAPVGIFPKARD
		L	L			AHTLALSVLAEVASVRLHQEE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24928	55296	A	25066	2	332	AGYSTRTALAIVNKPPSSAIPPT SGLASRKRNPASNDFNGCSRGC GGGGNAGRLNNGSKRSASTPP TIRPTNIAPP\AASPKAPPARWN VSSSGSAPAPRRRANPETQLR
24929	55297	Α	25067		3192	MNKKFKYKKSLLAAILSATLLA GCDGGGGSGSSSDTPPVDSGTGS LPEVKPDPTPNPETPPPTPDPE PTPEPIPDEPTPPPPEPTPPPPP PTEPIPDEPPNQNGAELSYN TEKTLTIRDSVFTYTENADGTIS LQDSNGRKATINLWQIDEANNT VALEGVSADGATKWQYNING ELVITGDNATVNNGKTTVDG KDSTGTEINGNNGKVIQDGDLD VSGGGHGIDITGDSATVDNKGT MTVTDPESM
24930	55298	Α	25068	1078	1317	
24931	55299	Λ	25069	135	361	SCSMLAGLCG*GSSSSVSITTCF ALSASTIA*PREPQQALPV*PLA LPNSSQDGTPMKATSIFSSPLCT RCTRPP
24932	55300	A	25070	469	841	RWWKQYAAAGFQCMCATAVS NLTRPVAA*TAAIPESKSPVLPN SPASTVRRS*PVSTMPPIRPGDG DHDPRFKAPSGTPHQPPRAGHS LIRRHG*TENCTAA*GQLRTPG DNGTVMSADTITFP
24933	55301	В	25071	1	2922	
24934	55302	Α	25072	1	3849	
24935	55303	Α	25073	1	2280	
24936	55304	A	25074	672	1045	GAVLSINCRTLSPAAASGENVA TPPVYTSNNTPIINKPKPLALAE ATGVIIAPKPPSSAAPMASPVTF CAVHKPLIRPNIASGVCVCSIVY CSNELTALNQPNSARQTTPKIHI GIRPNRPMARN
24937	55305	A	25075	650	1465	RKPICAADICQLSASAGYSTRT ALAIVSGLASRKRNPASADDFNG CSRGCGGGNAGRLNNGSKVI NVPAAASP*PQATPPVASNKPPI MGEITDPRRIYNNVIAPACIKF SRPTSAGVAANSAVTPSDAKKP SKHYSK*IASNDGSGSSALRHSP MKPMPQVPRASKITFLRS*RSA STPPTIRPTNIAPPVSVTESPTCQ VECVIIWICTGATPSKPRDIY MKRARNTARNAGCVSAGSSGS SAEVGSSNSKTSGSIASARAIET RCC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24938	55306	Α	25076	156	3092	LNRRWIANIAKLEAEQARKLK
		1				KTEKDSLKDEVLHSLLPRAFSR
		l				FSOTMMWIDTVNGLIMVDCAS
		l		1		AKKAEDTLAVLRKSLGSLPVVP
		l				LSMENPIELTLTEWVRSGSAAO
		l	ĺ			GFOLLDEAELKSLLEDGGVIRA
		1				KKODLTSEEITNHIEAGKVVTK
ł		1				LALDWOORIOFVMCDDGSLKR
						LKFCDELRDQNEDIDREDFAQR
		l				FDADFILMTGELAALIONLIEGL
						GGEAQHSGTGSLPEVKPDPTPN
						PEPTPEPTPDPEPTP
24939	55307	В	25077	61	2118	
24940	55308	Α	25078	132	280	RRRAALPERSGPGLDHRRVRH/
		ĺ		i		GCHVLPTPVTLVKRRKVSRVD
				1		AQWKSSV
24941	55309	Α	25079	1	1449	
24942	55310	В	25080	110	550	
24943	55311	Α	25081	657	805	RRRAALPERSGPGLDHRRVRH/
						GCHVLPTPVTLVKRRKVSRVD
						AQWKSSV
24944	55312	Α	25082	756	938	
24945	55313	A	25083	781	1257	
24946	55314	В	25084	1	2727	
24947	55315	Α	25085	1	2286	
24948	55316	Α	25086	1161	2024	VRSAVWPCLQRDPDCHHNRCG
				1		TGGTSRPGPARNPRIEPETCVG
						RIRNLGVLLYDADAMERAAST
						ENEKDLYQRQLDVFLDPNDPK
						VIEQAIKDGIPLSVIEAAQQSPV
				ļ.		YKMAMEWKLALPLHPEYRTLP
						MVWYVPPLSPIQSAADAGELGS
	l					NGILPDVESLRIPVQYLANLLTA
						GDTKPVLRALKRMLAMRHYK
						RAETVDGKVDTRALEEVGLTE
						AQAQEMYRYLAIANYEDRFVV
				İ		PSSHRELAREAFPEKNGCGLPF
						GDGCHGSDTKFNLFNSRRIDAI
	<u> </u>	ļ.		L		D\KTEPHP
24949	55317	Α	25087	664	1065	VAPEPHHGRKQLCREGLGVFH
						PTHHITHHLGVSLSLLITIFDAQS
				l		VHGPDDGCQGLDSVAVDNRLV
			1	l		LFHVFSGEAIFMDDLHLLHNGA
	1					FS*FSSPEQE*F/PRLWRR*CHPL
	L					*GFSQSPCSARGRLSPLRSEYIP

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	bod	in USSN	location of first	codon for last amino acid	*=Stop endon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24050	155210	_	0.5000	424	1663	PAGAFPDIANDFGEKSLLMPGG
24950	55318	A	25088	434	1003	AVINGDF\NNVLPVDLVDPQQV
				1		
						QEFVDHA WYRYPNDQVGRHPF
				l		DGITDPWYNPGDVKGSDTNIQ
						QLNEQERYSWIKAPRWRGNAM
		i	1		i	EVGPLARTLIAYHKGDAATVES
		l		1		VDRMMSALNLPLSGIQSTLGRI
		l			l	LCRAHEAQWAADAIENNYSRN
l		l		1		PSQGYSTVPRSPHPKVDPILTKP
						SGPAGPEMTRKQTQREDRPRSR
						PSMTTSPTSNLKPSVPAFKGVG
		l				YLDSLDRIGAADYQPTEQDILR
						TRVKTTGIVETHFTFKNLHFRT
						EQASVHACYCRLFDVEGQRSE
		l				RKKWIHCFEDVTAIIFCVALSG
						YDQVLHEDETTVLSTRIVDGHR
		l				YSDHSTIACPAFGTYTLLELKEL
						ALSCSTLLHIPHQRSPAGSFLAD
						NLNCTQAAVIPEFGGF
24951	55319	Α	25089	1	1247	MTFGGDQIFESLVYRSAFRHVY
						SRGSPWYLHTNSDLSFVESKKE
						LIAEHILETFPWNLKGLTEIPWG
						DASGESGAVGLGVLAAVHYHP
						QRQSLMEKLALNKDAVVLVIS
				l		TEGDTDQVIERLESDAVLRYGI
				l		EDVVTNLDVLERMQPSESLLRA
		İ		1		VLHTKHLMNPEVLAAARRIVC
İ				1		QVVEEIMARLAKEVRQAFSGV
				1		RDRRRRSFIPLARNFDFKSTLRA
ĺ		l		1		NLQHWHPQHGKLYIESPRFNSR
		i		1		IKRQSEQWQLVLLVDQSGSMV
				1		DSVIHSAVMAACLWQL\PGIRT
				1		HLVAFDTSVVDLTADVADPVE
			1	l		LLMKVQLGGGTNIASAGEYGR
			1	1		QLIEQPAKSVIILVSDFYEGGSSS
		l	1			LLTHOVKKCVOSGIKVLGLGA
		l	1			LDSTATPCYDRDTAQALGNVG
			1			AQI\AALMPGELGSLAWENLLA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hnd	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24952	55320	А	25090	1	1691	MGAYLIRRLLLVIPTLWAIITINF
				ŀ		FIVQIAPGGPVDQAIAAIEFGNA
		1		l		GVLPGAGGEGVRASHAQTGVG
		l				NISDSNYRGGRGLDPEVIAEITH
		l				RYGFDKPIHERYFKMLWDYIRF
						DFGDSLFRSASVLTLIKDSLPVS
		l				ITLGLCWYFVCRACVVTHALSL
ľ		l				WQSASIEVPRTSATAKARKTEP
						GRQTKRKVRSSQTVAARQRIAT
						LPHSMTVCNPGLFHSQMADAL
		1				AHRYYGFNIAEPWDNGSEAML
		1		ĺ		QRDIGLKSESRGLMAGKRCSCL
1		1				KGECGWSLDMQARVSTCFYVR
		ŀ		i		LLCGTELEDHRICHDTCDNKCG
		1				PQRRYVIKFRELCLVNSTVTLV
						DQEYELTVTDPELYDGSSQALA
1		1				GISDLSSIYATCDPGYSCTDRVT
		1				LVDVRKRQSKTGPYKEIGRYGI
		1				DRNRSPLNPGFRGKPDLMPSQC
İ		1			1	IACGACACACPANALTIQTDDQ
		1				QNSRTWQLYMGRCIY/CDGRCE
		1				EVCPTRAIQ\LTNNFVLTVTNKA
		1				DLYTRATFHLQRCSRCERPFAP
		i				QKTIALAAELLAQQQNAPQNR
		l			1	EMLWAQASVCPECKQRATLIN
		1				DDTDVLLVAKEQL
24953	55321	Α	25091	Ī	866	

3317

SEQ ID NO:   Met   SEQ ID NO:   Nucleotide	PAIPAGMKF ARYLVLLCQ WQSGPSCTC ERPGVGDVT YFTMLNSNK
sequence 09/540,217 codon for peptide of peptide sequence delection, "possible nucleoquence" 2388 CVQEPLITVSWRL SFR.CLFCFHLAY LH/SQGIKYLDFTC MLAWFGADYINTATEGKI ADILVENFIPGAII QEINPRLIFGSIKG VKAYENVAQAAG. WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WDGPPLVSAAALG WGGPPLVSAAALG WGGPPLVSAAALG WGGPPLVSAAALG WGGPPLVSAAALG WGGPPLVSAAALG WGGPPLVSAAALG	FAIPAGMKF ARYLVLLCQ VQSGPSCTC ERPGVGDVT YFTMLNSNK
24954 55322 A 25092 338 2388 CVQEPLITVSWRL SLFLRCL FCFIL A: LL/SQGIKVLDFTC MLA WFGADVIKIE RHQLRDIPDIDAL' RSIELNTKTAEGKI ADIL/ENFIPEGAII QEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAALG WDGPPLVSAAALG	FAIPAGMKF ARYLVLLCQ SVQSGPSCTQ ERPGVGDVT YFTMLNSNK
SLFLRCLFCFHLA/ LH/SQGIKVLDFTC MLAWFGADVIKIE RHQLRDIPDIDALY RSIELNTKTAEGKI ADIL/VENFHEGAII QEINPRLIFGSIKG VKAYENVAQAAG WDGPFLVSAAALG	ARYLVLLCQ GVQSGPSCTQ ERPGVGDVT YFTMLNSNK
SLFLRCLFCFHLA/ LH/SQGIKVLDFTC MLAWFGADVIKIE RHQLRDIPDIDALY RSIELNTKTAEGKI ADIL/VENFHEGAII QEINPRLIFGSIKG VKAYENVAQAAG WDGPFLVSAAALG	ARYLVLLCQ GVQSGPSCTQ ERPGVGDVT YFTMLNSNK
LH/SQGIKVLDFTC MLA WFGADVIKE RHQLRDIPDIDALY RSIELNTKTAEGKI ADIL/VENFREGKI IQEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAALG	SVQSGPSCTQ RPGVGDVT YFTMLNSNK
MLAWFGADVIKIE RHQLRDIPDIDALY RSIELNTKTAEGKI ADILVENFHPGAII IQEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAALG	RPGVGDVT /FTMLNSNK
RHQLRDIPDIDAL) RSIELNTKTAGGKI ADIL/VENFHIGAII IQEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAALG	YFTMLNSNK
RSIELNTKTAEGKI ADILVENFHFGAIE IQEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAALG	
ADILVENFHPGAII IQEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAAL	EVMENT IDE
IQEINPRLIFGSIKG VKAYENVAQAAG WDGPPLVSAAALG	
VKAYENVAQAAG WDGPPLVSAAALG	
WDGPPLVSAAALO	
LIGLLAALLHRELT	GDSNTGMHL
REEWAGFRARETA	
STVIATGGGILTE	
GIVVYLCAPVSVL	
VLRLAFLSSGILEF	
VYFGFSYLGELDF	
AAGFLALILAPEFF	
YHAKAQAVGAAD	
LAHPQRGEAELAS	
ELFITSPEGKTLAG	
QRAVLVGRSGSGS	
NVRLGPIVTDVPW	
EATAQVISSGSGA'	
LNKPVSNQNLVTO	
SAGSAPFGVLADN	
KDRLNQTWYQIRI	
LDAQPDNGLSVLT	
NTRFRHTSTTTSVI	
WLRDRGYATLSM NKINLPARAVVITI	
RYAYPVLKQYGM	
24955 55323 A 25093 1810 2399 STFRNSDDEPYIVE	
24935 33323 A 23093 11810 2399 STEANSDEE TVE	
MVNYFLOGDPYO	
HQHPSGLS*WVAC	
OPVRKRTRDNVOI	
VFRCSRRVLTGLV	
HREAAGEFSGEITG	
HFRLVLTTQAQRA	
GGTEPSAFPDTLPV	
24956 55324 A 25094 1 577 MPVSTAVATVIKT	
VGVPLYFRLRANP	
RLDSKGNIKRCRV	
WLORKLGNAARV	
PQYFSGDGKSGKI	
CREEPDAEECHGD	
EDGFFVTKDLYPN	
AVISPSQPPIIAPRV	
AHALARAIRQSTT	

SEQ ID	SEQ ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24957	55325	A	25095	51	407	TCPIRAQRVETLYDRAYREVFG
ŀ		[				WNPRGPTGRPNARHTG*SKEG
		1				GRTEADETDAADSGQRGMEQR
		1				SEMDRKPTGTTGQRSEKPRRTL
		İ				ECLALHETRIFLPQRKETHSSDA
						HDMPGPPML
24958	55326	A	25096	3047	4131	AHSGQMYMPLSSCIRSCILGSV
		1				VMTCGFPQKSAGQKRQKTADC
	1	1				RKRPQLYTKSLSLS/AVKAILAK
	1	ı				GYDPVKWRKKDKVLDAVLKE
		l				LESGKYSDGDKHAFDQMLHSI
l		l			1	GKQGGDPYLVMADFAAYVEA
		l				QKQVDVLYRDQEAWTRAAILN
		l				TARCGSSMESKRLDNAALAAGI
		l	İ			SPNYINAHGKPQSISAETKRRLL
l		l				DAMHQRTATKVAVTPVPNVM
		l			İ	VYTSGKKMPMVVEGSGEYSW
		1		1		LLTTEEGTQYKGHVTGGKAFN
ŀ		1				LPTKLPEGYHTLTLTQDDQRAH
		1				CRVIVAPKRCYEPQALLNKPKL
						WGACVQLYTLRSEKNWGIGDF
						GDLKAMLVDVAKRGGSFIGLN
1		i i				PIHALYPAIRRAPAHTARLLAV
24959	55327	Α	25097	524	697	AANWWWKSRRNWR*KMTAM
					İ	LDRIISHIIRTVRMSGSVAVTRAI
						AVPGLLLLLIIATA
24960	55328	Α	25098	I	1938	
24961	55329	Α	25099	33	226	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
24962	55330	IA	25100	1	2314	MDRAGDGPIRPLSGPTDVYGD
		l				VYLRDPGPNHGKTTNGPLRFV
						LLPFGQQVFPRVTPNFWNPVSS
						AALPARYMQTIENAAVWAQIG
			1			DKMVTVGNIRAGQIIAVEPTAA
						SYYAFNCGFGKAFIDKGHLEPV
						QGRQKVEDGLGDLYKPLSNQN
				ľ	1	LVTWKDTPVYNAPSAGSAPFG
		1				VLADNLRYPILHKLKDRLNQT
						WYQIRIGDRLAYISALDAOPDN
						GLSVLTYHHILRDEENTRFRHT
						STTTSVRAFNNQMAWARVDRO
1						YATLSMVQLEGYVKNKINNRA
l						TEREELRVSKITVLILGVIAIILG
					ŀ	VLFENQNIAFMVGLAFAIAASC
						NFPIILLSMYWSKLTTRGAMMO
					Į.	GWLGLITAVVLMILGPTIWVQI
ļ						LGHEKAIFPYEYPALFSITVAFL
	ŀ				ļ	GIWFFSATDNSAEGAHLRPIRR
						KKVYRFNYLRSDGPYQGWVSE
					1	RLLILRAISPGCSKLVHFPTLFDS
		1				LYRTLVKAGEKSGLLAPVLEKI
		l				ADYNENRQKIRSKLIQSLIYPC
						MLTTVAIGVVIILLTAVVPKITE
		1			İ	QFVHMKQQLPLSTRILLGLSDT
				1		LQRTGPTLLATVFIVAVGFWL
						WLKRGNNRHRFHAMLLRVALI
						GPLICAINSARYLRTLSILQSSG
						VPLLDGMNLSTESLNNLEIRQR
						LANAAENVRQGNSIHLSLE/QT/
		ŀ				AIFPPMMLYMVASGEKSGQLG
						TLMGAQSHWECATVNAASRIR
24963	55331	Α	25101	20	825	GFPRSRSCYASCTACRTHTYSA
				i		EK/QLTRALAKLARATSNEKLS
		l				QAFHAHLEETHGQIERIDQVVE
						SESNLKIKRMKCVAMEGLIEEA
l		1			1	NEVIESTEKNEVRDAALIAAAQ
		1				KVEHYEIASYGTLATLAEQLGY
		1				RKAAKLLKETLEEEKATDIKLT
				l		DLAINNSFYKEDIFMNRIEHYH
						DWLRDAHAMEKQAESMLESM
						ASRIDNYPELRARIEQHLSETKN
	l		1	I		QIVQLETILDRNDISRSVIKDSM
				I		SKMAALGQSTADTTKNSTHRQ
						SNTRQGN
24964	55332	Α	25102	2	269	GIIGLHLQQQEAVAVAIVRGAT
	1					RMLFATLVAVAAGERHYQRW
				1		ADC*CAAAG*NVVTVESRTAA
						ASSHYVGVSRQSHITAVISAPV
						DVPW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24965	55333	Α	25103	607	727	RQAVYRG**TAGQRANLLLLR
		1				RHSACALAAGESQSSCPAG
24966	55334	A	25104	465	574	
24967	55335	Α	25105	3	636	AHTSGFGDKESEKVSPQRKLHA
		l		i		MSRTFFWEN\LRCHGNLGSPTY
	1	1	ł			AFQISAIDRVNFALVVGLHLRH
		l				DYRNEKLGRSGRHYQAPVGNR
		l				SSADGMHRDPCSQLDICCILLG
		l				AGSIYGLYRYIEPQLPDVATLK
	1	l				DVRLQIPMQIYSADGELIAQYG
		1				EKRRIPVTDGPVMWFPFMIITTC
		l				VKGNFALNNQFREDMLNYNTE
						GIYGKNVNFENNKQT
24968	55336	Α	25106	434	1205	
24969	55337	A	25107	368	532	
24970	55338	Α	25108	722	934	
24971	55339	Α	25109	82	420	ARADPHRAHTAGVNGVNARLR
						IFNADTCLRRHAQPCTGGEKDF
						RVRFRVFKLGSIRAEGEKLAQL
		l				QRR*NRRRIQGDRSQPNRD/RA
		l				VPEDLPSKERMPGRTALTVNSR
		_				SEWT
24972	55340	Α	25110	618	788	WYPCCRNWRYLAGGDSGFCR
		l				GERA*R*IASQSGVT*AVATVV
		L.				FPSVLAGLRITGHS
24973	55341	A	25111	186	1198	QKTAVSTSITALTRWGS/SRA/G
	t	l		i		KRGAVLRSRVTRGKYHYPSSW
		1		ŀ		RETSSSVQNAPLMRQIKEVFLAI
	[	l				RIEQLLTKDEILELYLNKIYLGY
		l				RAYGVGAAAQVYFGKTVDQL
	1	l		l		TLNEMAVIAGLPKAPSTFNPLY
		l				SMDRAVARRNVVLSRMLDEG
		1				YITQQQFDQTRTEAINANYHAP
						EIAFSAPYLSEMVRQEMYNRY
	i	1				GESAYEDGYRIYTTITRKVQQA
						AQQAVRNNVLDYDMRHAIAA
		1	l			RHYVLWKPTANIRARYKAQGI
						ELPAVVPAGPDNPMGHHAIRL
		1				AAYGGVYLLHGTNADFGIGMR
						VSSGCIRLRDDDIKTLFSQVTPG
	L			L		TKVNIINTPIKVSAEPN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24974	55342	Α	25112	1087	3289	RLRSCGAQKNTFCNAAAGCRW
						RTTLSKMGGLLIAADLODPVO
						DMEMWOFHPTGIAC/AGVLVT
		l			l	E/GCRGEGGYLLNKHGERFMER
						YAPNAKDLAGRDVVARSIMIEI
		l				REGRGCDGPWGPHAKLKLDHL
						GKEVLESRLPGILELSRTFAHVI
		l				PVKEPIPVIPTCHYMMGGIPTKV
						TGOALTVNEKGEDVVVPGLFA
		l				VGEIACVSVHGANRLGGNSLL
						DLVVFGSARQVLHLQESIAEQG
		l				ALRDASESDVEASLDRLNRWN
		l				NNRNGEDPVAIRKALQECMQH
	ŀ					NFSVFREGDAMAKGLEOLKVI
						RERLKNARLDATSSEFNTORVE
		l				CLELHNLMETAYATAVYATFR
		ŀ				TERRGAHSR\FDFPDRDDENWL
	ŀ	ŀ		i		CHSLYLPESESMTRRSDYTLEA
						DEGRDMMLLDALIQLKEKDPS
						LSFRRSCREGVCGSDGLNMNG
		ŀ	İ			KNGLACITPISALNQPGKKIVIR
		l				PLPGLPVIRDLVVDMGQFYAQ
		l				YEKIKPYLLNNGQNPPAREHLQ
						MPEQREKLDGLYECILCACCST
						SCPSFWWNPDKFIGPGSLLAGY
						RSGLIAGIPKCSARYLSGEKRSV
				l		AWQQIAAEIGISIDAQFNESLKG
						ISRDESLRRILQHGGKEGDFNSQ
						ERAQLAYRKNLLYVHSLRELT
						VNAVLPGIRSLLADLRAQQISV
						GLASVSLNAPTILAALELREFFT
		ŀ				FCADASQLKNSKPGPGIFLAGC
24975	55343	A	25113	47	630	VGWETSFAQIRSRFLRIRFCRAY
						SSTLFVSAANPTT*G/QMVF*CG
						NGAQHKNILLLYRSIHGGFHFQ
		l				RGHHINTFNKRWRR**NRT*YO
		l	1	1		RDVRATTGSGGGDRKTHLAGA
		l				VIRDITHRIERFTRRAGGNHNV
		l	-			QMFQVVDGRKCATAISTVLDM
		l				FGDHFGRQKIASCQRWLAKTIR
		l				TVQQPICKNIVRKPGCHSLA
24976	55344	A	25114	731	829	- CQ

SEQ ID	SEQ ID NO:	Mei	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24977	55345	Α	25115	2	3744	RLPFKYPVKVKPLPAPFSKILLN
		l				SPAIPQLPITMNGSDFSLPEGPM
1						NRWENIQLTPETRLAPRAYFFS
		1				YDSVAQARTFARETSSLFLPLS
		1				GQW\NFHFFDHPLQVPEAFTSE
					İ	LMADWGHITVPAMWQMEGHG
		1				KLOYTDEGFPFPIDVPFVPSDNP
		1				TGAYORIFTLSDGWOGKOTLIK
						FDGVETYFEVYVNGOYVGFSK
		1				GSRLTAEFDISAMVKTGDNLLC
						VRVMQWADSTYEKDODMW,W
						SAGIFRDVYLVGKHLT
24978	55346	A	25116	1	2643	SAGIRET TETORIET
24979	55347	i A	25117	2499	2935	RSGGVACNCAVSASCMLVTVL
24919	33347	<u>۱</u> ^	23117	2477	2733	PWLSLPV/SVFGLWDGFFASLG
						VTALLAATPA\W*GVKT*CRPG
		1				
						RSP/SLTVRLGSVISPMIGGLLLA
1		1			ŀ	TGGVALLPLLSLPALPPPPQPRE
						HPLKSLLAGFRFLLASPLVGGIA
		L.				LLGGLLTMASAVRV
24980	55348	A	25118	676	1035	
24981	55349	Α	25119	1	1842	
24982	55350	A	25120	1	1341	DOLLIN D. OD
24983	55351	A	25121	563	1360	PSVLRCRNWVI*SPYCISLPSRV
1						SSLPFLVWIPVAR/CTAIGASRE
1	1	1				AMLGVLVEPMLLLGLWVAAQ
1	l					VAGSTNISNITDTVYHWPLSQSI
1	1					PLVLALCACAFATFIEMGKLPF
						DLAEAEQELQEGPLSEYSGSGF
	1					GVMKWGISLKQLVVLQMFVG
	1					VFIPWGQMETFTAGGLLLALVI
						AIVKLVVGVLVIALFENSMARL
l						RLDITPRDMIRIELDSWEQNGE
1	l					AIKRTGQPLLLSLLVRNLLDNA
						VRYSPQGSVVDVTLNADNFIVR
24984	55352	Α	25122	382	1424	VLLENLSEPPNQHDHEILTVQR
		1				KEEETALSCRLVLRKLTETEPVI
		1	l			IFEGIEAPATLPADEVPVGKDEN
l						DNVEVSRWGTPREFDFEVRDH
						VTLGEMHSGLDFAAAVKLTGS
						RFVVMKGQIARMHRALSQFML
		1	1			DLHTEOHGYSENYVPYLVNOD
						TLYGTGQLPKFAGDLFHTRPRH
1		1				ECFRHIGSLGLATPLVTECMQW
		ı				LFGIPHTLQLDAIIITCWIILNAIC
l		1				VACGLQKGVRIASDVRSYLSFL
l						MLGWVF\IVSGASFIMNYFTDS
1		1				VGMLLMYLPRMLFYTDPIAKG
l		1				GFPQGWTVFYWAWWVIYAIQ
l	1	l l		l		MSIFLARISRGRTVRELCFGMV
1	1	1		I		QEFGCKSSTKIDNADFNQA

ŠEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide scquence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide detetion, \-possible nucleotide insertion)
24985	55353	A	25123	416	610	
24986	55354	A	25124	662	811	AQQLPGMSDWQNSQEQHQMK N*VRLFMRTSRKLMDRLNVLIK LWSPNRT
24987	55355	В	25125	1	3264	
24988	55356	A	25126	489	3256	PRVFSATRSLVAMRRWYVRV RRIOYRRTOTAVFISTHGNYR EGQPVGTLIDDRYKANENVEL VHYAQPLLNEADSLAKVMPSDI PLKQRRWLGLOMLEGDIYSRA YAGEASQHLDAALARLRNEND PALHHADARYQCIAAICDVVS NTLTAEPSRFTTAVDKIVLNRFL GLPIFLYWYLLMFLANIGGAL QUEFDVGSVALFVHGIQWIGYT LHFPDWLTIFLAQGLGGGINTV LELYPQIGMWYLFLF
24989	55357	A	25127	779	910	
24990	55358	Α	25128	2203	2665	ACWARISAAVIQRSGMPGVRV CGRIKSCSKAVRCQRHVFATCV WNGRQVTSGAGTWSTIAWYSG VMSSAISSWSRPAIPFSAEA*TIG KSSC/YVGRVEVNEQIEYLIHNP IBTRARAVVIFVDNNNRLQAVS KRFFGYEARLRHRAVKCVNHQ QH
24991	55359	Α	25129	241	918	
24992	55360	А	25130	2142	2646	KGVCGTTNPAKIQAILQAFHEI FGEGSCHIASVAVESGVPEQPE GSEETRAGARNRVANARRLLP EADFWVAIEAGIDGDSTFSWVV IENASORGEARSATLPLPAVILE KVREGEALGPVMSRYTGIDES KKEGAIGVFTAGKLTRASVYH QAVILALSPFHNAVY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
24993	55361	A	25131	473	1765	KAWLMTGIVRHWKGRAVPPA
21775	33301	1	25151	1	1.700	EQLLEHLGNGKSFDSVAQAWD
		l				AAMADAKAEDTVLWGVEAFRI
l		l				NAAVAKDDTQIHTHMCYCEFT
l		i				DIMDSIAALDADVITIETSRSDM
		l				ELLESFEEFDYPNEIGPGVYDIH
		l				SPNVPSVEWIEALLKKAAKRIP
						AERLWVNPDCGLKTRGWPETR
		l				AALANMVQAAQNLRRGARAG
	1	l				CAADFAASARLAVGEALTNIA
	1	1				ATQIGDIKRIKLSANWMAAAG
		1				HPGEDAGLYEAVKAVGEELCP
		1				ALGLTIPVGKDSMSMKTRWQE
		l				GNEEREMTSPLSLVISAFARVE
						DVRHTITPQLSTEDNALLLIDLG
						KGNNALGATALAQVYRQLGD
1		1				KPADVRDVAQLKGFYDAIQAL
	ł	l				VAQRKLLAYHDRSDGGLLVTL
	1	l				AEMAVLSSLGQGGYFGHMII/D
	ŀ					SGQYPGKSKTGQSTPDVAAQA
				1		RQSWIP
24994	55362	Α	25132	602	2563	VVTTLTLVLTAVGSVLLLLFLV
l		l				MKARMHAFLALMVVSMGAGL
ŀ		1			ŀ	FSGMPLDKIAATMEKGMGGTL
l		1				GFLAVVVALGAMFGEILHETG
	İ	1				AVDQIAVKMLKSFGHSRAHYA
ĺ						IGLAGLVCALPLFFEVAIVLLIS
						VAFSMARHTGTNLVKLVIPLFA
						GVAAAAAFLVPGPAPMLLASQ
						MNADFGWMILIGLCAAIPGMII
						AGPLWGNFISRYVELHIPDDISE
		1				PHLGEGKMPSFGFSLSLILLPLV
1		1				LVGLKTIAARFVPEGSTAYEWF
		1				EFIGHPFTAILVACLVAIYGLAM
		1				RQGMPKDKVMEICGHAL\QPA
1		1				GIILLVIGAGGVFKQVLVDSGV GPALGEALTGMGLPIAITCFVL
1	İ	1			1	AAAVRIIQGSATVACLTAVGLV
		1			1	MPVIEQLNYSKRRGFTGRVEEN
		1				FGVCKGPSKYHSQHDAINRQG
					1	REASDAHGTLENLPLPLVPQPN
		1				AATALAALRASGLEVSENAIRD
l		1				GIASAILPGRFQIVSESPRVIFDV
		1	1		1	AHNPHAAEYLTGRMKALPKNG
		1			1	RVLAVIGMLHDKDIAGTLAWL
	1	1			1	KSVVDDWYCAPLEGPRGATAE
		1				OLLEHLGNGKSFDSVAQAWDA
					1	AMADAKAEDTVLVCGSFHTVA
					1	HVMEVIDARRSGGKLCQMHVN
					1	VQDKIDEEINQVHICLCLVLVIV
						SGCKYVGYSLKCSEHYYSLVR
	L	L_	L	L		BOCK I VOI BEKCSEHI TOEVK

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24995	55363	A	25133	518	1079	TQKETNKRCSPLVGWYPAFRM AHFLASERSCYQKLSNRKSHPM AVAGMYSGMTVANLLFEHSAG NVFKSGI*LALHLFIDRCF*YCG DGIGLFLGARYSRROERKSART ISLFAQPGPVVNFRRHDVWQRR CVCLVQLRKAIHDVYFRFFGNG DDLYYDVSWARDGAGKYAKW ODFRILFTTAHCSSD
24996	55364	A	25134	322	798	AQRAHVVGTVGKFDEDDADIL HHRHNHLAKVFGLRLFLIAELE FIKFRHPLYQLGDAFTKKLFHIL ILVVGGSIFNHWQQRRHQRFI VEFHLGQNAGNATGCVI*GSPL ERVCPS*ASRATRYACRRILIW SIARPAAKVSACCSAIATSK*RS KGQRVLLGNCHVEVAIREFT
24997	55365	Α	25135	440	906	CGFSSLSRLPHSSYSAHHAVAPS VLMSASGRPRWSQWYRWIFRA GVYTGSIWFFICSTVRPHDASQ RRLSSLT/QVSQDFTFQPVNHQL WAGGRPTAGITVGKQ*W*PFIK FTVPGDDSGDGRGQGFLQIAAG KCRAQTFFSFCRAGKHDPCRRT VS
24998	55366	A	25136	1059	1541	TAPLLRPGCRLS*SAAHPAAPA QSTNQCPGDRYAATLPAHHRH TNHG*IADVHQHISATPASAAS YAPGFLKDGAPASERHRETGC GRORPHPSLYKLSGILRPYQPA SFPG*QQRAVLSAR*LLPVQCSL HSQRCRRRPHRLHRSAPAPGIR ERRSRR

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24999	55367	A	25137	236	2211	OGALMSEDIFDAIIVGAGLAGS
		1				VAALVLAREGAQVLVIERGNS
		ŀ				AGAKNVTGGRLYAHSLEHIIPG
						FADSAPVERLITHEKLAFMTEK
		1	İ			SAMTMDYCNGDETSPSQRSYS
		1				VLRSKFDAWLMEQAEEAGAQI
		1				ITGIRVDNLVQRDGKVVGVEA
		ŀ		İ		DGDVIEAKTVILADGVNSILAE
		l			·	KLGMAKRVKPTDVAVGVKELI
						ELPK\$VIEDRFQLQGNQGAACL
		l				FAGSPTDGLMGGGFLYTNENT
		1			ł	LSLGLVCGLHHLHDAKKSVPQ
		l				MLEDFKQHPAV\APLIAGGKLV
						EYSAHVVPEAGINMLPELVGDL
		1				HERSLIFVASGPAGNSKETASD
						KLEEALPTKNWEVPGANWNTP
İ						GNGIPSVPEKLKGMLSAPNYRR
		1				MVLPAPLQILLLQNAKGGELLC
						AAGGQIAFNLGSAVGAYCGGM
		l				MLTLGLAYNYVALPAALLSFA
		1				AMSSLLLYGRYKRQQAADTPV
		l				LAKPLGQLDNAPFRCENVNLIR
				l	ŀ	EEIGFNALDKFKRTTGALLQLQ
					l	QALHPALGADLCGSTGFAVLFI
						SPVRGNTHLRHLVHIFGTDLDL
				1		NRHSVRADHRGVQRLIAVRFW
		l		l		NGDIVFHAARTRLVQAVHLAQ
						HAITGVRIIDDHAESVDVHDRV
l		l				KTLLFEHHFAVNRIKMLLPTTD
						AARYSRFLQTPFDFRKNLLDHL
25000	55368	Α	25138	1	1932	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1	i		sequence		
		<u> </u>				
25001	55369	Α	25139	1	1200	MAIPAFGLGTFRLKDDVVISSVI
		1			i	TALELGYRAIDTAQIYDNEAAV
1		1				GQAIAESGVPRHELYITTKIWIE
1		l				NLSKDKLIPSLKESLQKLRTDY
		1			į .	VDLTLIHWPSPNDEVSVEEFMQ
	į.	l				ALLEAKKQGLTREIGISNFTIPL
	į	1		1		MEKAIAAVGAENIATNQIELSP
						YLQNRKVVAWAKQHGIHITSY
						MTLAYGKALKDEGIARIAAKH
		l				NATPAQVILAWAMGGGPVE\W
						RR*QIWRGFSSAS*RHELYITTK
						IWIENLSKDKLIPSLKESLQKLR
						TDYVDLTLIHWPSPNDEVSVEE
1		1				FMOALLEAKKOGLTREIGISNF
1		1		1		TIPLMEKAIAAVGAENIATNQIE
		1				LSPYLONRKVVAWAKOHGIHI
		1				TSYMTLAYGKALKDEGIARIAA
		ľ				KHNATPAQVILAWAMGGGPVE
		ŀ				MAKVADMAGIFVSKLKTFNAG
						VKGSTLGASGPQYVMVPKKHA
	l					DOLRESLASGEIAAVOSTLVAD
1		i .				NTPLNSRVYTVRSGDTLSSIASR
1						LGVSTKDLQQWNKLRGSKLKP
						GOSLTIGAGSSAORLANNSDSIT
1	1	1				YRVRKGDSLSSIAKRHGVNIKD
1	İ					VMRWNSDTANLQPGDKLTLFV
		1				KNNNMPDS
25002	55370	A	25140	2237	2404	
25003	55371	A	25141	307	642	
25004	55372	A	25142	1449	2084	NAPRCAYY\VDVIAVTMPTTCC
Ι.						TLKISPLCRELILTLANRTTTQR
	1					AEPMTRRLIQVLFDELPQQPQQ
						QLHLPVSSHPKIRTMVEMMAK
						GPVEWGALGOWAGFFAMSER
		l				NLARLIVKETGLSFRQWRQQLQ
		1				LIMALQGLVKGDTVQKVAHTL
1		1				GYDSTTA\FITMLRKPGKTAGTS
1		1				LYHRRYGVSLLSSAWGQVGPP
1		1				RYCROANSVLSDRFCVLI
25005	55373	A	25143	981	1103	K TORQUES VESSER O VES
25006	55374	A	25144	222	379	-
25007	55375	A	25145	I	1452	
25007	55376	A	25146	500	854	
25009	55377	A	25140	1	1374	
25010	55378	A	25148	2	167	
25011	55379	A	25149	781	1047	
25012	55380	A	25150	1	783	
23012	22300	1^	123130	1.	1,00	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	coden for peptide	of peptide sequence	deletion, :possible nucleotide insertion)
1				sequence		
25013	55381	A	25151	1442	857	LVKNPVKRMEIQQKNLTLFEYL
		1				DWWDVLFLLLESELLFANTWL
1		1				AATSESVDDCSGVKPPSGKNGT
1		1				*AMPSWAKASIIASSARCAMLY
		1				SFCTQTISAILRASATCVGVTLL
						RPICFTRPCCCISASTVRLASIDP
						SAGP
25014	55382	Α	25152	3	4105	
25015	55383	Α	25153	2	269	YKNPYIAAKIQPKTHDTLTPINP
		1				GRIKLWLMTKRPMWVVPERSN
		1				*IAARSLG*VGRM**P*QAGAE
		1				ATMYAGSTPIASATGTIAASAA
		1		i		A
25016	55384	Α	25154	1	1370	MCPIEETASSFGGKPLSMVLVIQ
						MFMLLTGALIIILTKTNPASISK
		1				NEVFRSGMIAIVAVYGIAWMA
İ		1				ETMFAPACYGYYILPTYPSDLA
1	1	ı				AIQFDRSGTTHIGRFVINHSFILP
1		1				GLIGVSVSCVFGWIFAAIKRDA
						AAGRAKENVIFHHFPFQSVKAD
						IATNPFKRPGGAFIRITQTFRTV
		ŀ		l		QTFRLSAYRLDFAGDRLRISTPR
						AKMRTAFKKDHLRQRRRCIRQ
						RAPPARHNLVGAVALPATVAG
				l		VNFTFSNVPLDSSVLSSLLTDFS
						TAVGSIVMLAVIMGLMLAFDM
						GGPVNKVAYAFMLICVAQGVY
				l		TVVAIAAVGICIPPLGMGLATLI
		1				GRKNFSAEERETGKAALVMGC
		1		l		V\GVTEGAIPFAAADPLRVIPSI
		1	l			MVGSVGGAVTAALVGAQCYA
				l		GWGGLIVLPVVEGKLGYIAAV
						AVGAVVTAVCVNVLKSLARKN
		_				GSSTDEKEDDLDLDFEIN
25017	55385	A	25155	1	789	MKIIAGITPADSGTLEIEGNNYV
					1	RLTPVHAHQLGIYLVPQEPLLFF
				l	1	SLSIKENILFGLAKKQLSMQKM
						KNLLAALGCQFDLHSLAGSLD
						VADRQMVEILRGLMRDSRILIL
	1	1	l			DEPTASLTPAETERLFSRLQELL
	1	1		I	1	ATGVGIVFISHKLPEIRQIADRIS
		1	1			VMRDGTIALSGKTSELSTDDIIQ
		1				AITPAVREKSLSASQKLWLELP
	1	1		1	1	GNRPQHAAGTPVLTLENLTGE
	1	1	l			GFRNVSLTLNAGEILGLAG/TEL
		L				AETLYGLRTLRGGRIML
25018	55386	Α	25156	I	1332	

SEQ ID	leco in vo.	D4	SEQ ID NO:	Inc. de alla	[Nt. 4/3. tt614	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence		
25019	55387	IA	25157	1594	2220	MWVNPERGRAENTIIGGNATGI
23019	33361	^	23137	1394	2220	GTLNVQDQDSVITVRRLS*SAL
		1				KPGILVFKLTPAETERLFSRLQE
		1				LLATGVGIVFISHKLPEIRQIAD
		l				RISVMRDGTIAGTGFGDDFGFT
		l			İ	HPLRQQRLPQHLVSFMRAAVQ
1		l			1	QIFTLEIQRGVRPGCNVLAFGQ
						RGWTPGIVFQQVVELSLKFRIFL
		1				RTDKSFFQLAQSRHQDLWHVH
l						AAKLTKIGVK
25020	55388	A	25158	14	237	KTTSFPAKLFNACRISLLASAE/
23020	22360	<u>۱</u> ^	23136	'"	237	CQSEYFSIFSNMDLADTVMFL*
	l					GAIRFSDLVNEQIQHTFLIPGETI
					1	CRLSEVV
25021	55389	A	25159	h	1506	CKLSEVV
25022	55390	A	25160	158	639	SGC*PGRPSLN/GRLDVLSAWS
23022	33370		25100	150	007	VSILRLGGMALEGSIAYIVINFC
		1				DVKPQRFRGLSVPAASITVVLIC
				1		QFVLHRRELRRKLALPAHHLVT
		l				FTWGNVSAVDETRQWMVIKPS
ŀ		1				GVEYDVMTADD\RWWLR*PAV
		l				RWWKAAKNPLPIHQRIWRSTV
		l				AMPKLAVLC
25023	55391	Α	25161	2	2886	SVPTIIFFFLPVLRFWRPGIQQA
		l				KKCHLFATGTQSRRNTLRQRT
ľ		l				AKGIPQQRMTAKREEISIGILHV
		l				TPOORRECRGDNRFTARFRRTP
		l	l			WRLLGHCVSAAVTGVLPAVAG
		l				SPLAYSDTDEFYPVAGGTMSQ
ł						HLPLVAAQPGIWMAEKLSELPS
ł		1				AWSVAHYVELTGEVDSPLLAR
1		l		ł		AVVAGLAQADTLRMRFTEDNG
i		1	l			EVWQWVDDALTFELPEIIDLRT
		ł				NIDPHGTAQALMQADLPQDLR
		1				VDSGEPLVFHQTTLGFI
25024	55392	Α	25162	I	1659	
25025	55393	В	25163	200	646	
25026	55394	A	25164	I	3197	MPHRQHGPQMTPSHQRTTINR
		ı			i	DQREQQPIGTAAPQTRPQSAPY
1		l				CEPHTRRRTLQPHNRGFRTAKY
		1		i		TSTQARKYHMARPERSNDSDH
				l		PVHTRSRWNATQTERHTQHHV
		1				SPPSSLRTLRTNCTSHAHHRYH
1						RHAQWHRVGLLDVKPTGVPSN
		1				TVFSPPKNALWADRVDTSRGR
1		1				TTVEQDNHPNGGNVVGTPSDN
			l			NFWLETTGGDPNKEYYHHHHY
1						NEDYCRYYPLLIAEPLLFPSLSI
		$\perp$				KENILFGLAKKQLSMQKMK
25027	55395	В	25165	1	2505	

3330

NO: of peptide sequence of	SEO ID	SEO ID NO:	Mat	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
sequence   09/540,217   code for peptide sequence   defeion, impossible nucleotide insertion)   sequence   sequence   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion   defeion, impossible nucleotide insertion)   defeion, impossible nucleotide insertion   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible nucleotide   defeion, impossible n	NO:						
25028   55396   A   25166   159   1744   NSRISGLQQRYLMHIMVTQGG   MSLSIVHTRAALGVNAPPITVE   VIHSKGLPGLTMVGLPETTVKI   ARDRYWRSAINSGYEPAKKIT   NLAPADLPKEGGRYDLPIAIAL   LAASEQLTANKLDEVELVGEL   ALTGALRGVPGASSATEAISKS   RKIIVAKDNEDEVGLINGEGCL   ADHLQAVCAFLEGKHALERFK   PTDAVSRALQHDLSDVIGGEGC   GRRVLEITAAAGHNLLLIGPPG   TIGKTMLASRINGLIPDLSNEES   LESAAILSLVNAESVOKLWRQ   PERSPHHSASLTAMVGGAIPC   PFRSPHHSASLTAMVGGAIPC   PFRSPHHSASLTAMVGGAIPC   GRINNCTPECTLRYLNRLSGP   LDRFDLSLEIPLPPGILSKTVV   GRINNCTPECTLRYLNRLSGP   LDRFDLSLEIPLPPGILSKTVV   GESSATVKGRVMAARERQFKF   QNKLNAWLDSPEIRCPCKLEST   DAMWLEGTLHILGLSTRAWG   LLKVARTIADIDQSDITPTYGG   KADARNSGNVCPSSRALVQR   LKVARTIADIDQSDITPTYGG   KADARNSGNVCPSSRALVQR   LESEKLKNIFNRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPRPSGRLSYGT   RMFDIGVNLTSGRAFKTVPTAPFLLPLELRELLPLIP   AEKL*YTETDAPFLLPRDLSAK   STSRYHCVIEARAWFK   STSRYHCVIEARAWFK							
MSLSIVHTRAALGVNAPPITVE VHISKGLPGLTMVGLPETTVKI ARDRV/RSAINRSGVEYPAKKII NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEVELVGEL ALTGALROVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFW PTDAVSRALQHDLSDVIGQEG GKRVLETTAAAGHNLLLIGPFG TGKTMLASRINGLLPDLSSNES LESAAILSLVARESVORLWRQI PERSPHHSASLTAMVGGGAIPC GGHNRCTFEGTLRYLNRLSGP LDRAFEGGGHLSKTRAKI TYPARFQLVAAMMPSPTGHVY GGSSATVKQRVMAARERQFKI QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHLGLSIRAWG LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSOPAKTVMMI **RARLGR-**TTGLELRELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK				,			. ,
MSLSIVHTRAALGVNAPPITVE VHISKGLPGLTMVGLPETTVKI ARDRV/RSAINRSGVEYPAKKII NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEVELVGEL ALTGALROVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFW PTDAVSRALQHDLSDVIGQEG GKRVLETTAAAGHNLLLIGPFG TGKTMLASRINGLLPDLSSNES LESAAILSLVARESVORLWRQI PERSPHHSASLTAMVGGGAIPC GGHNRCTFEGTLRYLNRLSGP LDRAFEGGGHLSKTRAKI TYPARFQLVAAMMPSPTGHVY GGSSATVKQRVMAARERQFKI QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHLGLSIRAWG LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR LLKVARTIADIDQSDITPTYGG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSOPAKTVMMI **RARLGR-**TTGLELRELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK							
VHISKGLPGLTMVGLPETTVKI ARDRVIRSA IINSGYEYPAKITI NLAPADLPKEGGRYDLPIALAL LAASEQLTANKLDEYELVGEL ALTGALRGVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHILQAVCAFLEGKHALERFK PTDAVSRALQHDLSDVIGQECC GKRVLEITAAAGHNLLLIGPPG TIGKTMLASRINGLIPDLSNEGE LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEFERI TLDALREPIESGQHLSRTRAKI TYPARFQLVAAMPSPTGHVC GNHNRCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVV GGESSATVKGRVMAARERGFK QNKLNAWLDSPEIRCFCKLESI DAMWLEGTLHILGLSIRAWGR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR KADARNSGNVCPSSRALVQR RMFPGIGVILTSGRGNEEEDNI 25029 55397 A 25167 127 503 NRCLLUTLLRCKGRNREEEDNI EAESEKLKNIFNRPSGRLSYGI RMFPGIGVILTSGRGNAETTGHEL RARLGRTTGLELRELIPLIP ARKLYYETDAPYLLIPROLSAK STSRYHCVIEARAWFK	25028	55396	Α	25166	159	1744	NSRISGLQQRYLMHIMVTQGGL
ARDRYIRSAIINISGYEYPÄKKIT NLAPADLPKEGGRYDLPIAIAL LAASSQLTANKLDEVELVGEL ALTGALRGVPGAISSATEAIKS RKIIVAKDNEDEVGLINIGGECL ADHLQAVCAFLEGKHALBERR PTDAVSRALQHDLSDVIGQEC GKRYLEITAAAGHNLLIGPPG TGKTMLASKINGLPDLSNEEA LESAAILSLVNSEVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFDLEPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHYC GGNHNRCTPECTIRYLNRLSGPI LDRFDLSLEPILPPPGILSKTVV GESSATVKGRVMAARERGPK QKLNAWLDSPEIRCPCKLESI DAMWLEGTLIHLGLSIRAVGR LLKVARTIADIDQSDITPTYGG KADARNSONVCPSSRALVQR RUKHANGLPDLSAK 25029 55397 A 25167 127 503 NRCLLUTLLRCKGRNREEEND EAESEKLKNIFNRPSGRLSYGI RMFDIGVNLTTSGVAFATVILLPROLSAK STSRYHCVIERAWFK STSRYHCVIERAWFK STSRYHCVIERAWFK				İ			MSLSIVHTRAALGVNAPPITVE
NLAPADLPKEGGRYDLPIAIAL LAASEQLTANKLDEYELVÜGEL ALTGALRGUPGAISSATEAIKS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFN PTDAVSRALQHDLSDVIGQEQ GKRVLEITAAAGHNLLLIGPFG TGKTMLASRINGLIPDLSNEES LESAAILSLVNAESVOKLWRQ PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPAREQLVAAMMPSPTGHVY GHNINCTPEQTLRYLNRLSGP LDRFDLSLEIPLPPFGILSKTVV GESSATVKGRVMAAREROFKF QNKLNAWLDSPEIRCFCKLESI DAMWLEGTLHILGLSIRAWGR LLKVARTADIDQSDITPTYGG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLUTLRCKGRNREEEND EAESEKLKNIFNRPSGRLSVGI RMFPGIGVILTSGRAFKTREEND EAESEKLKNIFNRPSGRLSVGI RMFPGIGVILTSGRAFKTREEND EAESEKLKNIFNRPSGRLSVGI RMFPGIGVILTSGRAFKTREEDEND **RARLGLETTLECKGRNREEEND** **RARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **RARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNEEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND** **PARLGLETTLECKGRNREEEND*				ŀ			VHISKGLPGLTMVGLPETTVKE
LAASEQLTANKLDEYELVGEL ALTGALRGVPGAISSATEAIKS RKIIVAKDNEDEVGLINGEGGL ADHLQAVCAFLEGKHALERPR PTDAVSRALQHDLSDVIGGGEG GRRVLEITAAAGHNLLLIGPPG TGKTMLASRINGLIPDLSNEA LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFDLEPEFERI TLDALREPIESGQHLSSTRAKI TYPARFQLVAAMNPSPTGHYQ GGSATVKQRVAMARERQFK QKILNAWLDSPEIROFCKLESI DAMWLGGTLHLGLSIRAWG LLKVARTIADIDQSDITPTYCG KADARNSONVCPSSRALVQR RVETTAAPULFTCLSAK Z5029  55397 A 25167 127 503 NRCLLUTLLRCKGRNEEEDH EAESEKLKNIFNRPSGRLSYGI RMFPGIGVNLTSSQFAKTVMM **RARLGLR**TTGLELRELIPLIP AEKL**YFTDAPYLLFROLSAK STSRYHCVIEARAWFK	1						ARDRV/RSAIINSGYEYPAKKITI
ALTGALROVPGAISSATEAIRS RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFR PTDAVSRALQHDLSDVIGQEG GKRVLEITAAAGHNLLLIGPEG TGKTMLASRINGLLPDLSNEE LESAAILSLVNAESVQKLWRQ) PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNEPSTGHVC GGHNRCTFEQTLRYLNRLSGP LDRFDISLEIPLPPFGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRGPCKLESI DAMWLEGTLHILGJSRAWGR LLKVARTIADIDQSDIITPTYGG KADARNSGNVCPSSRALVQR LLKVARTIADIDQSDIITPTYGG KADARNSGNVCPSSRALVQR EASESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSQPAKTVMM **RARLGR.RTGLELEELLPLP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l			ŀ			NLAPADLPKEGGRYDLPIAIAL
RKIIVAKDNEDEVGLINGEGCL ADHLQAVCAFLEGKHALERFK PTDAVSRALQHDLSDVIGQEGC GRRVLEITAAAGHNLLLIGPPG TGKTKILASRINGLIPDLSNEE LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLIPDLEIPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHVY GNHNRCTPEGTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR RULLVLLRCKGRNREEEND EAESEKLKNIFNPSGRLSYGI RNFPGGVNLTSSQPALTVMMI *RARLGLR*TTGLELRELLPLIP AEKL*YFETDAPYLLGPROLSAK STSRYHCVIEARAWFK				l		İ	LAASEQLTANKLDEYELVGEL
ADHLQAVCAFLEGKHALERPK PTDAVSRALQHDLSDVIGQEG GRRVLEITAAGHNLLLIGPPC TOKTMLASRINGLPOLSNEE LESAAILSLVNAESVQKLWRQI PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPFERR TLDALREPIESGGHHSSTRAKL TYPARFQLVAAMNPSPTGHYC GRHNRCTPEQTLRYLNRLSGPI LDRPIJSLEIPLPPFGILSKTVY GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNV CPSSRALVQR 25029 55397 A 25167 127 503 NRCLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPGIGVNLTSSQFAKTVMMI **RARLGLR**TTGLELEELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK							ALTGALRGVPGAISSATEAIKSG
PTDAVSRALQHDLSDVIGQEQ GKRVLEITAAAGHNLLLIGPFG TGKTMLASRINGLLPDLSNEE LESAAILSLVNAESVQKLWRQI PERSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMPSPTGHVY GRHNRCTPEQTLRYLNRLSGPI LDRFDLSLEFILPPFGLLSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDITPTYG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLUTLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSGPAKTVMM *RARLGLR-TTGLELRELLPLP AEKL*YPETDAPYLLPRDLSAK STSRYHCVIEARAWFK					1		RKIIVAKDNEDEVGLINGEGCLI
GRRVLEITAÄAGHNILLIGIPG TGKTMLASRINGLIPDLSNEA LESAAILSLVNAESVOKLWRÖJ PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELPEEFRI TLDALREPIESGOJHLSRTRAKI TYPARFQLVAAMNPSPTGHYC GGHNRCTPEGTLRYLNRLSOPI LDRFDLSLEIPLPPFGILSKTVV GESSATVKGRVAMAERGPKF QNKLMAWLDSPEIRCFCKLESI DAMWLEGTLHILGJSRAWOR LLKVARTIADIDQSDITFTYCG KADARNSONVCFSSRALVQR ROMELLTLLRCKGRNEEEDN EAESEKLKNIFNRPSGRLSYGI RMFDIGVNLTSSGPAKTVMMI **RARLGLR**TTGLELRELLPLIP AEKL**YFTDAPYLLFROLSAK STSRYHCVIEZARAWFK				ł			ADHLQAVCAFLEGKHALERPK
TÜKTMLASRINGLPÖLSNEE LESAAILSLVARESVÖKLW?QI PPRSPHHSASLTAMVGGGAIPC POEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHYC GNHNRCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSQFAKTVMMI *RARLGLR-TTGLELRELLPLIP AEKL-YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	1						PTDAVSRALQHDLSDVIGQ\EQ
LESAAILSLVNAESVOKLWRQI PFRSPHHSASLTAMVGGGAIN PFRSPHHSASLTAMVGGGAIN PRESPHHSASLTAMVGGGAIN POEISLAHNGVLFLDELPEFERI TLDALREPIESGQIHLSRTRAKI TYPARFQLVAAMNPSPTGHVY GNHNRCTPEQTLRYLNRLSOPI LDRFDLSLEIPLPPPGILSKTVV. GESSATVKQRVMAARERQFK* QNKLNAWLDSPEIROFCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR RESEKLKNIFNPSGRLSVGI RMFDIGVNLTSSGPAKTVMMI *RARLGLR**LTGLELRELLPLIP AEKL**YETDAP*LLIPROLSAK STSRYHCVIEARAWFK				l			GKRVLEITAAAGHNLLLIGPPG
PFRSPHHSASLTAMVGGGAIPC PGEISLAHNGVLFLDELEPFERI TLDALRPIESGGHLSATRAKI TYPARFQLVAAMNPSPTGHYQ GNHNCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPPGILSKTVVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPERIGPGCLESE DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYGG KADARNSGNVCPSSRALVQR EASSEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQGAKTVMMI *RARLGLR*TTGLELRELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK		ł		ŀ			TGKTMLASRINGLLPDLSNEEA
PGEISLAHNGVLFLDELPFERI TLDALREPIESGQIHLERFERI TLDALREPIESGQIHLERTRAKI TYPARFQLVA AMMPSPTGHVC GNHNRCTPEQTLRYLNRLSOP LDRFDISLEPIELPPFGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIROFCKLESI DAMWLEGTLHLGLSIRAWOR LLKVARTIADIDQSDITPTYCG KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPGIGVNLTSSQFAKTVMM *RARLGLR-TTGLELRELLPLP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	ł						LESAAILSLVNAESVQKLWRQR
TI.DALREPIESGQİHLSRTRAKI TYPARFQLVAAMNPSPTGHYÇ GRHNRCTPEÇTLRYLNRLSGİP LDRFDLSLEIPLPPFGILSKTVV. GESSATVKQRVAARREPÇKE QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLİHLGLSIRAWQR LLKVARTIADİDQSDİİTPTYGG KADARNSGNVCPSSRALVQR ROMENDE VESTAVILLE VESTAVA VEŞEVLÜLLE VEŞEVLEYLE VE VE VEŞEVLEYLE VEŞEVLEYLE VE VEŞEVLEYLE VEŞEVLEYLE VEŞEVLEYLE VE VEŞEVLEYLE VE VEŞEVLEYLE VE VEŞEVLEYLE VEŞEVLEYLE VEŞEVLEYLE VE VE VE VE VE VE VE VE VE VE VE VE VE	l						PFRSPHHSASLTAMVGGGAIPG
TYPARFQLVAAMNPSPTGHYQ GNHNRCTPEQTLRYLNRLSGPI LDRFDLSLEIPLPPFGILSKTVV GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNV CPSSRALVQR EASSEKLKNKFNRSGRLSYGI RMFDIGVNLTSSQFAKTVMM **RARLGR**TTGLELRELLPLIP AEKL**YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l						PGEISLAHNGVLFLDELPEFERR
GNHNRCTPEOTLRYLNRLSOP LDRFDLSLEIPLPPPGILSKTVV GESSATVKQRVMAARERQFK QNKLNAWLDSPEIRCPCKLESI DAMWLEGTLHILGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR RS55997 A 25167 127 503 NRCLLITLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMM *RARLGR*TTGLELRELLPLIP AEKL*YFETDAPLLIPROLSAK STSRYHCVIEARAWFK		}					
LDRFDLSLEIPLPPPGILSKTVV. GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYCG KADARNSGNVCPSSRALVQR EASSELTLRCKGRNREEEND. EASSEKTLKNKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGR*TTGLELÆELLPLIP AEKL*YYETDAPYLLPRDLSAK STSKYHCVIEARAWFK							TYPARFQLVAAMNPSPTGHYQ
GESSATVKQRVMAARERQFKF QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIDQSDIITPTYGG KADARNGGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLLTLLRCKGRNREEEND. EAESEKLKNKFNRPSGRLSYGI RMFPIGVNLTSSQFAKTVMMI *RARLGLR*TTGLELEELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK			- 33		l		
QNKLNAWLDSPEIRQFCKLESI DAMWLEGTLIHLGLSIRAWQR LLKVARTIADIOSDHITPTYGG KADARNSGNVCPSSRALVQR NRCLLLTLRCKGRNREEND. EAESEKLKNIKFRNEPSGLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGR-*TTGLELRELLPLIP AEKL-*YETDAPYLLPRDLSAK STSRYHCVIEARAWFK							
DAMWLEGTLIHLGLSIRAWOR LLKVARTADIDOSDIITPTYCG KADARNSONVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLTTLRCKGRNREEEND EAESEKLKKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGR*TTGLELRELLPLIP AEKL-YVETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l						GESSATVKQRVMAARERQFKR
LILKVARTIADIDQSDITPTYÖC KADARNSGNVCPSSRALVQR 25029 55397 A 25167 127 503 NRCLLUTLERCKGRNREEEND EAESEKLKNIFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMM *RARLGER*TTGLELRELLPLIP AEKL*YETDAPYLEPROLSAK STSRYHCVIEARAWFK					l		QNKLNAWLDSPEIRQFCKLESE
25029 55397 A 25167 127 503 NRCLLITLIRCKGRNREEND. EAESEKLIKNERNEPSGLESYGI RMFDIGVNLTSSQFAKTVMML *RARLGR*TTGLELRELLPLIP AEKL-VYETDAPYLIPRDLSAK STSRYHCVIEARAWFK							DAMWLEGTLIHLGLSIRAWQR
25029 55397 A 25167 127 503 NRCLLTTLRCKGRNREEEND EAESEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQGAKTVMM *RARLGR*TTGLELEELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK	l						LLKVARTIADIDQSDIITPTYCG
EAESEKLKNKFNRPSGRLSYGI RMFDIGVNLTSSQFAKTVMML *RARLGLR*TTGLELRELLPLIP AEKL*YYETDAPYLLPRDLSAK STSRYHCVIEARAWFK							KADARNSGNVCPSSRALVQR
RMFDIGVNLTSSQFAKTVMML *RARLGER*TTGLELÆELLPLIP AEKL-YVETDAPYLIPRDLSAK STSRYHCVIEARAWFK	25029	55397	Α	25167	127	503	NRCLLLTLLRCKGRNREEENDA
*RARLGR*TTGLELRELLPLP AEKL*YETDAPYLLPRDLSAK STSRYHCVIEARAWFK							EAESEKLKNKFNRPSGRLSYGD
AEKL*/YETDAPYLLPRDLSAK STSRYHCVIEARAWFK					l		RMFDIGVNLTSSQFAKTVMML
STSRYHCVIEARAWFK							*RARLGLR*TTGLELRELLPLIP
					l		AEKL*/YETDAPYLLPRDLSAKP
25030   55398   A   25168   3   406							STSRYHCVIEARAWFK
	25030	55398	Α	25168	3	406	

SEO ID	ISEO ID NO:	Me	SEO ID NO:	Nucleotide	Nucleotide location of lost	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
		1		sequence		
25031	55399	I <sub>A</sub>	25169	11	1252	MFDIGVNLTSSOFAKDRDDVV
25051	33399	<u> </u> ^	23103	ľ	1232	ACAFDAGVNGLLITGTNLRESO
		l				QAQKLARQYSSCWSTAGVHSH
		1				DSSQWQAATEEAIIELAAQPEV
		1				VAIGECGLDFNRNFSTPEEOER
		l				AFVAQLRIGADLNMPVFMHCR
İ						DAHERFMTLLEPOMVENYETLI
					İ	FEAHSTDYOTPOSLROLVIDHF
		1		1		AILKVGPALTFALREALFSLAAI
		1				EEELVPAKACSGLROVLEDVM
				İ		LDRPEYWQSHYHGDGNARRLA
		ı				RGYSYSDRVRYYWPDSQIDDA
		1				FAHLVRNLADSPIPLPLISOYLP
		l				LQYVKVRSGELQPTPRELIINHI
		1				ODILAHTTOPVKANKONKEEH
		1				AMPNIVLSRIDERLIHGOVGVO
		İ		l		WVGFAGANLVLVANDEVAED
		ı				PVQQNLMEMVLAEGIAVRFWT
		l				LOKVIDNIHRAADROKILLVCK
		i				T*WKWYWOKGSPYVSGRCKK
		1			l	LSTTFIAPPIDRKSCWFVKHPPIS
25032	55400	A	25170	2	319	YSSVFSLSASASFSSSRFRPLPT*
						KREKKTPISNROYIGIANSVCEK
		1			1	TSGGVSNIPTTNAPTSTYGRFLR
		1				KSSGEVIPIQHSSTIATGTSKETP
						NAINSAITKLK
25033	5540I	Α	25171	1	1011	MIPHPKLEGDRSTQALPPTPVIR
		1				VTERRNLNWVGTTIGFVHTGK
	Į.	1			ł	PLSFVYDMADIIKFDTVVPKAF
	1	l		l	ļ	EIARRNPGEPDREVRLACRDIFR
		1				SSKTLAKLIPLIEDVLAAGEIQPF
		l				APPEDAQPVAIPLPVSLGDAGH
	İ	ı				RRRRSGRVSEVSWRSGVMSFR
		l				RASGDKPQPKPKVMPEHAECPF
	1	l		l		AARRGQMMSICPCFALKIDIAD
		l				NKFFNGETSPLFSQSQAKLARQ
	1	1				FHQKIAGYRPTPLCALDDLANL
		l		1		FGVKKILVKDESKRFGLNAFK
	1	ı				MLGAPEKCHRRKNDF*RRSDRI
		1				VLIRL*REFSSHQKGLRDRPAH
						KAVLGDNQLFSGGTGAPVWPG
		1				FAKRAVMF/TPLKNLLSAISIFN
						AKHGHILIIWPRLAAGGHSACS
		1			1	GITFGFGCGLSPLARRKLMTPE
						RQLTSDTRPDRLLRWPASPSET
1		1				GSGMATGCASSGGAGGCISPA
		1				ASTSSISGINLANVLLLRKISLH
1		ĺ				AKRTSRSGSPGLRRAISKAFGTT VSNLMMSAIS
25034	55402	-	25172	ı	510	A 2INFIMIM2VI2
25034	55402	A B	25172	1	1482	
23033	153405	ρ_	2110	11	1702	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
25036	55404	А	25174	704	1069	RLWQADCKENAGGDYYWTFF PQPTFVSTQKYYCHVDNSCYM NFDFSAPEYHAHWRYGLLMVG ESQHGLGANAIQASQCFKAAN QPLGADATFLQQIKGEIICFGLFI TGVFSIDSAFCDIT
25037	55405	А	25175		639	MARWUCDFPYGVLPTLNAM PESTRKQIMPWTRLSGSLHTWN FTPNRRIGRYPSGLPPDSANRPR REPDACRSLHSPAKYRGNPNBD RLDHQQNGLPARGKDTPRSNK PSISQWTNTKPQPRHQPRGKG HKSPAPEMPKPPQATSSTREQT KYGAAELWRSPWKTRYIELKA RGPMACVTISLNVCCAHLVRL VMVTLKQTDPIRNLGEMPSKSQ TKKAREVHLHSLHLQELQQE EPPARKRKTQWAVSEKK
25038	55406	Α	25176	82	356	AQCEEYRVPQTLKRNPKQCFDI SIRGGSQPCGIFSTPVRNTLQNM GQMGWLVAPG*WLWREIRKH NRWCACPRKPGRAGISMALRW GSGHA

SEQ ID NO:	SEQ ID NO:		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	noa	09/540.217	codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or pepude sequence	detection, (-possible nucleotide insertion)
25039	55407	Α	25177	I	2635	MNKSGKYLVWTVLSIMGAFAL
		i				GYIALNRGEQINALWIVVASVO
		ŀ				IYLIAYRFYGLYIAKNVLAVDP
	1					TRMTPA VRHNDGLDY VPTDKK
						VLFGHHFAAIAGAGPLVGPVLA
						AQMGYLPGMIWLLAGVVLAG
		ł				AVQDFMVLFVSTRRDGRSLGE
		l				LVKEEMGPTAGVIALVACFMI
		1				MVIILAVLAMIVVKALTHSPWC
	}					TYTVAFTIPLALFMGIYLRYLRF
						GRIGEVSVIGLVFLIFAIISGGWV
	ı					AESPTWAPYFDFTGVQLTWML
						RLINRSIMMDFSLTEEQELLLAS
						IRELITTNFPEEYFRTCDQNGTY
		1				PREFMRALADNGISMLGVPEEF
						GGIPADYVTQMLALMEVSKCG
				ł.		APAFLITNGQCIHSMRRFGSAE
						QLRKTAESTLETGDPAYALALT
						EPGAGSDNNSATTTYTRKNGK
					ĺ	VYINGQKTFITGAKEYPYMLVL
				1		ARDPQPKDPKKAFTLWWVDSS
						KPGIKINPLHKIGWHMLSTCEV
		ĺ				YLDNV*TSVWRTCACPALRRA
						TQRYRRQSRAGNLRTSGEAIRR
		1				DMEWTSLRSE\DWEKGDTIKQC
					1	ISAATSCVYGVTGEGILEGGDA
						QILREPLPGTKLGLLNWPVFDA
						LESRSTRERDGKPGGEICGETA
	1				ĺ	NILIRGPENRPLRRDPPGKP

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25040	55408	A	25178	216	1829	TVCRCHFVTTKHIGRERNQRAR
23040	33404	ľ`	23170	1.0	1025	OCLVGKTTDTQQHNCDIRVGE
1		1				OADHTRANHOHCTORYDHLTG
						NDOVHTKPTLEQRRQVTTEDT
]						TEVSKQHRHPGEHRDLFQRTLN
1						ISADDORRLLLELONDNLNHNR
		ļ			i	IWLRLAAQPEDHIYGCGEQFSY
1				l	l	FDLRGKPFPLWTSEQGVGRNK
				l		QTYVTWQADCKENAGGDYYW
		l			i	TFFPQPTFVSTQKYYCHVDNSC
		l		l		YMNFDFSAPEYHELALWEDKA
					1	TLRFECADTYISLLEKLTALLGR
						OPELPDWIYDGVTLGIQGGTEV
						COKKLDTMRNAGVKVNGIWA
						ODWSGIRMTSFGKRVMWNWK
						WNSENYPOLDSRIKOWNOEGV
						OFLAYINPYVASDKDLCEEAAO
ļ						HGYLAKDASGGDYLVEFGEFY
						GGVVDLTNPEAYAWFKEVIKK
					İ	NMIELGCGGWMADFGEYLPTD
						TYLHNGVSAEIMHNAWPALW
		l				AKCNYEALEETGKLGEILFFMR
		l				AGST/GDIGG\YTTLFEMKRSKE
						LVLRWCDFSAFTPMMRTHEGN
						RPGEHWAF/DGDAKHRHLAVY
25041	55409	Α	25179	277	488	
25042	55410	В	25180	260	1500	
25043	55411	Α	25181	1	764	MQEWGRYTILSGCCNSALKGD
		l				VCLLYGFRVAGRRQASE*TPGA
		l				YNRVPSSKK*GFQLVLLPFSAN
		l				GKSPAY*RFSKSFAEDGEKDAG
		ı				FPHPYAEAGYDNGGRRSGAGT
		ı				LLSR*I*TGAGRGAWRV*RLTG
		l				E*MAGKRT*VTASGYSQR*IMV
l		l		l		FLWSLYRSYRL/GRVRQHNGPR
		l				YLPVLARNWKMSAWVAAAW
		l				QGLTDMKRKTMKIRSGS\IVILA
		l				SGYAATAA*PLSGDRIFLP*PGK
		L				TG*RHGGTPSCAGFTGDY
25044	55412	В	25182	1	3117	
25045	55413	В	25183	270	388	
25046	55414	Α	25184	2154	2279	
25047	55415	Α	25185	614	623	RPNSGAR*GRGDKRSTQSVPET
	1	1		I		VRLLFCAGTFDQQPGNARWDD
		1		1		QYRCIRSGIVGVRAVLLGGDIL
				<u> </u>		DTQPLPVELAETLGKSAE

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		05/540,217	sequence	or popular sequence	, , , , , , , , , , , , , , , , , , , ,
25048	55416	A	25186	1208	2813	CYGVAWPFDPTLKFEFWRYFT
						HALMHFSLMHILFNLLWWWY
			i		l	LGGAVEKRLGSGKLIVITLISAL
		1				LSGYVQQKFSGPWFGGLSGVV
						YALMGYVWLRGERDPQSGIYL
						RRGVIIFAPIWIVRRWFEMTPTQ
						WSNYFFENLFKYEWVQTRSPA
						GAIQFEAVDAPEIIPDPFDPSKK
						RKPTMLVTDLTLRFDPEFEKISR
						RFLNDPQAFNEAFARAWFKLT
						HRDMGPKSRYIGPEVPKEDLIW
						QDPLPQPIYNPTEQDII\DLKFAI
		l				ADSGLSVSELVSVAWASASTFR
					l	GGDKRGGANGARLAL\MPQTR
						TGDVTRRQPIRAL\PVLE\KIQKE
		l				SGKASLADIIVLP\GLFVVEKSA
		1				SAAGLSIHVPFAPGRVDARQDQ
					l	\TAIGMFELLEPIADGFRNYRAR
						LDVSTTESLLIDKAQQLTLTAPE
				l		MTALVGGMRVLGANFDGSKN
						GVFTDRVGVLSNDFFVNLLDM
		l				RYEWKATDESKELFEGRDRET
		l				GEVKFTASRADLVFGSNSVLRA
		l				VAEVYASSDAHEKFVKDFVAA
		l				WVKVMNLDRFDLL
25049	55417	Α	25187	1520	1960	PVPLNFGWQRSTEVLICHVNSP
		1		1		STAAMTISPWRR**RRRTKQLS
		l				APLLLGVSAIGW/LTIILVAFMA
		1				WLLAKT/AFGRSFYATGDNLQG
		1				AR/QLGVRTEAIRIVAFSLNAER
		1				DFDDLRDSGPLIAMILFIMPTLS
						SISSRRLNPGVPSEI
25050	55418	A	25188	1155	1778	SASGGVMLKFIQNNREITALLA
		l	1			VVLLFVLPGFLDRQYLSVQTLT
						MVYSSAQILILLAMGATLVMLT
		1				RNIDVSVGSITGMCAVLLGMLL
						NAGYSLPVACVATLLLGLLAGF
		l				FNGVLVAWLK/IPAIVATLGT\L
					1	YRGLMSLWTGGHWFEGYPRIE
	1	l				KPSPPVAGVHHWCVTQIGGLRF
						AVAKRVGPDLPGDNKGAKGVL
	1	1	1			NTLDNYGVDGKCV

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide		in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25051	55419	A	25189	1	2227	I MVTIAGIILGGLALVGLITYFGK
23031	33417	^	23107	1	1221	WTYLWKEWLTSVDHKRLGIM
					ĺ	
			ŀ		1	YIIVAIVMLLRGFADAIMMRSQ
						QALASAGEAGFLPPHHYDQIFT
						AHGVIMIFFVAMPFVIGLMNLV
			İ			VPLQIGARDVAFPFLNNLSFWF
			İ			TVVGVILVNVSLGVGEFAQTG
			i			WLAYPPLSGIEYSPGVGVDYWI
						WSLQLSGIAVAHIAAQNVAVLI
						ISSDLEEIELMADRVYVMHQGE
						ITHSALTERDINVETIMRVAFGE
						SQRGVMLKFIQNNREITALLAV
						VLLFVLPGFLDRQYLSVQTLTM
						VYSSAQILILLAMGATLVMLTR
						NIDVSVGSITGMCAVLLGMLLN
						AGYSLPVACVATLLLGLLAGFF
						NGVLVAWLKIPAIV\ATLGTLG\
						LYRSIMLLWTGGQWIEGLPAEL
						KQLSAPLLLGVSAIGWLTIILVA
						FMAWLLAKTAFGRSFYATGDN
						LQGARQLGVRTEAIRIVAFSLN
						GCMAALAGIVFASQIGFIPNQT
				1		GTGLEMKAIAACVLGGISLLGG
						SGAIIGAVLGAWFLTQIDSVLV
						LLRIPAWWNDFIAGLVLLAVLV
						FDGRLRCALERNLRRQKYARF
			i			MTPPPSVKPASSATSDFICIGIVA
						LPLTMVIVSGGIDISFGSTIGLCA
						IALGVLFQSGVPMPLAILLTLLL
1 1						GALCGLINAGLIIYTKVNPLVIT
						LGTLYLFAGSALMLSEEQKNTK
						KTRQREDKKKEKKKQRKREEK
25052	55420	Α	25190	1055	1206	SFALFSSSSPRSRP*FASTKS*TL
		l				TTGQVLPSTNVRFLTGNWGPPV
						VATG
	55421	В	25191	1	1386	
25054	55422	A	25192	1	449	MQDPLLALLEDYNKGDLEKQV
						PPAQSGPQPGKAGRDRPIVIML
						DPGHGGEDSGAVGKYKTREKD
						VVLQIARRLRSLIEKEGNMKVY
						MTRNEDIFIPLQVRV/AKAQKQ
				I		RADLFVSIHADAFTSRQPSGSSV
						FALSTKGGMCSYRGSGCLQ
25055	55423	Α	25193	1536	1941	STSNQNSTALCRRRGLVHCIDG
						ANDDDSVMVWPSGSGRPWSAE
						PGAPQR\YAQLVVEDVELDLLH
				l		FIVFGDDVMLNVVLQGQAFML
				l		ALGLVTNVGVLAHAHHHALVS
				l		GVPNDGGGTWVGGRCVQQSQ
ı I		i	1	l		LCTCWSHCQ

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25056	55424	Α	25194	240	855	SRAGYAPAAAQKVASPYVRRE
		1				R*NOSD\PAVLTGIGERGK*LLS
		1				RDFFIAPLAGMIVEKRGAVHLA
		1				RWSVPVERKGQWQPAGLWAQ
		l				FFLADIVCPAATALPDTTAEDQ
		i				HIDHPAVVHVHVIPVVNTCAED
		l				NHRAPMRFMGGIGKFTGDGFN
		l				LARHPGNLLTPGWGVRFDFSVI
		l				FRTVFIFQPAIEAVIRQYQIINAD
						HRTGVAID
25057	55425	Α	25195	840	1157	QYAPTAQPARPADPFALPTVQA
		l				RLTPFCYLVAKGDWCVYRRSY
i						SLWHSVASPRVRQSPRLGY*GY
		l				TANSPGILLAPLSLRGEMFLPQD
		l				APKSVPPYKRGKSVAIN
25058	55426	A	25196	1076	1339	LVCVASMPVEISTDASASSGVI
		1				VISSAMSGSWSAETKRRLAMV*
		ı				PEPLHLWAISIPTTSGRFTSSLIS
						PFPAR*YSPARYIPRVWRV
25059	55427	Α	25197	2	118	
25060	55428	Α	25198	1809	3145	ARHKQHAYGYRYRQSPRCYGV
		l				SGKKRGLRYYGSWLAISGSSRI
		l				TR/LLCMYLRRFFIGVIGADIAN
						MGISAGAMWLLSVSQVSLAAV
						SQVVAVRVWPASSYTRVTVES
						NRQLKYKQFALSNPERVVVDIE
					l	DVNLNSVLKGMAAQIRADDPFI
		1			ľ	KSARVGQFDPQTVRMVFELKP
	l			ĺ		NVKPQLFALAPVAGFKERLVM
				1		DLYPANAQDMQDPLLALLEDY
				1		NKGDLEKQVPPAQSGPQPGKA
		1				GRDRPIVIMLDPGHGGEDSGAV
		1				GKYKTREKDVVLQIARRLRSLI
		1				EKEGNMKVYMTRNEDIFIPLQV
1		1			İ	RVAKAQKQRADLFVSIHADAF
		l				TSRQPSGSSVFALSIQRGARPVG DRYVDHTMFDMVQSLTIADSL
		l				KFGKAVLNKLGKINKLHKNOV
		l				EQAGFAVLKAPDIPSILVETAFI
		l				SNVEEERPNGQPGHPLDPATTM
		l				GTLIDCAHADSVQ
25061	55429	A	25199	1	277	O I DIDONII NDOVQ
25062	55430	A	25200	902	1006	
25063	55431	Α	25201	2	1265	
25064	55432	Α	25202	409	525	
25065	55433	Α	25203	91	431	NHKPGNIDVARRIQRGFAGDQI
		ŀ				GHLRPVERQCSPDKRRFIAADG
	1					REIRGKQRAGHIFQLLSRCLLQI
	1	l	1			LNHCQRRAAHFRFQLSNQRHQ
	1	1		1		QLLPV/HYHAAEREYPAGACLV
	1			l	i	RWLL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25066	55434	Α	25204	3	71	
25067	55435	Α	25205	1	1212	
25068	55436	A	25206	1	2786	MAAVIEQIRRAVLALVTGVVIH GOIPPVVDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGFGRLPFNRIGLIRRITRRIRGR LFGLYFILLLINRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRW FTDKTGSSNGLAPQGQCSAQ GELINEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQULDAIAAFILAALDGTLD DFIVARETEGQSGLKRVYHSPG APDIREFIRDAIP
25069 25070	55437	A	25207	48	402	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPPS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI DETCGHLWAYVWPSCAAVIGL
23070	33436		23200			YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
2507I	55439	Α	25209	1	912	

SEQ ID	SEQ ID NO:	T54-4	Icro in vo.	ISC. de al ac	Thirt-day to come of the	I
NO:	of peptide	hod	in USSN	Nucleotide location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide
1.0.	sequence	""	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	l '			sequence		
		L				
25072	55440	Α	25210	1	1857	MRVCARACVRTRTRMCVYAH
		1				TCVCVRTYAYVRVRVRVHVRA
l						RVRVCAYARTRVRNSLSILPFIQ
1						LTLATPIHHIHQEEFNIRGIVPVL
		1				RRVKPDLAIGIDITPSCDTPDLH
		l				DYSEVRINGGVGITCLNYHGRO
		1	İ			TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
						GWEIGFSPLALLLAFLCSTSPGF
						GDPDGLGVIAYQDTVRPNAAT
						AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
						KAVTELNQHAPLAMVGDGIND
				ì		APAMKAAAIGIAMGSGTDVAL
	1	i				ETADAALTHNHLRGLVQMIEL
						ARATHANIRONITIALGLKGIFL
		1				VTTLDDRVVAGSAGRYGGDGA
	1	[				GDSECVKIVAQEIRQTDRNIER
						DRSPRPSGERVRVRGKGGIEAN
						QPLSTAFTNQITIRQSIRLFSNQF
		ŀ				VFHKGISRVVAGSSAIISNVSPG
						CILRTPNCRRGFPISCTGEGKAA
						YGWQRDGGHAEYLLAEEKDLI
						LLPDALSYEDGAFISCGVGTAY
		ŀ			1	
						EGILRGEVSGSDNVLVVGLGPV
		1				GMMAMMLAKGRGAKRIIGVD
						MLPERLAMAKQLGVMDHGY*I
		l				LPDVY/V*IGVARVSWMNGRID
		1			i	SELRTRVRAYAHTRTRARTCTR
		1				TRTRTYAYVRTHTHVCAYTHM
		ļ				RVRVRTHARAHTR
25073	55441	Α	25211	3	1180	SKLGTRRSVVWA*SPSTSPTLW
1						CSTFSAAGHSSMKRMNEFVDL
l						LPAQQRMKGENWYRGTADAV
	ŀ		ŀ			TQNLDIIRRYKAEYVVILAGDHI
						YKQDYSRMLIDHVEKGARCTV
			l			ACMPVPIEEASAFGVMAVDEN
			ŀ			DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
		1				RDENSSHDFGKDLIPKITEAGLA
				1		YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
						PAGPPLPLPAARSEAPKAAGTV
1		1	l	l		ASVPSIAPARLRPVPDPVELVLV
İ	1	1	l	l		AAEFITPGDPTPRLHGSGFIDIR
1		ı		l		QIHHQTRSHLEGVKTGIRFLNH
l				1		FSGNPQGGIAHVNGVARFQVK
		1		l		QCHQAWGQQYAARLRFQARGI
						SLQIAIHRVDIIHRFDVRQL
25074	55442	Α	25212	16	543	
25075	55443	Α	25213	1	3387	

SEO ID	ISEO ID NO	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25076	55444	ĪA.	25214	1688	2234	LSVGKTFPVLVPAAFRKVSATO
		1		1.000	1	AAVPGTPSILALPSYSTTPFGVC
1		İ				TSASMNVPVLTLRIRTRVTGEV
						AAIKPFSMANAPTPDSILPQLGV
						VSTRCS*TITCANR*STSARGSL
1		İ				ERLIMATLL/WVAGTFD*SVWF
ł						GHDTDVVTLYRFHEALCYSVT
1				1		LRTPHRRVLRFKSQHPGELACF
				1		SPVA
25077	55445	A	25215	905	4761	PPHNWMPSNATPGIAFVWCAY
23077	33443	ľ	23213	100	17701	GAI/LPGDAPVPVVDDYRKVVR
				1	1	KDTKGLIARWKYFWMSVIALG
İ				1	l	VAFALYLAGKDTPATQLVVPFI
						KDVMPOLGLFYILLAYFVIVGT
				1		GNAVNLTDGLDGLAIMPTVFV
		1			ŀ	AGGFALVAWATGNMNFASYL
				1	1	HIPYLRHAGELVIVCTAIVGAG
1				į.		LGFLWFNTYPAQVFMGDVGSL
				•		ALGGALGIIAVLLRQEFLLVIM
					i	GGVFVVETLSVILQVGSFKLRG
25078	55446	A	25216	269	1219	QRIFRMAPIHHHYELKGWP
23076	33440	Α.	23210	209	1219	QTRTRRVQLQDLIEYVAIHQW/ FSDKHPVPFYSCIFDDSITNCYS
					1	WSISKDGYFIFGGAYPMKDGQT
					ļ	RFLTMKDKMSAFQFQFGKTVK SEKCTVLFPSRGODFVCGKDNA
						FLIGEAAGFISASSLEGIIYALYS
						TDIPRSVLLKQPDKLNPAYWRA
					1	TRLVCITLFGOIVNTICMAAPDL
		1				,
		1				RKWIMLSPVAHKGHHLEWVLF DMQILPVPRPSGCICSGSSTFFC
		1				NWGCPYDRPQWQLYPSMCLC
		1				VHIGPAPVRSEKVESKRAISKV
						DQDSAFRGCCRSGNRNGGRKI VAVSLKKVSGAAKPCGHFRST
						RYRVAYSTIIN
25079	55447	A	25217	1	1158	KIKVAISIIIN
25080	55448	A	25218	1156	1899	LKLGIRYPQCQRLVTHSLDGISL
		1				PLHTAH*SQSNSAENTHRAISLK
						AVPPFFTAERRGVNAEEHRNGR
						LINGECRORFNVLRVANGVRN
						VQFAKARDRNDIASFRQIGFDT
						FQTEVAQHFTDFRVAGFAFAID
		1	l			DSDLLVRLHFTALDAANADNA
		1	l			NIAVVIELRNLHLERTVKVNVR
		1	1			RRNVVNNRLVQRGHVFRHIFV
		1	l			VQTRDTVQRRSVNDREVQLLV
l	1	1	l			GRVEVNEQIEYYADAFVIMLER
						LCKVLCCR
25081	55449	A	25219	1	2583	LCKYLCCK
23001	22449	J^A	23217	1	2203	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /-possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \≔possible nucleotide insertion)
		1		sequence		
25082	55450	A	25220	278	787	TLLSATROVYALLSTKPAFFSS
		1				HSSFSTSSRLISSRAASSMDVAF
		1				PIAFSASKTVSIKFFSR*KLLRNS
	1	1				HRPPFMVMRSIIRSPSNVFMAS*
		1				FRFVSIPTLRIDAVRRSTIWCSTT
	1	l				ARFSSRADAKFIKNVFQQAIPDS
						AAKWFFPVPGFPLNAKFVHPVI
		İ				SSSAMDFA
25083	55451	A	25221	866	1144	
25084	55452	Α	25222	19	1203	NWNLTPYASLTGFTADNPEYH
						LSNGMKSKSVDTRSIYRELGAT
	1	1				LSYNMRLGNGMEVEPWLKAA
	1					VRKEFVDDNRVKVNSDGNFVN
		l		i		YLSGRRGIYQAGKDLDRFKNL
	Ì			i		VLVHAARYAADLSYLPLMQEL
		1				EKRYEGKLRIQTVVSRETAAGS
		l		l		LTGRIPALIESGELESTIGLPMN
				l		KETSHVMLCGNPQMTRRLIPAS
						VEVYHDSLC\RKIWHGWEQHIT
						ARYLVGADGANSMVRRHLYP
	1	1				DHQIRKYVAIQQWFAEKHPVPF
		1		l		YSCIFDNSITNCYS WSISKDGYF
		1		l		IFCGAYPMKDGQTRFTTLKEK
						MSAFQFQFGKTVKSEKCTVLFP
		l				SRWQDFVCGKDNAFLIGEAAG
		1				FISASSLEGISYALDSTDILRSAL
						RKPIRTEQGANGAIRELEKFRPA
25085	55453	В	25223	58	359	
25086	55454	A	25224	4	329	
25087	55455	A	25225	1	1008	
25088	55456	A	25226	1	1335	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	deletion, \=possible nucleotide insertion)
25089	55457	A	25227	3	1886	HRINITAENDCRRLHGSIRDI.S SLIQAVGRIAAFYIGDVFAARF NDALTVVERLVKYTLYGSQIKL YNIETAVPSVLEVPDLIDVHAQYS LAGGCRLSSAHWLAQYCSBIHR QNTQOFVTLISTTMDAITPLIST KVQDKLLISACHILVSLATINAT PVFLISIPAVGKYFNRITDASAL RLVDKAQVLVCRALSNILLIPW PNLIPINEQQWPVRSINHASLISA LSRDYRNLKYPSAGAPQRKMPL PNEQQWPVRSINHASLISA LSRDYRNLKYPSAGAPQRKMPL PNEQQWPVRSINHASLISA LSRDYRNLKYPSAGAPQRKMPL FULFULFORLRKILWENIS GESTRSSTDFAYOFGCRESVQ VSLGLIFPAFHHQSDVTDEMLSF FLTERGLRVQMGVPFTEQIQT FLMRFTRFQLAESILHEGSTGC RVVEKFLKILQVVVQEPGQVFK FFLPSIIALCMEQVYPIIAERSP DVKAELFELLFTLHFNUWFF KSTVLASVQRGIAVEGOMENEP QFSAIMQAFGQSFLOPDIHLFK KSTDLLQGEGHRIFSYMASV DFNDGFFAAFLPEFLITSCNDGV DANGKSVLGRNFKKMDRLCPCL DGANDSLAPWGLWKLLGPCLL DSGNDSLAPWGLWKLLGPCLL DSGNDSLAPWGLWKLLGPCLL PGGTRDFLLVAT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide locatinn of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25090	55458	A	25228	689	3053	VDCRMS/FSYIEKFTDFLRLFVS VHLRRIESYSOFPVVEFLTLLFK
	1		İ	1		,
1				ŀ		YTFHQPTHEGYFSCLDIWTLFL
						DYLTSKIKSRLGDKEAVLNRYE
						DALVLLLTEVLNRIQFRYNQAQ
						\LEEL\DDETLDDDQQTEWQRY LRHSLEVVAKVMELLPTHAFST
	l					LFPVLQDNL\EVYLGLQQFIVTS GSGHRLNITAENDCRRLHCSLR
					Į.	DLSSLLOAVGRLAEYFIGDVFA
l						
						AR\FNDALTVVERLVKVTLYGS
						QIKLYNIETAVPSVLKPDLIDVH
				i		AQSLAALQAYSHWLAQYCSEV
						HRQNTQQFVTLISTTMDAITPLI
					!	STKVQDKLLLSACHLLVSLATT
		1			1	VRPVFLISIPAVQKVFNRITDAS
					1	ALRLVDKAQVLVCRALSNILLL
						PWPNLPENEQQWPVRSINHASL
					ŀ	ISALSRDYRNLKPSAVAPQRKM
						PLDDTKLIIHQTLSVLEDIVENIS
	l				l	GESTKSRQICYQSLQESVQVSL
					İ	ALFPAFIHQSDVTDEMLSFFLTL
						FRGLRVQMGVPFTEQIIQTFLN
	ĺ					MFTREQLAESILHEGSTGCRVV
						EKFLKILQVVVQEPGQVFKPFL
						PSIIALCMEQVYPIIAERPSPDVK
i		1				AELFELLFRTLHHNWRYFFKST
ł		ı				VLASVQRGIAEEQMENEPQFSA
i						IMQAFGQSFLQPDIHLFKQNLF
		l				YLETLNTKQKLYHKKIFRTAML
		ŀ				FQFVNVLLQVLVHKSHDLLQE
		_				EIGIAIYNMASVDFDGFFAAFLP
25091	55459	Α	25229	1	853	MISVANEIAEAGFDPQGRTSED
		l				LLDLAESRVFKIAESRANKDEG
		l				PKNIADVLDATVARIEQLFQQP
		1				HDGVTGVNTGYDDLNKKTAG
		l				LQPSDLIIVAARPSMGKTTFAM
1					1	TLVENAGR\MLQDKP\VLIFSLE
		1			1	MPSEQIMMRSLASLSRVDQTKI
		l				RTGQLDDEDWARISGTMGILLE
1		l	1		1	KRNIYIDDSSGLTPTEVRSRARR
		1			I	I\AREHGGIGLIMIDYLPLMRVP
		l	1			ALFONRTLEIAEISRSLKALAKE
1		1	1	ĺ	1	LNVPVVALSHLNRSLEQRAEER
					l	PGNSDLGESGSIEQDADLIL

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25092	55460	IA	25230	206	1073	VKITSWLMSNSALPGTLKLLAL
23092	33400	l^	23230	200	1075	ILKCSTCVRVLPRSELRNLER/O
		1				GQLDSVGGFA/YLAEL/SKNTPS
		1				AANISA/YADIVRERAVVREMIS
		1				
		1				V/ANEIAEAGFDPQGRTS/EDLL DLAESRVFKIAES/RANKDEGR
		1				
		1				NPMFDDRGKRGEPSDLIIVAAR
	1	1				PS/MGKTTFAMNLVENAAML/Q
		1				DKPVLIFSQTKI/RTGQLDDEDW
		1				ARISGT/MGILLEKRNIYIDDSSG
l	1	1				L/TPTEVRSRARRIAREH/GGIGL
						IMIDYLQLMRVP/ALSDNRTLEI
					l	AEISRSLKHFEKLALICGCRNNG
						TTRYCKSLLA
25093	55461	В	25231	1	483 635	
25094	55462	В	25232	287	2469	MRCDICL ACCRED ATCRETTION
25095	55463	Α	25233	1	2469	MPSDISLASCRLRATSRLFTDHR
1		1				RQSDCMTAINRIPIVDDEDNVR
1		1				RFETHCANNVRTALHLFADIHP
1						DVVLMDIRMPEMDGIKALKEM
1		1				RSHETRTPVILMTAYAEVETAV
i		1				EALRCGAFDYVIKPFDLDELNLI
1	1	1			ŀ	VQRALQLQSMKKEIRHLHQAL
ŀ	1			1		STSWQWGHILTNSPAMMDICK
						DTAKIALSQASVLISGESGTGKE
		1				LIARAIHYNSRRAKGAFIKVNC
						AALRESLLESELFGHEKGLFER
		1			1	ANEGTLLLDEIGRM/PLVLQAIL
i		1				RILQEREFERIG/GHQTIK/VDIAS
	1					LLAPTRLQAMVKEGTFREDLFY
						RLNVIHLILPPLRDRREDISLLA
		i				NHFLQKFSSENQRDIIDIDPMA
	1	1				MSLLTAWSWPGNIRELSNVIER
		1				AVVMNSGPIIFSEDLPPQIRQPV
		1				CNAGEVKTAPVGERNLKEEIKR
		1			i .	VEKRIIMEVLEOOEGNRTRTAL
		1				MLGISRRALMYKLQEYDATGF
		1				FRDGMTIMVGGFMGIGTPSRLV
		1				EALLESGVRDLTLIANDTAFVD
						TGIGPLIVNGRVRKVIASHIGTN
1		1				PETGRRMISGEMDVVLVPQGTL
	1	1				IEQIRCGGAGLGGFLNPTGVGT
1		1	1		1	VVEEROTSIDTSTRKRPFELGRP
1	1					SRNNDKGIRPRSGAGSEEYPRT
1	1					
1		1	1		1	LHDSLKRLQTDYLDLYQVHWP
		1	İ	1		LRPFYCFGKLGYSWTDSAPAVS
1			ļ		1	QLDTLDALAEYQRAGKIRYIGV
	1	<b>!</b>		ļ		SNETAFGVMRYLHLADKHDLP
25096	55464	A	25234	1	891 1614	
25097	55465	A	25235 25236	1	946	
25098	55466	Α	23230	П.	240	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25099	55467	A	25237	1055	11474	NGVKSKPPPNHOTGSAPGFSAI
23099	33407	A	23231	1033	14/4	KNRTFAWPTLPNTSCWANTML
		Ì			1	
1	1	1				IGSRELGIRSSQSGPLLGVRVWC
1						/CRCRGTQG/HSQGKDG/IPENGI
						RAYKFTSS*ASFRNSACFRQPSR
ŀ		1		1		IKPLRKATWLLCGLSTRHLITK
L	<del></del>	ļ.,				RLSSPDWA
25100	55468	Α	25238	2036	2743	DLLIRQMPLLSRRVIPVIRVPVT
					1	GVLWKSFTPRITIFGH/ALIDQH
	}	ı			1	SMIVAAQGLTPDHQLLLQIYDR
	ł			1	1	ARVSASRIVHQAQIYGDAVVR
	ļ					YAFIEHRAEVFDFASIEGNEENN
	İ					VWLCDCAKVYGHAQVKAGIEE
1	l				1	DAIPTIHYSSQVAEYAIVEGNCV
1	İ	1			1	LKHHVLVGGNAVVRGGPILLD
						EHVVIQGESRITGAVIIENHVEL
1		1		1		TDHAVVEAFDGDTVHVRGPKV
1		1				INGEERITRTPLAGLL
2510I	55469	Α	25239	2234	2571	IMSSVDSSLVLPLKAMVPSRITL
		1				IRSAIWRISG/RLMRDKNNTHAS
		1		1		SKQLLQATKQAFGFRRGKRGG
		ŀ			l	RFIEDQNPRVAHQPAEDFHHLA
1						IGDIQRSCQTMQIKLAAQRRQQ
1	ŀ	1		į.		VLH
25102	55470	Α	25240	659	1206	WKSTSNTAKAKPGSVMAVDLR
				1		IPIRFGVMLSAA/FGDDVVDLIA
		1		l	1	QVDLVTTAVGPVVLERIAPAIA
		ı		1	ŀ	KGQVKRKEQGHESPLNIIACEN
		1		i	l	MVRGTTQLKGHVMNALPEDA
		ı			i	KAWVEEHVGFVDSAVDRIVPP
		1			1	SASATNDPLEVTVETFSEWIVD
		ı			1	KTOFKGALPNIPGMELTDNLM
		ı		1		AFVERKLFTLKH
25103	55471	A	25241	332	683	ALPGR*RHVHLPGSAYEWNDA
		Γ.				EPAQESDELSLKMLTAICWLTA
		1	l	l	1	TA/STSLKI*R*KVALRCLVGRIR
		1			1	RLRRIROOCOLLMRRSRVLSGR
		i i		i .		LSSV
25104	55472	A	25242	1	841	MVKVAGECRVRASAHLPGLNR
25101		Γ.		1	***	STKNTEDRGANNOEGTNTOKT
		1		İ		RGETNERLKKNEHRDLRLARY
						PAKENNKQGDKNKPRTYEKLT
					i	GTVTHQEPPHHADQSPGLCLFR
		ı		1		TSRAQVERGPTVLLLISQENQIE
1						
1			1	1	l	RYDSDNHSQLNLCLRVPTVTTQ
		1		1	1	RRDYDIAERYRQKGIKLPARKE
l	l		l			RLMTIAERLRQEGHQIGWQEG
1		1	l	1		KLEGLHEQAIKIALRMLEQGFD
		ŀ		1		RDQGIA/RRASCQRQQRQSSLPT
						P/EHCCAISGATARKPAALPAAR
		L.,		L		IRRILVSIIRCTSGCPALSG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop eodon, /-possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \≔possible nucleotide insertion)
25105	55473	A	25243	240	651	RCPPQSCLLAEGRWCG*K/CRK
	i					VSV*SNRYR*SRLSLGELLRAYS
	1					RNRDLPGF/SSGSARVLVATDV
						AARGLDIKSLELVVNFELAWEP
		1				EVNVHRIGRTARAGNSGLAISF
						CAPEEAQRANITSRPPHPAHIAS
		1				DHQSTP
25106	55474	Α	25244	1455	1643	RDPHQICVAESVYLAAFVLLCA
		l				GLCVRRRSTTGARNAAAAC*N
						GLW*AEAQCPAYYVCPVVG
25107	55475	Α	25245	549	641	
25108	55476	Α	25246	1378	2084	PNFGYSPPASSCGQVSQNSS*LQ
		l				CSVSGRDKMLRTGPCARTVSSS
		1				YLMGVSFSRDA**DAR*VCACH
		1				NTIAALSASAERFTSCERASHSE
		1				ARSGCCNSVRVMSNNPCCPRSL
1		1				IGVYDILFFQESTAKRCKRSLSG
		1				SGSACGKSRVRFTPYRPARRTP
		l				LRSTTSPISAASFPSGWECNAAS
	1					TCSAALRSTAITSLPSLAKFRAS
						SPSNSQTPRTAGLTGSAASESSI
ŀ		1		l		PQPQAAANS
25109	55477	Α	25247	1134	1428	GPCGCCSSNVARCASQTSSRFA
		1				AV/WHGAIGAR*LNADNRPLWI
1		1				EITREHAELPGKTGRRMETKQR
l						RAITFTQRQNGFESHTPGAVFFS
	1			l		INNRCQFGDR
25110	55478	A	25248	96	535	RPQTTVQPALYVAEQSICSQPC*
			l			*FSTKCDRKPAAVLAPAGYAAL
ŀ				l		PVLFSSAKLDGSWLRWNSASG
				l		RRQNGSFSCAALASKRPASASS
				l	1	KLNSA**SLPSAVFAAPVRVAA
					1	SMIISGFCALASIRPSASTRRPSA
l	1	l			1	SVFITSTFLPLR

SEQ ID			SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
25111	55479	A	25249	1471	3026	SPLRSSVACRGWHRKNNRRGW
		Γ.				CPRRGDPARPVRDSLO\HATAII
ı		1				VATPGRLLDHLQKGTVSLDAL
i		1				NTLVMDEADRMLDMGFSDAIL
i		1				DVIRFAPASRQTLLFSATWPEA
i	1	1		ļ		AAISGRVQRDPLAIEIDSTDALP
i	ŀ	ŀ				PIEQOFYETSSKGKIPLLQRTLV
i	1	l				RFANGSARVLVATDVAARGLD
l	Į.	1	l			IKSLELVVNFELAWDPEVHVHF
l	ļ		i	1		IGRTARAGNSGLAISFCAPEEA(
ı		1		1		RANIISDMLQIKLNWQTPPANS
ı		1				SIATLEAEMATLCIDGGKKAKN
l	l			1		RPGDVLGALTGDIGLDGARAKN
ì		1		ļ.		
ì		1		1		IAVHPAHVYVAVRQAVAHKA
ì						WKQLQGGKIKGKTCRRCYPLA
ì				1		APYVRHCSLVGRAASHQALWH
l						VAGFGLYALFRRTGGCRLRCR
ì				1		YSGGLRLIRPTVAAGICRPDKT
ſ		ŀ		i		RKRRIRHRAPFPDAARAPYPAY
	l	1		1		RSQYNQFFFTNSDFSFIGPKPSM
í		1				LQSMLCAPCNQADVFHFGANV
	1	1				SASKSYLFTFRSLMMVTLSPCS
		1		1		QQIAVSIFNDQLVAFLCRFCVV
25112	55480		25250	196	330	PLRRHIHGQMYMPLSS
25112	55481	A	25251	62	617	NRRLPSGGDEMSAQVSLELHH
23113	33461	n	23231	02	017	RI/SQF/LVQESSCWTDW/KFRD
		1		1		GVAOLRPKEVRF\TMRTTVNGC
		i i				TRVPRKGVQPPTTWIFNDTKDQ
						LERRIARLETGMAWAEEPPSRT
		į.		l		RHLISNCQISETDIPNVFAVRVN
		1				YLLYRAQK\ERDETFYVGTRFD
	l	1		1		KVPPSE\DTTWRCLKRDIVLDO
	1	1		l		AVITSHNLSVLF
25114	55482	A	25252	1	318	AVITSHINESVEI
25115	55483	A	25253	1	510	
25116	55484	A	25254	9	79	
25117	55485	A	25255	ĺ	361	
25118					1245	FSQIYLARSALSSAHSSRSPWQF
	55486	A	25256	863		
	55486	Α	25256	863	1245	
	55486	A	25256	863	1245	SVWTLVRSVTNLETSANSALG
	55486	A	25256	863	11245	SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR
	55486	A	25256	863	1245	SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW
	55486	A	25256	863	1245	SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE
25119	55486	A	25256	909	1069	SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI
25119						SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW
25119						SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSKIJELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW YYP*GLCSVPLVDISVLVPVPCC
25119						SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW
	55487	A	25257	909	1069	SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLISLCLADEAFPSSKYIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW YYP*GLCSVPLVDISVLVPVPCC
25120	55487	A	25257 25258	909	1878	SVWTLVRSVTNLETSANSALĞ NLWLRRATAHALKALSPNFWR LAHLISLCLADEAFPSSKYIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI GILSPFLVFVRFVKDQIVVDVW YYP*GLCSVPLVDISVLVPVPCC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25124	55492	Α	25262	1599	1776	WFPASSMSQPKKAQDQTDSQP
		1				NSTRGTERSWYHSF*NGSKO*K
						KSNSSPTHFMRPASS
25125	55493	Α	25263	1	162	
25126	55494	Α	25264	1	3370	MNRAPIPKQSKDKTSRETKNTS
						RSKTRERTDELEGLSTDNHAET
		l				QHAETNTDMTHERYTQIRNHT
		1		l		YKTTHQMEDKRTKPKREKEIH
		1				NRPDDMAKAGIPRSILNTGHPG
l		1		i		KLMQTEVHHVRTLKIMLKVYS
İ	l	l				RALOEELOFSSKAIGRLFPCAD
		l				DLLETHSHFLAQTHERSGYVPL
	l					CVCATHTKFYEFMEDVNTAYT
		İ				KRHTMFRSLSMVSECLFSLING
		l				DDMFVTFAAMQAQQGRSSLV
l		l				WLFSQLYLYSFISLFIYMV
25127	55495	В	25265	44	238	
25128	55496	Α	25266	1	444	MPAEFITG\ERS\SEGFF\RIHAGI
	İ				\	EQAISRGLAYAPYADLKNLDD
		l				KTIASFOOOLSDMGYKFOFITL
1		l			1	AGIHSMWFNMFDLANAYAQG
		l				EGMKHYVEKVQQPEFAAKKD
	i e	l				GYTFVSHQQEVGTGYFDKVTTI
		l				IQGGTSSVTALTGSTEESQF
25129	55497	Α	25267	710	1395	DLPGISSKWVIAVIFGHLIVGIFI
		İ				PPAIIVRAGIT*RQVR/WIAAHE
		l				GKAPQQIIIMAHLDTYAPLSDA
		l			l	DADANLGGLTLQGMDDNAAG
		l				LGVTLQLAERLKNTPTEYGIRF
		l				VATSGEEEGKLGAENLLKRMS
		l				DTEKKNTLLVINLDNLIVGDKL
		l				YFNSGVQTLEARHQRSFNTVKP
		l				WPDSVISNRPFAGNTGSVDDND
		l				EIQRNLNDTNYNRMWEYNNRG
		1				VGSKVVAEAKK
25130	55498	Α	25268	2	2105	
2513I	55499	Α	25269	754	1133	RAANQHQTVDLTRLQTRIAQR
	1	1				LFNRHSQAIEQRQPQIFQFVLVK
	l				1	FAFPRFFLILPANVQWRLIATFC
						RFHTGVQGCQFTLVKRGPGDIR
						DYQQTNLDWYNSRNTTKLDES
						VNRV/HAAIQS*RQNGL
25132	55500	В	25270	1	1275	
25133	55501	С	25271	1	1167	

NO: of peptide sequence had in USSN mortal and in USSN more period sequence of peptide of peptide sequence of peptide of peptide sequence of peptide of peptide sequence of peptid	Common 1 4	Tono	1	1222-2-2-2-2			
25134   55502   A   25272   275   2424   SPAMHPQSFT/WQNNLDDNTIA SPQQHLSDMGYKFQFITLAGIH SMWFNMFDLANAYAQGGGMK HYVEKQQFFTAGIH SMWFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQQFFTAGIH SWMFNMFDLANAYAQGGMK HYVEKQFTTAGIH SWMFNMFDLANAYAQGGMK HYVEKQFTTAGIH SWMFNMFDLANAYAQGGMK ATALHYYTAKCAPPKTAGAK GENERAL SWMFNMFDLANAYAGGMTALSDLFG CRTSQRCPDKTRQRIRQPAR ALDVGCGYTALSDLFG CRTSQRCPDKTRQRIRQPAR ALDVGCGYTALSDLFG CRTSQRCPDKTRQRIRQPAR ALDVGCGYTALSDLFG CRTSQRCPDKTRQRIRQPAR ALGTSFKRLCAHYSRMKCWRI SGLRGAPFNICKCRRLRRIPG LRLRFPHSRVVFIFGGGNPR AKQRCTGEVEKCHQPQHGTK CCARGGFAACLVFEVVVVFWT SLPDSFCRKSFFTRIRGSMYPSL WDFPPGVDGRKGTSWMOYP PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSQPPIPLKFQAILQ/FHEIFGGSGHLASVAVESGYPP QFGSEETRAGARNRVANARR LLPFADFWAHEAGIGGDSTSS WVVIENASQRGARSATLPLPA VILEKVREGEALGFVMSRYTGI DEIGRREGAIGVTAGKTSKTWOYP QFGSEETRAGARNRVANARR LLPFADFWAHEAGIGGDSTSS WVVIENASQRGARSATLPLPA VILEKVREGEALGFVMSRYTGI DEIGRREGAIGVTAGKTAGA GMEKLPLGGFWTTQEAVRT GMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT GAMEKLPLGGFWTTQEAVRT AAASDLTTSGCOPTDEKATTG AAASDLTTSGCOPTDEKATTG AAASDLTTSGCOPTDEKAFT FOR THE AAAACDGTTVSHQCGJSDMG YKFQFTTLAGIH SMWFNMFDLANAY GAGGMKHVVEKVQQFE FAAAACDGTTVSHQCGTGV FFKVTTTUGGTFDKAAFT FKAACCGTTPAGKLTARS AAAACDGTTCPTVLVARTT AAASDLTTSGCOPTDEKAFT FKAACCGTTPAGKLTARS AAAACDGTTCPTVLVARTT AAASDLTTSGCOPTDEKAFT FAAACCGTTTAGATT AAAACDGTTTCAAACTGTTTAGATTAGATAGATTAGATTA	SEQ ID					Nucleotide location of last	
25134 55502 A 25272 275 2424 SPAMHFQSFT/WQNNLDDNTIA SFQMLSDMGYKFQFITLAGIH SNWFMMFDLANAYAQGEGM HYYEKVQOPEFAAAKDGYTFV SHQQEVGTGGYVASGNSLLIM RALNAAWGIIDCSNHFARLRC SVWSIPRSDLRCAAAFRTGRLA CCPAGDEKPYPSLRSSRWSGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGYTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLEG LHRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMKCWRII SGLRGARPKIVCRIRRLRRIRP IRLRFPHSRVYFFGGGNPRR AKQROTGEEVEKCHQPQHGTR CCARGFACLVFEVVVFWFY SLPDSFCRKSFFTRIRGSMVPSL WDFPPGVDGRKGKTSWNGVP PCVTCGIGLTCPSPCVGGLU PHEIFGEGSCHIASVAVESGVPP PCVTCGIGLTCPSPCCFGLU PHEIFGEGSCHIASVAVESGVPP QPFGSEETRAGARNANARR LLPEADFWVAIEAGIBGDSTFS WVVIENASQRGERASATILLPA VILEKVREGEALGFVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWTOZEAVRT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAJHAKYPGKLAVNCSSTW WQRNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWTNNFOLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJSDMG YKFQFTTLAGIBAWTNFOLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJSDMG YKFQFTTLAGIBAWTNMFOLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJSDMG	ino.		11100				
SFQQHLSDMGYKPQFITLAGIH SMWFMMFDLANAYAQGGGMM HYVEKVQQPEFAAAKDGYTFY SHQQEVGTGYYAASGNSLLLM RALNAAWGIIDSNIHFALRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA ALDVGCGYTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPCXTALSDLGG CRTCTA			l				, , , , , , , , , , , , , , , , , , , ,
SFQQHLSDMGYKPQFITLAGIH SMWFMMFDLANAYAQGGGMM HYVEKVQQPEFAAAKDGYTFY SHQQEVGTGYYAASGNSLLLM RALNAAWGIIDSNIHFALRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA CCPAGDERYPYSILSSRWGGRC ATALHYYTAKRCPPKTRQRA ALDVGCGYTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPPCXTALSDLGG CRTSQRCPCXTALSDLGG CRTCTA							
SMWFMRFDLANAYAQGEGMM HYVEKVQPEFAAKDGYTFV SHQQEVGTGYYAASGNSLLM RALNAAWGIIDCSNHFARLRC SWWSIPRSDLRCAAAFRTGRIA. CCPAGDERPYPSLRSSRWGGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGYTALSDLIGG CRTSQRCRPDKTRQRRRQPAR LLRSCPFYFLRRAGAPVGI YCTGTPITPLESTRLFAPLPINC SMAGMYGIQPYPHPAIGARC LMRCTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMRCWRII SGLRGARPNKIVCRIRRLRRIPP LRLRFPRHSRVVFIFGGGNPRR AKQROTGEEVEKCHOPQHGTIK CCARGGFAACLVFEVVVVFVY SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLEFQAILQ/ FHEIFGEGSCHIASVAVESGYPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTFS WVVIENASQRGARSATLLPLA- VILEKVREGEALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGPVTGCEAVRT VRARLQADVTGVFTVLVARTT ADASDLITSDCDPYDSEMTIGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPLELARRR AQAHAKYPGKLLAYNCSSESN WQNILDDKTIASFQQQLSDMG YKFQFTTAGIBRMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSGVGTGY FFRAKTUTINGGTFDKAFT	25134	55502	A	25272	275	2424	SPAMHFQSFT/WQNNLDDNTIA
HYYEK VQQPEFAAALÖGYTFV SHQQEVGTGVYAASGNSLLLM RALNAAWGIIDCSNIHFARLRE SVWSIPRSDLRCAAAPTGRLA CCPAGDEKPYPSLRSSRWSGR ATALHYYTAKRCEPDKTRQRR RQPARALDVGCGYTALSDLPG CRTSQRCRPDKTRQRRRRIRPAR ALDVGCGYTALSDLPG GCTSQRCRPDKTRQRRRRIRPAR ALDVGCGYTALSDLRGAALHG SLANYRVNFLERIPDAMILES LLRSCPFVFPLLRRLRAGAPVGI YCTGFPTPLPSTRLFAPLPNEC SMAGMYGGLQPVPHPAIGARC LMRCLTHLRPTMGTGSMAEE ALGTSFKRLCAHYSMRCWRIII SGLRGARPNKIVCRIRRLRRIRP LELRPRHSRVYFFGGGNPRR AKQROTGEEVEKCHOPQHGTR CCARGGFAACLVFEYVVVFWT SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVP PCVTCGIGLTCPSPCCPGLSL DGYPEKVSVGPPPLKFQALQA FHEIFGEGSCHIASVAVESGVPE QPFOSEETRAGARNAVARRR LLPEADFWAIEAGIDGDSTFS WVVIENASRGERASTALPLAP VILEKVREGEALGPVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VRARLQADVTGVFTVLVARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAJHAKYPGKLLAVNCSSFN WQRNLDDKTIASFQQDLSDMG YKFQFTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQEVGTGY FGKVYTTIJQGGTFDKAFT			1				
SHOQEVGTGVYAASGNSLLLM RALNAAWPGIDCSNHFARLRC SVWSIPRSDLRCAAFTTORLA CCPAGDERPYPSLRSSRWGGRC ATALHYYTAKCREPIXTRORR RQPARALDVGCGVTALSDLPG CRTSQRCRPDKTTRQRRIRQPAR ALDVGCGVTALSDLRGALHGE SLANYRVVNFLFRLPDAMILSV LLRSCFPVFPLLSBLRGAALPGG YCTGTPITPLPSTRLFAPLPNRC SMAGMYGGLQVPHPAIGARC LMRCLTHLIRPTMGTSMAEE ALGTSFRRLCAHYSRMRCWRII SGLRGARPNICVCRRIRLRIRGP LRLRFPRHSRVVFIPGGGNPR AKQROTGEEVEKCHOPOHGTIK CCARGGFAACLVFEVVVVFWT SLPDSFCRRSFPTRIRGSMVPSL WDFPPGVDGRRGKTSWNOYPG PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLFFQAILO FHEIFGEGSCHLASVAVESGVPF QPFGSEETRAGARNRVANARR LLPFADFWAHEAGINGDSTSS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRREGAIGVFTAGKLTAG 25135 55503 A 25273 I 441 25136 55504 A 25273 I 441 25136 55504 A 25273 I 441 25137 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLTISDCDPYDSEMTIGE RTSGGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQRILDDKTIASFQQU.SDMG YKFQFTTLAGIBRWTNMFDLA NAYAQGEGMKHVVEKVQQPE FAAAKDGVTFVSHQUSGTDY FFEKTYTTINGGTFDKAFT			Ì				SMWFNMFDLANAYAQGEGMK
RALÑAAWGIIDCSNIFIARLRC SVWSIPRSDLRCAAAFRTGRLA CCPAGDEKPYPSLRSSRWSGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGYTALSDLGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLGG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLGG SLANYRVVNI-ERLPDAMILSV LLRSCPYPFLLRRLRAQAPVGI YCTGFTIFTLPSTRI-PADPINGE SMAGMYGGLQPYPHAJGARC LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMKCWRII SGLRGARPKRIVCRIRRLRRIRP IRLRPPHSRVVFIFGGONPRR AKQROTGEEVEKCHOPQHGTK CCARGFAACL VFEVYVVFWT SLPDSFCRKSFFTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PC-VTCGLGLTCPSPCVGGLLC DGYPEKVSVGPPIPLKFQAILQ/ FHEIFGEGSCHLSVAVESGVFP QPFGSEETRAGARNANARR LLPEADFWAIEAGIBGDSTFS WVVIENASQRGERASATLLPA- VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25135 55503 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFFWTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRR AQAJHAKYPGKLAVNCSSSFN WQRNLDDKTIASFQQQLSDMG YKFQFTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONDM	1		1				HYVEKVQQPEFAAAKDGYTFV
SVWSPRSDLRCAAAPRTGRLA CCPAGDEKPYPSLRSSRWSGRC ATALHYYTAKRCRPDKTRQRR RQPARALDVGCGVTALSDLPG CRTSQCRPDKTRQRRIRQPAR ALDVGCGVTALSDLRGAALHG SLANYRVNFLFRLPDAMILSV LLRSCPFVPFLLRRLRAGAPVGI YCTGTPITPLPSTRLFAPLPNRC SMAGMYGGLGPPPHPAIGARG LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMRCWRII SGLRGARPNIKUCKIRRLRRIRP LELRFPRHSRVVFIFGGGNPRR AKQROTGEEVEKCHOPOHGTK CCARGGRAACLVFEVVVVFWT SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGTSWNOFPU PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLKFQAILQA FHEIFGEGSCHIASVAVESOVPE QPFGSEETRAGARNRVANARR LLPEADFWWALEAGIDGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25135 55503 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQADVTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSGGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAHAKYPGKLLAYNCSSFSN WQRNLDDKTIASFQQQLSDMG YKFQFTTLAGIBRWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQUSGNTOV YFGPTTLAGIBRWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAARDGYTFVSHQUSGNTOV PFOKVETTINGGTFDKAFT			l				SHQQEVGTGVYAASGNSLLLM
CCPAGDEKPYPSLRSSRWGGR ATALHYYTAKRCRPDKTRQRR RQPARALDVGGVTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGGVTALSDLEG CRTSQRCRPDKTRQRRRQPAR ALDVGGVTALSDLEG SLANYRVVNPEFRLPDAMILSV LLRSCPFYPFLRRLAGAPVGI YCTGTPITPLESTRLFAPLPNRC SMAGMYGGLQPYPHPAIGARC LMRCLTHLRPFMGTGSMAEE ALGTSFKRLCAHYSRMRCWRII SGLRGARPNKIVCRIRRLRRIPP LRLRFPRHSRVVFIFGGGNPRR AKQRQTGEEVEKCHQPQHGTIK CCARGGFAACLVFEVVVVFVV SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLKFQAILQV FHEIFGEGSCHIASVAVESGVPP QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTTS WVVIENASQRGARSATLLPLA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVTGCFART VRARLQAD/VTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPLELARRR AQAHAKYPGKLLAYNCSSFSN WQRNLDDKTIASFQQUISDMG YKFQFTTLAGIBRWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSJGNDG YKFQFTTLAGIBRWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSGTGY FFKVTTIIQGGTPDKAFT			l				RALNAAWPGIIDCSNHFARLRC
ATALHYTAKRCRPIKTRORR RQPARALDVGCGVTALSDLFG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLFG CRTSQRCRPDKTRQRRRQPAR ALDVGCGVTALSDLRGAALHG SLANYRVNPLERIPDAMILSV LLRSCPFVPFLLRRLRAGAPVG YCTGFTFTPLESTRLFAPLPNEC SMAGMYGGLQPVPHPAIGARC LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMCEWEII SGLRGARPNKIVCRIRRLRRIRP LELRPPHSRVVFFIGGGINFRR AKQROTGEEVEKCHQPQHGTK CCARGGFAACLVTEYVVVFVT SLPDSFCRKSEPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVP PCVTCGLGLTCFSPCCPGLSL DGYPEKVSVGPPPLKFQGLIQA FHEIFGEGSCHIASVAVESOVFE QPFGSETRAGARNVANARR LLPEADFWAIEAGIDGDSTFS WVVIENASRGREARSATLPLPA VILEKVREGEALGPVMSRVTGI DEIGRKEGAIGVFTAGKLTRAS  25136 55504 A 25273 1 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAHAKYPGKLAYNCSES WQRNLDDKTIASFQQQLSDMG YKFQFTLAGIBAWWNNFEDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSUSDMG YKFQFTLAGIBAWWNNFEDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSUSTMY FFEKVYTTILIQGGTPBKAFT	1		l				SVWSIPRSDLRCAAAFRTGRLA
ROPARALDVGGGYTALSDLPG CRTSQRCRPDKTRQRIRQPAR ALDVGCGYTALSDLRGALING SLANYRVVNFLFRLPDAMILSV LLRSCFPVFPLLERRAGAPYGI YCTGTPITPLESTRLFAPLENEC SMAGMYGGLQPVPHPAIGAGRC LMRCLTHLIRPTMGTGSMAEE ALGTSFRILCAHYSRMRCWRII SGLRGARPNIVCKRRILRRIPP LRLRFPRHSRVVFIFGGGNPR AKOROTGEEVEKCHOPOHGTK CCARGGFAACLVFEVVVVFVTV SLPDSFCRRSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNOYPP QPTCGLGLTCPESPCCPGLSLC DGYPEKVSVOPPIPLFFQAILO FHEIFGEGSCHIASVAVESGVFP QPFGSEETRAGARNRVANARR LLPEADPWAIGAGIGDGSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGFVMSRYTGI DEIGRREGAIGCVFTAGKLTAGS 25136 55504 A 25273 I 441 25136 55504 A 25273 I 441 25137 STORM ALGERIAN			l				CCPAGDEKPYPSLRSSRWSGRG
CCTSGRCRPDKTRQRARQPAR ALDVGCGVTALSDLRGAALHG SLANYRVVNI-ERLPDAMILSV LLRSCPFVPFLLRRLRAGAPVGI VCTGFTIFTLESTRI-FAPLPING SMAGMYGGIQPVPHAIGARG LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMKCWRII SGLRGARPNKIVCRIRRLRRIRP IRLRPPHSRVVFFGGGNPRR AKOROTGEEVEKCHOPOHGTK CCARGFAACL VFEVVVVFWT SLPDSFCRKSFFTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PC-VTCGIGLTCPSPCVCFBLL DGYPEKVSVOPPPILFFQAILO/ FHEIFGEGSCHIASVAVESGVPF QPFGSEETRAGARNVANARR LLPEADFWAIEAGIBGDSTFS WVVIENASQRGEARSATIL-PLA- VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFFWTO-EAVRT GAMEKLPLGGFFWTO-EAVRT ADASDLITSDCDPVDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRR AQAIHAKYPGKLAVNCSSFS WQRNLDDKTIASFQQQLSDMG YKFQFTTAGIBAMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONG YKFQFTTAGIBAMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONG			l			ł	ATALHYYTAKRCRPDKTRQRRI
ALDVGCGVTALSDLRGAALHG SLANYRVVNFLFRLPDAMILSV LLRSCPFVPFLJRRLRAGAPVGI VCTGTPTPTLPSTRLFAPLPNRC SMAGMYGGLGVPPPHAGARG LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMCWRII SGLRGARPNKIVCRIRRLRRIPP LRLRFPPHSRVVFIFGGGNPRR AKQROTGESVEKCHOPOHGTK CCARGGFAACLVFEYVVVFWT SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGTSWNOVP PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVCPPPLKFQAILQA PHEIFGEGSCHIASVAVESOVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTFS WVVIENASQRGEASATIPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS 25136 55504 A 25273 1 441 25136 55504 A 25273 1 441 25136 AVSNCSEGLSKEWGPRPCRIR GMEKLPLGGKFWPTQEAVRT VRARLQADVTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTLTAGIBRWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSKQQPSTGY FFKVTTINGGTFDKAFT			l				RQPARALDVGCGVTALSDLPG
SLANYRVVNFLERLPDAMILSV LLRSCPFVFPLLRRLAGAPVGI YCTGTPITPLESTRLFAPLPNRC SMAGMYGGLQPVPHPAIGARC LMRCLTHLRPFMGTSMAEE ALGTSFRILCAHYSRMRCWRII SGLRGARPKIVCRIRRLRRIPP LRLRFPRISRVVFIFGGGNPRR AKQRQTGEEVEKCHQPQHGTIK CCARGFAACLVFEVVVVFW SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLEFQAILQ/ FHEIFGEGSCHIASVAVESGVPP QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTTS WVVIENASQRGARSATLLPEA VILEKVREGEALGPVMSRYTGI DEIGRREGALGPVMSRYTGI DEIGRREGALGFVMSTYGE GMEKLPLGGFFWTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPLELARRR AQAHAKYPGKLLAYNCSSESN WQNILDDKTIASFQQQLSDMG YKFQFTTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONDG YKFQFTTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONDG							CRTSQRCRPDKTRQRRIRQPAR
LLRSCPVPPLLRRLRAGAPVG YCTGPITPLPSTRLFAPLPNRC SMAGMYGGLQVPHPAIGARC LMRCLTHLRPTMGTGSMAEE ALGTSFRRLCAHPSSMACWHI SGLRGARPNKIVCRIRRLRRIRP LRLRPPHSRVVPFPGGONPRE AKQRQTGEEVEKCHQPQHGTK CCARGGFAACLVTEVVVVFVT SLPDSPCRKSEPTFIRGSMYPSL WDFPPGVDGRKGKTSWNGVP PC-VTCGLGLTCFSPCCPGLSLC DGYPEKVSQPPPLKFQALQ FHEIFGGSCHIASVAVESOVPE QPFGSEETRAGARNVANARR LLPEADPWAIEAGIDGDSTFS WVVIENASRGEARSATLPLPA VILEKVREGEALGPVMSRVTGI DEIGRKEGALGFVMSRVTGI DEIGRKEGALGFVMSRVTGI DEIGRKEGALGFVMSTVGARG S5504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFWFTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRCLAV APYADLVWCETSTPDLELARRI AQAHAKYPGKLAVNCSSES WQKNLDDKTIASFQQQLSDMG YKFQFTLAGIBAWWNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQEVGTGY FEKVTTILQGGTDRAFT			l				ALDVGCGVTALSDLRGAALHG
YCTGTPITPLESTRLFAPLENEC SMAGMYGGLQPVPHPAIGARC LMRCLTHLIRPTMGTOSMAEE ALGTSFRILCAHYSRMRCWRII SGLRGARPNICKCRRIR.RIRPS LRLRFPRHSRVVFIFGGGNPRR AKQRQTGEEVEKCHQPQHGTIK CCARGGFAACLVFEVVVVFVTV SLPDSFCRRSFPTRIRGSMYPSL WDPPPGVDGRKGKTSWNGVPP PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLFFQAILO/ FHEIFGEGSCHIASVAVESGVPP QPFGSEETRAGARNRVANARR LLPEADPWAIEAGIGDGSTES WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRREGAIGVFTAGKLTASK 25136 55504 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/TGVPTVLVARTL ADASDLTISDCDPYDSEFMTGE RTSGGFFRTHAGIGAISRGLAY APYADLVWCETSTPDLELARRI AQAHAKYPGKLLAYNCSSESN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQSJGMG YKFQFTTLAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQSVGTGY FFKVTTINGGTFDKAFT							SLANYRVVNFLFRLPDAMILSV
SMAGMYGGIQPYPHAIGARC LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMCWEII SGLRGARPKIVCRIRRLRRIRP IRLREPPHSRVYPFIGGONPRE AKOROTGEEVEKCHOPOHGTK CCARGGFAACLVFEYVVVFWT SLPDSFCKKSFPTRIRGSMYPSL WDFPPGVYDGRKGKTSWNGVP PCVTCGIGLTCPSPCCPGISLC DGYPEKVSVGPPIPLKFQAILQ FHEIFGGSGCHISAVAVESGVFP QPFGSEETRAGARNVANARR LLPEADFWAIEAGIBGDSTFS WVVIENASQRGEARSATLLPA- VILEKVREGEALGPVMSRYTGI DEIGREGAIGVFTAGKLTRAS 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFWFTQEAVRT VRARLQAD/TGVFTVLARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLAYNCSSFW WQNLDDKTIASFQQQLSDMG YKFQFTTAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQSVGTGY FEKVTTIIQGGTDKAFT			1				LLRSCPFVFPLLRRLRAGAPVGP
LMRCLTHLIRPTMGTGSMAEE ALGTSFKRLCAHYSRMRCWRII SGLRGARPNKIVCRIRRLRRIPP ILRLRFPRHSRVVFIFGGGNPRR AKOROTIGEEVEKCHOPOHGTK CCARGGFAACLVFEYVVFWT SLPDSFCKRSFPTRIRGSMVPSL WDFPPGVDGRKGSTSWNOYPP PCVTCGLGTCPESPCCPGLSLC DGYPEKVSVCPPPLKFQAILQO FHEIFGEGSCHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWWAIEAGIDGDSTFS WVVIENASQRGEARSATI-PLPA VIILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS 25135 55504 A 25273 I 441 25136 55504 A 25273 I 441 25136 FSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			1				YCTGTPITPLPSTRLFAPLPNRC
ALGTSFKRLCAHYSRMRCWRII SGLRGARPNKIVCRIRRLRRIP LRLRFPRISRVVFIFGGGNPRR AKQRQTGEEVEKCHQPQHGTK CCARGGFAACLVFEVVVVFWT SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVDGRKGKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVGPPIPLKFQAILQ/ FHEIFGGSGHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTFS WVVIENASQRGARSATLPLAY VILEKVREGEALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VKRALQAD/VTGVPTVLVARTT ADASDLTSDCDPYDSEMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSSFSN WQNILDDKTIASFQQQLSDMG YKFQFTTAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONG YKFQFTTAGIBMWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQQEVGTGY FEKVYTTIJQGGTDKAFT			1				SMAGMYGGLQPVPHPAIGARC
SGLRGARPNKIVCRIRRLRRIRP LRLRPPHSRVVPFGGGONPR AKORQTGEEVEKCHQPOHGTK CCARGGFAACLVTEVVVVFVT SLPDSPCRKSFPTFIRGSMYPSL WDFPPGVDGRKGKTSWNGVP PC-VTCGIGLTCFSPCCFGLSL DGYPEKVSVGPPIPLKFQAILQA FHEIFGGGSCHIASVAVESGVPE QPFGSETRAGRARNVANARR LLPEADPWAIEAGIDGDSTFS WVVIENASRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVTAGKLTRAS 25136 55504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFWFTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRCLAY APYADLVWCETSTPDLELARRI AQAIHAKPYGKLAYNCSFS WQKNLDDKTIASFQQQLSDMG YKFQFTLAGIBAWWENNEDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FEKVYTTIJQGGTPDKAFT			l				LMRCLTHLIRPTMGTGSMAEE
SGLRGARPNKIVCRIRRLRRIRP LRLRPPHSRVVPFGGGONPR AKORQTGEEVEKCHQPOHGTK CCARGGFAACLVTEVVVVFVT SLPDSPCRKSFPTFIRGSMYPSL WDFPPGVDGRKGKTSWNGVP PC-VTCGIGLTCFSPCCFGLSL DGYPEKVSVGPPIPLKFQAILQA FHEIFGGGSCHIASVAVESGVPE QPFGSETRAGRARNVANARR LLPEADPWAIEAGIDGDSTFS WVVIENASRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVTAGKLTRAS 25136 55504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGFWFTQEAVRT VRARLQAD/TGVPTVLVARTT ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRCLAY APYADLVWCETSTPDLELARRI AQAIHAKPYGKLAYNCSFS WQKNLDDKTIASFQQQLSDMG YKFQFTLAGIBAWWENNEDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FEKVYTTIJQGGTPDKAFT	i		1				ALGTSFKRLCAHYSRMRCWRIL
AKOROTGEEVEKCHOPOHGTK CCARGGFAACLVFEYVVVFWT SLPDSFCRKSFPTRIRGSMYPSL WDFPPGVVDGRKGKTSWNGVP PCVTCGIGLTCFSPCCPGLSL DGYPEKVSVGPPPLKFQALLQA FHEIFGEGSCHIASVAVESGVPE QPFOSEETRAGARNRVANARR LLPEADPWAIEAGIDGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGREGAIGVFTAGKLTRAS 25136 55504 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQAD/TGVFTVLVARTT ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLAYNCSSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSJONG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTVSHQUSGVTGY FEKVYTTIJQGGTDKAFT			ı				SGLRGARPNKIVCRIRRLRRIRPI
CCARGGPAACLVFEYVVFWT SLPDSFCRKSFTTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PCVTCGGLTCPESPCCPGLSLC DGVPEKVSVGPPPLKFQAILQO FHEIFGEGSCHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGOSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTARS 25136 55504 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQADVTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FEKVYTTIQGGTPDKAFT			l				LRLRFPRHSRVVFIFGGGNPRR
CCARGGPAACLVFEYVVFWT SLPDSFCRKSFTTRIRGSMVPSL WDFPPGVDGRKGKTSWNOVP PCVTCGGLTCPESPCCPGLSLC DGVPEKVSVGPPPLKFQAILQO FHEIFGEGSCHIASVAVESGVPE QPFGSEETRAGARNRVANARR LLPEADFWVAIEAGIDGOSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTARS 25136 55504 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQADVTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FEKVYTTIQGGTPDKAFT	1		l				AKOROTGEEVEKCHOPOHGTK
WDFPPOVDGRKGKTSWNGVPC PCVTCGLGLTCPESPCCPGLSLC DGYPEKVSVCPPPLKFQALQO FHEIFGEGSCHIASVAVESGVPE QPFGSETRAGARNVANARR LLPEADFWVAIEAGIBGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRVTGI DEIGRKEGAIGVFTAGKLTRAS  25136 55504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQADVTGVPTVLVARTI ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WGNILDDKTIASFQQQLSDMG YKFQFTLTAGIBAWWTNMFDLA NAYAGGEGMKHYVEKVQQPE FAAAKDGYTFVSHQGVGTGY FDKVTTIIQGGTPDKAFT			1				CCARGGFAACLVFEYVVVFWT
PCVTCGLGLTCPESPCCPGLSLC DGYPEKYSVGPPIPLKFQAILQA FHEIFGEGSCHIASVAVESOVPE QPFGSEETRAGARNRVANARR LLPEADPWAVIEAGIGDOSTES WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGVFTAGKLTRAS 25135 55503 A 25273 I 441 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/VTGVPTVLVARTL ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAV APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAARCDGYTFVSHQQSVGTGV FFKVTTIIQGGTPDKAFT			l	1		ì	SLPDSFCRKSFPTRIRGSMVPSL
DGYPEKVSVCPPIPLKFQALLQA FHEIFGEGSCHIASVAVESGVPE QPFGSETRAGARNRVANARR LLPEADPWAIEAGIBGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VERALQADVTGVFTVLVARTT ADASDLITSDCDFYDESFMTGE RTSEGFFRTHAGIEQAISKGLAV APYADLVWCETSTPDLELARRI AQAIHAKYPGKLAVNCSSFS WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQSVGTGY FEKVYTTIJQGGTFDRAFT			l				WDFPPGVDGRKGKTSWNGVPG
DGYPEKVSVCPPIPLKFQALLQA FHEIFGEGSCHIASVAVESGVPE QPFGSETRAGARNRVANARR LLPEADPWAIEAGIBGDSTFS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSRYTGI DEIGRKEGALGFVMSTYGEAVRT VERALQADVTGVFTVLVARTT ADASDLITSDCDFYDESFMTGE RTSEGFFRTHAGIEQAISKGLAV APYADLVWCETSTPDLELARRI AQAIHAKYPGKLAVNCSSFS WQKNLDDKTIASFQQQLSDMG YKFQFTTLAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQSVGTGY FEKVYTTIJQGGTFDRAFT			l				PCVTCGLGLTCPESPCCPGLSLG
FHEIFOEGSCHIASVAVESGVPE QPFGSETRAGARNRVANARR LLPEADPWVAIEAGIDGDSTFS WVVIENASQRGEARSATLPLPA VILEKYREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25135 55503 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQ/EAVRT VRARLQAD/VTGVPTVLVARTT ADASDLTISDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRS AQAHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFTLTAGIBAWWTNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FDKVTTIQGGTPDKAFT			l				
QPGGSETRAGARNRVANARR LLPEADFWVAIEAGIDGDSTS WVVIENASQRGEARSATLPLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVMSRYTGI DEIGRKEGALGPVTGAGKLTRAS  4 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQEAVRT VRARLQAD/VTGVPTVLVARTT ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRR AQAIHAKYPGKLLAYNCSSFSN WQRNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWTNMFDLA NA YAQGEGMKHYVEKVQQPE FAAARDGYTVSHQQEVGTGY FEKVYTTIJQGGTPDKAFT			l				
LIPEADFWAIEAGIDGDSTES WVVIENASQRGEARSAIT.PLPA VILEKVREGEALGPVMSRYTGI DEIGRKEGAIGVFTAGKLTRAS  25136 55504 A 25273 I 441  25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQAD/VTGVPTVLVARTI ADASDLITSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSPN WGNILDDKTIASFQQDLSDMG YKFQFITLAGIBRWFNMFDLDL NAYAGGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FPKVTTIQGGTPDKAFT			l	1			
25135 55503 A 25273 I 44I 25136 55504 A 25273 I 44I 25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWPTQ'EAVRT VRARLQAD/TGVPTVLVARTE ADASDLITISGCPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFGPTTAGIBRWFNMFDLA NA YAQGEGMKHYVEKVQQPE FAAARDGYTFVSHQQVGTGY FEKVYTTIJQGGTPDKAFT			l				
VILEKVREGEALGPVMSRYTGI			l	l			
DEIGRKEGAIGVFTAGKLTRAS	i		l				
25135   55503			l				
25136 55504 A 25274 3 2919 AVSNCSEGLSKEWGPRPCRHR GMEKLPLGGKFWFTQEAVRT VRARLQAD/VTGVPTVLVARTI ADASDLTSDCDPYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSN WQKNLDKTIASPQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIQGGTPDKAFT	25125	55502	<u> </u>	25272	1	441	DESCRICTION TO THE PROPERTY OF
GMEKLPLGGKFWPTQ/EAVRT VRARLQAD/VTGVPTVLVARTE ADASDLITSDCD/PYDSEFMTGE RTSEGFFRTHAGIEQAISRGLAY APYADLWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FPKVTTIQGGTPDKAFT							A VSNCSEGI SK EWGPRPCRHP
VRARLQAD/TGYPT\L\ARIT ADASDLTSDCDPYDSEMTGE RTSEGFFRTHAGIEQAISRCLAY APYADLVWCETSTPDLELARRI AQAIHAKYPGKLAYNCSFS WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWFNMFMEDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FEKVTTIIQGGTPDKAFT	23130	33304	ľ	23214	ľ	2515	
ADASDLTSDCDPYDSEFNTGE RTSEGFFRTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAIHAKYPOKLLAYNCSPSFN WQKNLDMKTIASFQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FPKVTTIQGGTPDKAFT			l				
RTSEGFERTHAGIEQAISRGLAY APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIBAWWENMEDLA NAYAQEGMKHYVEKVQQPE FAAAKDGYTFVSHQSVGTGY FEKVTTIIQGGTPDKAFT	ı		l				
APYADLVWCETSTPDLELARRI AQAIHAKYPGKLLAYNCSPSTN WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FPKVTTIQGGFPDKAFT			1		ì		
AQAIHAKYPGKLLAYNCSPSFN WQKNLDDKTIASFQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQVGTGY FPKVTTIQGGTPDKAFT			l		l		
WQKNLDDKTIASFQQQLSDMG YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT			l		i		
YKFQFITLAGIHSMWFNMFDLA NAYAQGEGMKHYVEKVQQFE FAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT			1	1	l	1	
NAYAGGEGMKHYVEKVQQPE FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT	İ		1		l	1	
FAAAKDGYTFVSHQQEVGTGY FDKVTTIIQGGTPDKAFT			1			1	
FDKVTTIIQGGTPDKAFT			1	l	l		
			1	l	I		
[25137   55505   A   25275   432	25125	55505	I.—	250#5	430	5.00	FDKVTTIIQGGTPDKAFT
	25137	55505	A	25275	432	549	

NO: of p	O ID NO: No eptide l'ence		SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25138   555		4	25276	652	2689	KFSVGYAVONFNATVSTKOFO VFSEQNTSSYFAEPQLDVNYYQ NDVVHFVTTRDDMPEATRYHL EPTINLPLSNNWGSINTEAKLLA HYQQTINLDWYNSKNTTKLDE SVNRWMPOFKVDGRMVFERD MEMLAPOYTOTLEPRAQYLLYV PYRDQSDIYNYDSSLLQSDVSG LFRDRTYGGLDRIASANQVTTG VTSRIYDDAAVEEFNISVGQIV YFTESRTGDDNITWENDDKTGG QVDTRLDNVATSNSSIEYRRDE DRLVQLNYRYASPEYIQATLEPN VHHITMEHHMKTRTQQIEEL QKEWTOPRWEGITRRYSAEDV VKLRGSVPFECTLAQLGAK WRLLHGESKKGYINSLGALTG GQALQQAKAGIEAVYLSGWQV VKLRGSVPFECTLAQLGAK WRLLHGESKKGYINSLGALTG GQALQQAKAGIEAVYLSGWQV ADANLAASMYPDQSLYPANS VPAVVERINNTFRRADQIWSA GIFEOPRYVDYFLPIVADAG GFGGVLNAFELMKAMIEAGAA AVHFEDQLASVKRMRHMGRT ASDQPWLAYAPYADLVWCEPP PPDLELARRRAQAIHAKYPGKL LAYNCSPSHWGNLDHOKYGKL HYVEKYQGEGYAR WRYNMFDLANAVAQEGMK WRYNMFDLANAVAGEGMK WRYNMFDLANAVAGEGMK HYVEKYQGEFAAAKDQYTFV SHQQEVGTGYPDKYTTIIQGT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25139	55507	IA	25277	1134	1695	I FPDPARLPPVSVNHHITMEHLH
23139	33307	ΙΑ .	23211	134	1093	
	1	1				MKTRTQQIEELQKEWTQPRWE
	1	1			l	GITRPYSAEDGGKLRGSVNPEC
		1				TLAQLGAAKMWRLLHGESKK
		1				GYINSLGALTGGQALQQAKAG
	1	1				EAVYLSGWQVAADANLAASM
l		ŀ				YPDQSLYPANSVPAVVERINNT
1				į		FRRADQI/QWSAGIEPGDPRYV
1		1				DYFLPIVADAEAGFGGVLNAFE
1					1	LMKAMIEAGAAAVHFEDQLAS
1		1				VKKCGHMGGKVLVPTQEAIQK
1				ŀ		LVAARLAADVIGVPTLLVART
		i				DADAADLITSDCDPYDSEFITGE
1		1		1		RTSEGFFRTHAGIEQAISRGLAY
İ						APYADLVWCETSTPDLELARRI
1		1				AQAIHAKYPGKLLAYNCSPSFN
	1					WQKNLDDKTIASFQQQLSDMG
						YKFOFITLAGIHSMWFNMFDLA
						KAYAOGEGMKHYVEKVOOPE
						FAAAKDGYTFVSHQQENRSSK
		1				QQQPLLTVGRIRRSRRIRQSVPR
		1		l		TGIGCASRRFNTAKPWADAVIS
1	1					
1		1				NRPFAGNTGSVDDNDEIQRNLN
		1		i		DTNYNRMWEYNNRGVGSKVV
25140	55508	A	25278	230	380	AEAKK
25140	55509	A	25279	432	1247	PSQEPSVHGRWMA*KGHSRIV*
23141	33309	^	23217	1732	1247	WRAYD*TH\FNPVLKKSVSLGS
	1	1				NIRHMLAEEATTEELDGT\GPV
i	1	1	1			LV*PNRH*PAYWMRAYLNLKK
1						MSCRSFRRKA*RW*CETOTVV
1	1					
1	1					HRDRVDQGNNHFDVVARHYH
1						LYAFLRKERQLIFFKFKYARIQY
		_				AG
25142	55510	Α	25280	243	430	RRPSYSVLQRLPSAVLLPYY*R
						DWYHRTAGRRRDGNAGRQHQ
		_				NGCYPDPPDRDGRRSAFRNP
25143	55511	A	25281	10	638	SSVPTAGSRYNHLRAPRYSPLF
1		1	ŀ			ANYSMSDRCCKPFG/LDSSTG*
		1				WFQ*RSVPLPILLPDTSRHQL*C
1	1	1	ļ.			SDPTRNGPA\QACQRFFHIVERV
	1	1				ARVHHARFAATVTVDHVVIDQ
1	1	1	1	1		RFFQICRT/PWCRLHRHHWRSS
1	1	1				GTR*TF*SPARHFCLLHNDSSYR
i		1		1		STARPTCSGTDVPDRRCSDAHL
1	1	1	1			CDHWSGSRAHADTDAECWCL
		1				NPQPAPSLLQCRR
25144	55512	A	25282	803	1622	· · · · · · · · · · · · · · · · · · ·
25145	55513	A	25283	498	686	RRPSYSVLQRLPSAVLLPYY*R
1	1	1				DWYHRTAGRRRDGNAGRQHQ
1		1	1	1		NGCYPDPPDRDGRRSAFRNP
1	1		1	L	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nueleotide insertion)
25146	55514	Α	25284	1	2063	MKNFMENVLRYLSDDKWKPD
		1				AKASMTVGTNLDTVYFKRHGQ
	l	l				VTGNSAAFDFHPDFAGISVEHL
	İ	1				SSYGDLDPQEMPLLILNGFEYV
	İ	1				TQVGNDPYAIPLRADTSKPKLT
						QQDVTDLIAYLNKGGSVLIMEN
						VMSNLKEESASGFVRLLDAAG
	1			ł		LSMALNKSVVNNDPQGYPNRV
		1				RQQRATGIWVYERYPAVDGAL
		1				PYTIDSKTGEVKWKYHVENKP
		l				DDKPKLEVASWLEDVDGNRKR
						NFSNDARANGTAAFTDCETQT
		l				VVHRDRVDQGHNHFDLVARH
		1				YHLYAFRQFDGTSHVSSTEVEL
		1				RTVAFEERSMTAAFISWTECTL
					ļ	QIRTCPQNPTGKVWTCDELEIM
		1				ADLCERHGVRVISDEIHMDMV
						WGEQPHIPWSNVARGDWALLT
		l				SGSKSFNIPALTGAYGIIENSSSR
					İ	DAYLSALKGRDGLSSPSVLALT
	1					AHIAAYQQGAPWLDALRIYLK
			•		1	DNLTYIADKMNAAFPELNWQIF
	1	1			i .	QSTYLAWLDLRPLNIDDNALQ
		1				KAL\IDQEKVAIMPGYTYGEEG
		l				RGFVRLNAGCPRSKLEKGVAG
					1	LINAIRAKKSATMIDTTLPLTDI
		1				HRHLDGNIRPQTILELGRQYNIS
		1			1	LPAQSLETLIPHVQVIANEPDLV
					1	SFLTKLDWGVKVLASLDACRR
					1	VAFENIEDAARHGLHYVELRFS
	1					PGYMAMAHQLPVAGVVEAVID
						GVREGCRTFGVQAKLIGIM
25147	55515	Α	25285	3	371	
25148	55516	Α	25286	63	180	
25149	55517	Α	25287	2	205	
25150	55518	Α	25288	495	707	REFSSHQKGLRDRPAHKAVLG
		1			1	DNQLFSGGTGAPVWPG/HSENV
		1			1	VPVDPT\MKRLPDDVNHPALDY
	1	1				YWRLSFA

NO:	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
25151   55519   A   25289   I   1713   MTWAYSPSYGKPLSVPQGIIG MTRRGMDVTLAHPEGYDLIF VVEVAKNAKASGGSFRQV MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVPRSWAPY MEGAFKDADIVALISHEM SCKEGRSDQKAYDEKSRPDE PIDDNVVLIKGGVLQVRSGDV RVKTLADRIGFISHSQVTDLL CAFFVIGIMIGMITFOFSTESF MCNAAGLIFAGIMLGFMRAA PTFGYIPQGALSMVKEFGLM MAGGIQVDGNTIYPHIWKSC GVLFAKQYLLRIGIILYGFRI SQIADWIGSIIDVLTLSSTFI ACFLQQK VFGLDKHTSWLIG GSSICGAAAVLATEPVVKAE KVTVAVATVVIGFGVAHFLY YPLMSQWFSPETFGIYIGSVII GVDVPNASLMIENPERILGL LHQLRGRVGRGAGLLTACCS KRRILKAAPEVTRTGLADDR GLPQTGYGLASMQGLDVVV LSPQGTDTFAMLDAFRANEA AAPLPLTANSDCNGYWRLDL LHQLRGRVGRGAGLLTACCS KRRILKAAPEVTRTGLADDR GLPQTGYGLASMQGLDVVV LSPQGTDTFAMLDAFRANEA AAPLPLTANSDCNGYWRLD HCWPADISGVSCKGGEVTEG EKYRIATYKEASWKPYILAA CPVNTTPNQVHCSSNC HCWPADISGVSCKGGEVTEG EKYRIATYKEASWKPYILAA CPVNTTPNQVHCSSNC CPVNTTPNQVHCSSNC CPVNTTPNQVHCSSNC CPVNTTPNQVHCSSNC GEVTEG EKYRIATYKEASWKPYILAA CPVNTTPNQVHCSSNC GUTEG EKYRIATYKEASWKPYILAA CPVNTTTPNAMATTPNAMATA CPVNTTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATTPNAMATT						of peptide sequence	deletion, \=possible nucleotide insertion)
MTRIGMDVTLAHPEGYÖLLE VVEVAKNNAKASGGSRQV MEEAFKDADIVYPKSWAPYY MEERTELLRANDHEGVKAP HCLAQNAQHKUWHISIEME EPITREGEAQNKHGRPAEING SCKEGRSDCKAYDEKSRPDE PIDDNVVLNKGDVLQVSGDV RVKTIADRIGFISHSQVTDLL CAFFVIGLMIGMITPOFSTSST MGNAAGLLFAGIMLGFMRA PITGYIPQGALSMVKFGILM MAGEIQVDGNTIYPHIWSSC GVLFAKQYLLRLGIILYGFRL SQIADVIGSGIIDVLTLSSTFL ACFLGQKVFGLDKHTSWLIG GSSICGAAVLATEPVVKAE KVTVAVATVVIGTVAILTY! YPLMSQWFSPETFGIYIGSVII GVDVPNASMIIENPERIGL. LHQLRGRVGRGAGLLTACC KRRILKAAPEVTRTGLADDR GLPLQTGYELASMQGLVDVU LSPQGTDTFAMLDAFRANEN AAPLPLANSDCNGYWRLL DHEGLKALLEKQCLAQNAQ-D WHCTEEMMELTRDGGALY HCWPADISGVSCKEGEVTEG EKYPIATYKEASWKPYIIAAN CPVNTPNQVHCSSNC  25153 55521 A 25291 235 780  TYRNNHQTIGVAFLFQTIKF HGGGKTGFGFRRGKA GIFLYNNQLQPDIVHGGFCTF HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNKMPRIGVG GWAYLQGYPVRFGVWPLEE AYACGKFNGAIRAGDAAQL YAQAFQLHGIPIDAGGAGVW					sequence		
MTRIGMDVTLAHPEGYÖLLE VVEVAKNNAKASGGSRQV MEEAFKDADIVYPKSWAPYY MEERTELLRANDHEGVKAP HCLAQNAQHKUWHISIEME EPITREGEAQNKHGRPAEING SCKEGRSDCKAYDEKSRPDE PIDDNVVLNKGDVLQVSGDV RVKTIADRIGFISHSQVTDLL CAFFVIGLMIGMITPOFSTSST MGNAAGLLFAGIMLGFMRA PITGYIPQGALSMVKFGILM MAGEIQVDGNTIYPHIWSSC GVLFAKQYLLRLGIILYGFRL SQIADVIGSGIIDVLTLSSTFL ACFLGQKVFGLDKHTSWLIG GSSICGAAVLATEPVVKAE KVTVAVATVVIGTVAILTY! YPLMSQWFSPETFGIYIGSVII GVDVPNASMIIENPERIGL. LHQLRGRVGRGAGLLTACC KRRILKAAPEVTRTGLADDR GLPLQTGYELASMQGLVDVU LSPQGTDTFAMLDAFRANEN AAPLPLANSDCNGYWRLL DHEGLKALLEKQCLAQNAQ-D WHCTEEMMELTRDGGALY HCWPADISGVSCKEGEVTEG EKYPIATYKEASWKPYIIAAN CPVNTPNQVHCSSNC  25153 55521 A 25291 235 780  TYRNNHQTIGVAFLFQTIKF HGGGKTGFGFRRGKA GIFLYNNQLQPDIVHGGFCTF HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNKMPRIGVG GWAYLQGYPVRFGVWPLEE AYACGKFNGAIRAGDAAQL YAQAFQLHGIPIDAGGAGVW	25151	55510	Ι	25280	1	1713	MTWAYSPSYGKPI SVPOGUGI
VVEVAKNNAKASGGSFRQV   MEEAFKDADIVYPKSWAPYA   MEERTELLRANDHEOYKAP   MEERTELLRANDHEOYKAP   HCLMQNAQHKDWHISIEM   EPITREGEAQNKHGRPAAINN   SCKEGRSDQKAYDEKSRPDE   PIDDNVVLNKGDVLQVSGDJ   RVKTIADRIGFISHSQVTDLL   CAFFVIGLMIGMITPGFSTFST   MGNAAGLLFAGIMLGFMRA   MAGEIQVDGMTYPHIWSC   GVIFAKQYLLRLGIILYGFRL   SQIADVGISGIIDVLT.ISSTFL   ACFLQQKVFGLDKHTSWLLG   GSSICGAAAVLATEPVVKAE   KVTVAVATVVIGTVAILYJ   YPLMSQWFSPETFGIYIGSVII   GVDVPNASLMIIENFERLGLJ   LHQLRGRVGRGAGLLTACCC   KRRFLKAAPEVTRTGLADDR   GLPLQTGYELASMQGLUDV   LSPQGTDTFAMLDAFRANCH   LAPQGTOTFAMLDAFRANCH   AAPLPLTANDCNGYWRRLJ   ASGRFREVTGMEEAFKDAD   YPQSWAPYKVMEERTVLLR   DHEGLKALLEKQCLAQNAQ   DWHCTEEMMELTRDGEALY   HCWPADISGSVSCKEGEVTEG   EKYRIATYKEASWKPYILAA   CPVNTFNQVHCSSNC   EKYRIATYKEASWKPYILAA   CPVNTFNQVHCSSNC   CEKYRIATYKEASWKPYILAA   CPVNTFNQVHCSSNC   CEKYRIATYKEASWKPYILAA   CPVNTFNQVHCSSNC   CEKYRIATYKEASWKPYILAG   GILVNNQLQYRVOTQSRIIA   EVTDVEINLFCHPLCIIMQIFT   HISEELATFIVRGFRFRRGKA   GILVNNQLQYDVINRGFCT   HDVRGIKHFTLVEHVITGSGI   NTTRTFFFRRGKA   GILVNNQLQYDVINRGFCT   HDVRGIKHFTLVEHVITGSGI   NTTRTFFFRRGKA   GILVNNQLQOPVNRGPNKWPLIGV   GWAVLQGVPVRFGVWPLPE   AYACGKRNGAIRAGDAAQL   YAQAFQLHIGDDAGDAVR   CAQAFQLHIGDDAGDAVRA   CAQAFQLHIGDAGGAVRA   CAQAFQLHIGDDAGDAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CAQAFQLHIGDDAGGAVRA   CACAFTA CACAFTA   CACAFTA CACAFTA CACAFTA CACAFTA CACAFTA CACAFTA CACAFTA CACAFTA CACAFT	23131	33313		1310	ľ	1	
MEEAFKDADIVYPKSWAPYY MEERTELLRANDHEGVKAP HCLAQNAQHKIDWHSIEEM EPTREGEAQNKHGRPAEINK SCKEGRSDQKAPDEKSRPD BIDDNVYLNKGDVL,OVSGDA RVKTIADRIGFISHSQVTDLL CAFFVIGLMIGMITGFSTSTSS MGNAAGLLFAGIMLGFMRA PTFGYIPGGALSMVKEFGLM MAGEIQVDGNTIYPHIWKSC GVLFAKQYLLRLGIILGYFRIA SQIADVGISGIIIDVLTLSSTFT ACFLGQKVFGLDKHTSWLIG GSSIGGAAVALATEPVVKAE KVTVAVATVVIFGTVAIFLYI YPLMSQWFSPETFGIYIGSVII GVDYPNASLMIENPRELGL- LHQLRGRVGRGAGLLTACC: KRRFLKAAPEVTRTGLADDB GLPLQTGYELASMQGLVDV- LSPQGTDTFAMLDAFRANEN AAPLPLTANSDCNGYWRLL- DHEGLKALEKQCLAQNAQF DWHCTEEMMELTRDGGELY HCWPADISGVSKEGEVTEG EKYYRLATYKEASWKPYIJAAN CPVNTPNQVHCSSNC  25153 55521 A 25292 1 2783 MTYRNNIQTGVAFLFQTKF GGGKYFGLTFOKFRGKA GIFLVNNQLQPDIVHGGCTE HDVGRIKHFTLVEHVITGSGI NTRFTFFRAGNKMPRLGVC GWAVLQGYPKRGVWPLEE AYACGKFRGAIRAGDAAQL YQAGFQLHGFIDAGOGNWR					i		
MEERTELLRANDHEGVKAP					l		
HCLVQNAQHKIOWHISIEEM			l		l		
EPITEGEAONKHGRPAEIN   SCKEGRSDQKAYDEKSRPDE   PIDDNVVLNKGDVLQVSGDV   RVKTIADRIGFISHSQVTDLL   CAFFVIGLMIGMITPGSTFISS     MONAGQLFAGIMLGFMRA     PTFQYIPQGALSMVKEFGLM     MAGEIQVDGNTIYPHIWSCC     GVLFAKQYLLRLGIILYGFRL     SQIADVIGSGIIDIVLTLSSTFI     ACFLGQKVFGLDKHTSWLIG     GSSICGAAAVLATEPVVKAE     KVTVAVATVVIFGTVAIFLY      YPLMSQWFSPETFGIYIGSVII     GVDVPNASIMIENPERIGLI     LHQLRGRVGRGAGLLTACC     KRRFLKAAPEVTRTGLADDR     GLPLQTGYELASMQGLVDV     LSPQGTDTFAMLDAFRANEN     AAPLPLTANSDCNGYWRRL     AASGRFREVTGMEEAFKDAD     YPQSWAPYKVMEERTVLLR     DHEGLKALEKQCLAQNAQP     DWHCTEEMMELTRDGEALY     HCWPADISGVSCKEGEVTEG     EKYPLATYKEASWKPYIJAAN     CPVNTPNQVHCSSNC     25153   55522   A   25292   1   2783   DGGVKTEDGVROTGSRIA     EVTOVERILFCHPLCIMQIFT     HISEELATFIVRGFRFRRGKA     GIFLVNNQLQPDIVHGFCTF     HDVRGIKHFTLVERIVITGSGI     NTRFTFFRAGNKMPRIGVG     GWAVLQGVPVRFGVWPLPE     AYACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAQL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAGL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAGL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAGL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAAGL     YAQAFIQLHGPIDAGGOVRH     YACGKFNGAIRAGDAACL     YACGKFNGAIRAGDAACL     YACGKFNGAIRAGDAACL     YACGKFNGAIRAGDAACL     YACGKFNGAIRAGDAACL     YACGKFNGAIRAGDAACL     YACGKFNGAIRAGDAACL     YACGKFNGA			l				
SCKEGRSDGKAYDEKSRPDE   PIDDNVVLNKGDVLQVSGD/RVKTIADRIGFISHSQYTDLL							
PIDDNYUNKGDVLQVSGDZ RVKTIADRIGFISHSQVTDLL CAFFVIGLMIGMITGPSTIFSS MGNAAGLLFAGIMLGFMRA PTFGYPGGALSMYKEFGLM MAGEIQVDGNTIYPHIWSC GVLFARQYLLRLGIILYGFRL SQIADVGISGIIIDVLTLSSTFL ACFLGQKVFGLDKHTSWLIG GSSIGGAAVLATEPVVKAE KVTVAVATVVIFGTVAIFLYI YPLMSQWFSPETFOLYIGSVII GVDVPNASLMIENPERLGLL LHQLRGRVGRGAGLLTACC: KRRFLKAAPEVTRTIGLADDB GLPLQTGYELASMQGLVDV- LSPQGTDTFAMLDAFRANEN AAPLPLTANSDCNGYWRELY LSPQGTDTFAMLDAFRANEN DHEGLKALEKQCLAQNAQ- DWHCTEEMMELTRDGEALY HCWPADISGVSKEGEVTEG EKYRLATYKEASWKPYIJAAN CPVNTPNQVHCSSNC    25153   55521			ı				
RVKTIADRIGEISHSQYTDLL	]		l				
CAFFVIGLMIGMITFOFSTESS   MGNAAGLLFAGIMLGFMRA   PTFGYIPQGALSMVKEFGLM   MAGEIQVDGNTIYPHIWKSC   GULFAKQYLLKIGIILYOFRI   SQIADVGISGIIDVLTLSSTFL   ACFLGQKVFGLDKHTSWLIG   GSSIGGAAVLATEPVVKAE   KVTVAVATVVIFGTVAHELYI   YPLMSQWFSFEFTGYIGSVI   GVDVPNASLMIIENPERLGL.   LHQLRGRVGRGAGLLTACC: KRRFLKAAPEVTRTIGLADDB   GLPLQTGYELASMQGLVDV-LSPQGTDTFAMLDAFRANEN   AAPLPLANSDCNOYWREL.   LSPQGTDTFAMLDAFRANEN   AAPLPLANSDCNOYWREL   DHGLKALEKQCLAQNAQP   DWHCTEEMMELTRDGEALY   HCWPADISGVSCKEGEVTEG   EKYRIATYKEASWKPYIIAAN   CPVNTPRQVHCSSNC   CFVNTPNQVHCSSNC   CFVNTPNQVHCSSNC   CFVNTPNQVHCSSNC   CFVNTPNQVHCSSNC   CFVNTPNQVHCSNC   CFVNTPN			1				
MONAGGLEAGIMLÖFMRA   PTFGYIPQGALSMVKEFGLM   MAGEIQVDGMTIYPHIWSC.   GVLFAKQYLLRLGIILYGFRL   SQIADVIGSGIIDVLTLSSTIF!   ACFLGQKVFGLDKHTSWLIG   GSSICGAAAVLATEPVVKAE   KVTVAVATVVIFGTVAIFLY  YPLMSQWFSPETFGIYIGSVII   GVDVPNASIMIENPERIGLI.   LHQLRGRVGRGAGLLTACC: KRRFLKAAPEVTRTGLADDR   GLPLQTGYELASMQGLVDV   LSPQGTDTFAMLDAFRANEN   AAPLPLTANSDCNGYWRRL.		i	1		1		
PTFGYIPQGALSMYKEFGLM   MAGEIQVDGNTIYPHIWKSC   GVLFAKQYLLRLGIILYOFRL   SQIADVGISGIIDVLTLSSTFL   ACFLGKKYFGLDKHTSWLIG   GSSICGAAAVLATEPVVKAE   KVTVAVATVVIGTVAILTJ   YPLMSQWFSPETFGIYIGSVI   GVDVPNASLMIIENPERLGL.   LHQLRGRVCRGAGLLTACC   KRRFLKAAPEVTRTGLADDR   GLPLQTGYGLASMQGLLDVJ   LSPQGTDTFAMLDAFRANDE   AAPLPLTANBCOLONYWRIL.   ASGRFREVTGMEGAFKDAD   PYQSWAPYKVMEERTVLLR.   DHEGLKALLEKQLLAQNAQ   DWHCTEEMMELTRDGEALY   HCWPADISGVSCKEGEVTEG   EKYBLATYKEASWRYPILAAD   CPWTTPNQVHCSSNC   EKYBLATYKEASWRYPILAAD   CPWTTPNQVHCSSNC   S5522   A 25292   1 2783   MTYRNNHQIGVAFLFQTKFG   DGGVKTFDGYRVOTQSRIA   EVTDVEINLFCHPLCIIMQIFT   HISEELATFIVRGFRFRRGKA   GIFLVNNQLQPDVHRGFCRF   GDVKRTFGGYRVOTQSRIA   EVTDVEINLFCHPLCIIMQIFT   HISEELATFIVRGFRFRRGKA   GIFLVNNQLQPDVHRGFCRF   HDVRGIKHFTLVEHVITGSG   NTERTFFFRRGNKMPRLGV   GWAVLQGVPVRFGVWPLPE   AYACGKFNGAIRAGDAAQL   YAQAFQLHIGDIAGDGAVRPL	İ		l				MGNAAGLLFAGIMLGFMRANH
MAGEIQVDGNTIYPHIWKSC							
GVLFAKQYLLRLGIILYGFRL	1		i			1	
SQIADVGISGIIIDVLTLSSTFL	ļ		l				
ACFLGQKVFGLDKHTSWLIG   GSSICGAAAVLATEPVVKAE   KVTVAVATVVIEGTVAILLY    YPLMSQWFSPETGIYIGSVII   GVDVPNASIMIENPERIGLI   LHQLRGRVGRGAGLLTACCS   KRRFLKAAPEVTRTGLADDR   GLPLQTGYELASMQGLVDV   LSPQGTDTFAMLDAFRANEN   AAPLPLTANSDCNGYWRRLI   AAGRFREVTGMEEAFKDAD   YPQSWAPYKVMEERTVLLR.   DHEGLKALEKQCLAQNAOP   DWHCTEEMMELTRDGEALY   HCWPADISGVSCKEGEVTEG   EKYPLATYKEASWKPYIIAAN   CPVNTPNQVHCSSNC   25153   55522   A   25291   2783   DGGVKTEGGYRGTS   A   25292   1   2783   DGGVKTEGGYRGTS   GGVKTEGGYRGTGRFRFRGKA   GIFLVNNQLQPDIVHGGFCTF   HISEELATFIVRGFRFRRGKA   GIFLVNNQLQPDIVHGGFCTF   HDVRGIKHFTLVEHVITGSGI   NTRFTFFRAGNKMPRIGVO   GWAVLQGVPVRFGVWPLEE   AYACGKFNGAIRAGDAAQL   YAQAFQLHGPIDAGGOVRF			l				
GSSIGĞAAVLATEPVYKAE							ACFLGOKVFGLDKHTSWLIGA
VPLMSQWFSPETFGIVIGSVII   GVDVPNASLMIIENPERLGL/   LHQLRGRVGRGAGLITACCS     KRRFLKAAPEVTRTGLADDR     GLPLQTGYELASMQGLVDV     LSPQGTDTFAMLDAFRANEA     AAPPLTANSDCNGYWRRL/   ASGRFREVTGMEEAFRDAD     YPQSWAPYKVMEERTVLLR     DHEGLKALLEKQCLAQNAQ     DWHCTEEMMELTRDGEALY     HCWPADISGVSCKEGEVTEG     EKYRIATYKEASWKPYIIAAN     CPVNTPNQVHCSSNC     25153   55521   A   25291   235   780     25154   55522   A   25292   1   2783   MTYRNNHQIGVAFLFQTKFI     DGGVKTFGGYRTGG     GGVKTFGGYRVQTGSRTIA     EVTDVEINLFCHPLCIIMQIFT     HISEELATFIVRGFRFRRGKA     GIPLVNNQLQPDVINRGFCTE     HDVRGIKHFTLVEHVITGSG     NTRFTFFRRGNKMPRLGVC     GWAVLQGVPVRFGVWPLPE     AYACGKFNGAIRAGDAAQL     YAQAFQLHIEDDAAGDAYNE     YACGBYNGAIRAGDAAQL     YAQAFQLHIEDDAAGDAYNE     YACGBYNGAIRAGDAADL     YAQAFQLHIEDDAAGDAYNE     YACGBYNGAIRAGDAADL     YAQAFQLHIEDDAAGDAYNE     YACGBYNGAIRAGDAADL     YAQAFQLHIEDDAAGDAYNE     YACGBYNGAIRAGDAADL     YACGBYNGA			l				GSSICGAAAVLATEPVVKAEAS
GVDVPNASLMIIENPERIGLA   LHQLRGRVGRGAGLLTACCS   KRRFLKAAPEVTRTGLADDB    GLPLQTGYELASMQGLVDV    LSPQGTDTFAMLDAFRANEO    LSPQGTDTFAMLDAFRANEO    AAPLPLTANSDCNGYWRRLA   AAPLPLTANSDCNGYWRRLA   AAPLPLTANSDCNGYWRREATVLRL   DHEGLKALEKQCLAQNAQH    DWHCTEEMMELTRDGEALY    HCWPADISGVSCKEGEVTEG    EKYPLATYKEASWKPYIIAAN    CPVNTPRQVHCSSNC    25153   55521   A   25291   235   780     25154   55522   A   25292   1   2783   MTYRNNHQTGVAFLFQTKFG   DGGWKTFDGYRVQTGSRHA    EVTDVEINLFCHFLCIIMQFT    HISELATFIVEGYRFRGRAGA   GIFLVNNQLQPDIVHRGFCTE    HDVRGIKHFTLVEHVITGSGI    NTRFTFFRGRNKMPRLGVC    GWAVLQGVPVRFGVWPLPE    AYACGKFRGAIRAGDAQLA   YAQAFQLHGPIDAGGGVRF	1						KVTVAVATVVIFGTVAIFLYPA
LHQLRGRVGRGAGLITACCS   KRRFLKAAPEVTRTGLADDR GLPLQTGYELASMGGLVDV LSPQGTDTFAMLDAFRANED   AAPLPLTANSDCNGYWRLL			l				YPLMSOWFSPETFGIYIGSVIEV
RRFLKAAPEVTRTGLADDR			l		ļ		GVDVPNASLMIIENPERLGLAQ
GLPLQTGYELASMQQLVDV-    LSPQGTDTFAMLDAFRANEN     AAPLPLTANSDCNGYWREL-    25152   55520   A   25290   629   1054   ASGRFREVTG/MEEAFKDAD     YPQSWAPFKWMEERTVLEL,     DHEGLKALEKQCLAQNAQ+     DWHCTEBMBLTRDGEALY     HCWPADISGVSCKEGEVTEG     EKYRIATYKEASWKPYIIAAN     CPVNTPNQVHCSSNC     25153   55521   A   25291   235   780     Z5154   55522   A   25292   1   2783   MTYRNNIQTGVAFLFQTKFG     DGGVKTFDGYRVQTGSRIA     EVTDVEINLFCHFLCIIMQIFT     HISELATFIVRGFRFRRGKA     GIFLYNNQLQPDIVHGGCTF     HDVRGIKHFTLVEHVITGSG     NTRFTFFRAGNKMPRLGVC     GWAVLQGVPVRFGVWPLPE     AYACGKFRGAIRAGDAAQL     YAQAFQLHGPIDAGGGVTR							LHOLRGRVGRGAGLLTACCST
LSPQGTDTFAMI.DAFRANED			1				KRRFLKAAPEVTRTGLADDRSS
AAPLPLTANSDCNGYWRRL/   25152		ĺ					GLPLQTGYELASMQGLVDVVR
25152   55520	1		1				LSPQGTDTFAMLDAFRANENG
PROSMAPYKVMEERTYLLR.  DHEGLKALEKQCLAQNAGE DWHCTEEMMELTREGCELTY HCWPADISGVSCKEGEVTEG EKYRIATYKEASWKPYIIAAN CPVNTPNQVHCSSNC  25153 55521 A 25291 235 780  25154 55522 A 25292 1 2783 MTYRNNHQIGVAFLFQTKFF DGGVKTFDGYRVQTQSRHA EVTDVEINLFCHELCIIMQIFT HISEELATFIVERFFRERGA GIFLVNNQLQPDIVHRGFCTE HDVRGIKHFTLVEHVITGSGI NTERTFFREAGNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFQLHGPIDAGGOVRE	1		l				AAPLPLTANSDCNGYWRRLAG
DHEGLKALERQCLAQNAQPDWHCTEEMMELTRDGEALY	25152	55520	Α	25290	629	1054	ASGRFREVTG/MEEAFKDADI/V
DWHCTEEMMELTRDGEALY HCWPADISGVSCKEGEVTEG EKYBLATYKEASWRPYILAA  25153 55521 A 25291 235 780  25154 55522 A 25292 1 2783 MTYRNNHOIGVAFLFOTKFI DGGVKTFDGYRVOTOSRIA EVTDVEINLFCHPLCIIMQIFT HISEELATFIVRGFRFRRGKA GIFLVNNOLQPDIVLRGFCTE HDVRGIKHFILVEHVITGSGI NTRRTFFRRGNKMPRLGVC GWAVLQGVPVRFGVWPLPE A YACGKFNGAIRAGDAAQL YAQAFICLHEIDPLAGGOVRF							YPQSWAPYKVMEERTVLLRAN
HCWPADISGVSCKEGEVTEG							DHEGLKA\LEKQCLAQNAQHK
EKYPIATYKEASWKPYIIAAN CPVNTPNQVHCSSNC 25153 55521 A 25291 235 780  Z5154 55522 A 25292 1 2783 MTYRNNHQTGVAFLFQTKFF DGGVKTFDGYRVQTQSRNIA EVTDVEINLFCHFLCIIMQIFT HISEELATFIVRGFRFRRGKA GIFLVNNQLQPDIVHGGFCTF HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFQLHGPIDAGGOVRF			1			ł	DWHCTEEMMELTRDGEALYM
CPVNTPNQVHCSSNC			1				HCWPADISGVSCKEGEVTEGVF
25153   55521			l				EKYRIATYKEASWKPYIIAAMI\
25154 55522 A 25292 I 2783 MTYRNNHQIGVAFLFQTKFG DGGVKTFDGYRVQTOSRHA EVTOVENIL-FCHPLCIMQFIF HISEELATFIVRGFRFRGKA GIFLVNNQLQPDIVHRGFCTE HIDVRGIKHFTLVEHVITOSGI NTRFTFFRAGNNKMPRLGVC GWAVLQGYPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGGGVYR							CPVNTPNQVHCSSNC
DGGVKTFDGYRVQTQSRHA EVTDVEINLFCHFLCIIMQIFT HISEELATFIVEGFFFRRGA GIFLVNNQLQPDIVHRGFCTF HIDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL. YAQAFQLHGPIDAGDGVNF	25153	55521	Α	25291	235	780	
EVTDVEINLECHELCIIMQIFT HISEELATFIVRGFRFRRGKA GIELVNNQLQPDIVHGGCTE HDVRGIKHFTLVEHVITGSGI NITRTFFRAGNKMPRLGVC GWAVLQGVPVRFGVWDLEE AYACGKFNGAIRAGDAAQL YAQAFQLHGPIDAGDGVNR	25154	55522	Α	25292	1	2783	MTYRNNHQTGVAFLFQTKFCIE
HISEELATFIVRGFRFRRGKA GIFLYNNOLOPDIVHRGFCTE HIDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGGGVYR			1				DGGVKTFDGYRVQTQSRHAEQ
GIFLVNNQLQPDIVHRGFCTE HDVRGIKHFTLVEHVITGSGI NTIRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL. YAQAFQLHGPIDAGDGVNR			1				EVTDVEINLFCHPLCIIMQIFTV
HDVRGIKHFTLVEHVITGSGI NTRFTFFRAGNNKMPRLGVC GWAVLQGVPVRFGVWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGDGVAF			1				HISEELATFIVRGFRFRRGKAAI
NTRFTFFRAGNNKMPRLGVC GWAVLQGYPVRFGVWPLPE AYACGKFNGAIRAGDAAQL, YAQAFIQLHGPIDAGGVYR							GIFLVNNQLQPDIVHRGFCTEH
GWAYLGGYPYRFGYWPLPE AYACGKFNGAIRAGDAAQL YAQAFIQLHGPIDAGDGYNF						1	HDVRGIKHFTLVEHVITGSGFG
AYACGKFNGAIRAGDAAQL, YAQAFIQLHGPIDAGDGVNR			1			1	NTRFTFFRAGNNKMPRLGVGA
YAQAFIQLHGPIDAGDGVNR			1			1	GWAVLQGVPVRFGVWPLPEYP
			l				AYACGKFNGAIRAGDAAQLAA
			1		1	I	YAQAFIQLHGPIDAGDGVNRA
DHRAGDFFEIVFQNLFAIADV			1			i	DHRAGDFFEIVFQNLFAIADVD
LAINHAVNAQLRLRNP	l .		L				LAINHAVNAQLRLRNP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first eodon for peptide sequence	codon for last amino aeid of peptide sequenee	*-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
		l				
25155	55523	Α	25293	365	722	TSCLSALAIK/QQHLDEKKELG
		1				HLSAGARRLILGIIVTF/CADSG
		1			İ	VNLRYSAV*PAGAVYLPDAAV
		1				GGSADRTADAGALLGANVDCA
				1	1	VADRFLPLYLVALHLYAELGRS
						GQPGVRAYSALR
25156	55524	Α	25294	798	1094	
25157	55525	Α	25295	1	2780	MGIVA\$A\$VQAAEIYNKDGNK
						LDVYGKVKAMHYMSDNASKD
						GDQSYIRFGFKGETQINDQLTG
	İ					YGRWEAEFAAWTDMFPEFGG
	1	1				DSSAQTDNFMTKRASGLATYR
ļ		1			İ	KTTSSAYRWPELNLQYHRCTS
		1				AARAMLLSGRPVMQINERTAV
l		1				RRQMTVYLRVERIHEIDPLVSL
		1		1		SHSMSVIPIDVERPIAAAPCTPG
		l				LWRTKTPLRVPSTYPLRLPGRA
			1			RVVCHRTFRLHLCKDWVFMFS
						GLLIILVPLIVGYLIPLRQQA
25158	55526	Α	25296	66	300	QSTYCDNPPVPVSRGL*P*RRSS
1		1				STSSAGYQK*RYCQHRHDPASR
1		ŀ				IRTVQRTDSQRTVKRKFMLLVP
1						EASVPASEIC
25159	55527	A	25297	240	424	RCSRDEHDFQLIANLRIVVITFA
		i i				TFA*CTA*LPLGNHSVVAAH*A
						G*GGAPVTAQVFVQHG
25160	55528	A	25298	1	1425	
25161	55529	Α	25299	I	471	
25162	55530	A	25300	1269	1390	
25163	55531	A	25301	601	1119	VAAGAV*RGH*NVQLGKLFFV
		1		1		ASDLRINAIAGGVVVFS*FIQGL
		1	l	i .		TNAIGSGFNNARCRKPTGQVA
		1		1		ADGGRDAGFFTIANNQCTYAA
				1		GIFFQCSGEFVGIQFQFAIAGIGR
		1		1		DTNLRQRFIAGRTDGITQHRFQ
1				1		LRLNRPQRGVAEQCTIARTLAIS
						SRMAVYLVRLLKVSISEL
25164	55532	Α	25302	1666	1769	RLKRHPPLRPSWPPY*TGAHVW
						HFSPLANWKPGI
25165	55533	Α	25303	1	1970	MKDDIFFRTSGGGVTLSGGEVL
				1		MQAEFATRFLQRLRLWGVSCA
	ŀ			1		IETAGDAPASKLLPLAKLCDEV
	1			1		LFDLKIMDATQARDVVKMNLP
	1	1	1	I		RVLENLRLLVSEGVNVIPRLPLI
		1				PGFTLSRENMQQALDVLIPLNIR
	1	1				QIHLLPFHQYGEPKYRLLGKTW
l	1	1		1		SMKEVPAPSSADVATMREMAE
l		1	1	I		RAGLQVTVGEKWGVSIETQGA
l		1		1		LGTENRLADEDIRRADVALLIT
1	1		1			DIELAGAERFEHCRYVQCSIYA
1	1		1	1	1	FLREPQRVMSAVREV

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25166	55534	A	25304	2804	3494	LSLAEWKCLNPSQRALYREVM
23100	33334	^	23304	2804	3434	LENYRNLEAVGQLQPQSTQRIP
						*GRICNGDRLTSQKGLDL\VLEA
			-			LPGLL\EOGGQLALLGAGDPVL
						QEGFLAAAAEYPGQVGVQIGY
						HEAFSHRIMGGADVILVPNRFE
i		l				PCGLTQLYGLKYGTLPLVRRTG
						GLADTVSDCSLENLADGVASG
i						FVFEDSNAWSLLRAIRRAFVLW
						SRPSLWRFVQRQAMAMDFSW
		L				Q\VAAKSYRELYYRLK
25167	55535	A	25305	1	1306 1658	
25168	55536	A	25306	2611	2826	
25169	55537	A	25307			
25170	55538	Α	25308	609	2359	PPPKIAPV WGCRKKSLPARSKSI
1						FCFALFFPFFLNGEIILPESPCPF
1	:					WTLFRNDGGKKRDPLAPVYLL
						GKLTISPGPICPDMIGVLFDSTV
						RREVAHIGNVQHRFCGPLFLKL
						VEFIDFILTIDIAAIIRQYLVVICE
					1	VDQRINQIAIATRIFRTGYTAAD
ŀ						LRQIILMQLLIFLVVFTRFVALT
l l	ł				1	TQFFHFFRCVTKNKDIVSTDMI
					1	QHLDIRTVQRTDSQRTVKRKLH
					1	VTGAGSFRPCQRNLFRQICRRN
	l				1	DQLRQANAVVRDEHDFQLIAN
l					1	LRIVVDHFRYVIDQMNNVLRH
ŀ					1	VIGRSRLTAKNIHARYPLRIRVG
ŀ						LDAVIAEMASGLDPFWRPDVV
l						HAHDWHAGLAPAYLAARGRP
1		ĺ				AKSEFTVHNLAYQGMFYAHH
1	ı					MNDIOLPWSFFNIHGLEFNGOIS
l						FLKAGLYYADHITAVSPTYARE
1						ITEPOFAYGMEGLLQORHRERR
1						LFGVLNGVDEKIWSPETDLLLA
						SRYTRDTLEDKAENKROLONA\
1						MGLKVDDKVPLFAVVSRLTSQ
1						KGLDLVLEALPGLLEQGGQLA
l						
1				1		LLGAGDPVLQEGFLAAAAEYP
1		1	1		I	GQVGVQIGYHEAFSHRIMGGA
						DVILVPSRFEPCGLTQLYGLKY
1		l	1			GTLPLVRRTGGLADTVSDCSLE
		ĺ				NLADGVASGFVFEDSNAWSLL
I		l	1			RAIRRAFVL/WSRAGSWRYSAR
1		l				AIRCCRKVSLRRQRNTPVRWAF
1	1	ı	1	J _		RLAITKHFRIALWAARTSFWCP

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
25171	55539	A	25309	1028	1632	TSASAGTARNFSSNFAVRTTGH STSEATSSSRSILS KSALPHEL SASALMFFVIGDDFPTSRRISG Y*SALSMVNSGSPIKRWPRITRS DYMPRMVAGMTLSPMQQGHG VHRTHEVHVVAPQRISFGIGSF AREVATIFESSASVFRR*YRNH APPALLTLCSVCLQRRTPGQSPG RVFRHDDPVAFRQVSYFQRQTP IA
25172	55540	Α	25310	1	336	
25173	55541	A	25311	1889	2257	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTVCTGRTKCTSL APQRISFGIGSFAREVATRRPYR DIKEGFSQREAALLPQSLRVPQ TGTWSAAGAQA
25174	55542	В	25312	1	735	
25175	55543	Α	25313	1439	1744	SAMTFPRSRRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPMQQGHVPWQLMVVL WNTRQRWKPSSPDRYVNRAMS LPSRKGEMLKPAPCRK
25176	55544	A	25314	1209	1972	SAMTPPRSRISGY*SALSMVN SGSPIKRWPRITRSD*MPRMVA GMTLSPSSRVTVCTGRTKCTSL AGVILSPSSRGYSFARGEVATIFCSSA SVHFALHMGAIQQPFAFIGSQT LSLVNGNTATTPCPPSALLGLP SASNAWAIAGPRFSISSSGASA RLATFSARRRGASKPLNGCLR ATLSSPDKFQQGSTGGMLWGV LKHSPKFSITADGREFTLHWPN TGAMTGCATPGEYVWYSTEDN TGRKYPHPWEL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
25177	55545	A	25315	ļi .	1521	METQHRLMRTFQPRQQDWTY
						ALWGGVKLRWLFFFLWGLFLF
						AGEEELGIRQTRTNDFLVTGDN
						LLRIFRFDVGNEDKVRQQFAVV
						RIHREVFLVTFHGVNQRFSRHR
	İ				İ	EEFLFEFCVTPKLNEGTTQRTN
						NRGIAVLNTGHRHPDLVAAVE
l						QQLQQFTHTAYQIVPYESYVTL
ľ	i					AEKINALAPVSGQAKTA\FFHP
					İ	GSETG\ENGVKMVRAHTGTPG
						V\IAFRGG\FHGRTYMTMALTG
						KVAPYKIGFGPFP\GSVYHVPYP
	1					SDLHGISTQDSL\DAIERLFKSDI
						EAKQVAAIIFEPVQGEGGFNVA
						PKELVAAIRRLCDEHGIVMIAD
l		1				EVQSGFARTGKLFAMDHYADK
		1				PDLMTMAKSLAGGMPLSGVVG
		1				NANIMDAPAPGGLGGTYAGNP
1					i	LAVAAAHAVLNIIDKESLCERA
İ		1				NQLGQRLKNTLIDAKESVPAIA
		1				AVRGLGSMIAVEFNDPQTGEPS
						AAIAQKIQQRALAQGLLLLTCG
				_		AYGNVIRFLYPLTIPDAQFDAA
25178	55546	Α	25316	114	187	RSTISSVRYGDDAFKP*RQAWN
						VL
25179	55547	Α	25317	105	317	YLFFLSRFNHWISMEKKLGLSA
		1			i	LTALVLSS\SWARVFSVCRKIW
		1			1	RQLPARQHCSSAGVLLALAFYC
						WPLPC
25180	55548	Α	25318	1	593	
25181	55549	Α	25319	1	729	
25182	55550	A	25320	l	1005	
25183	55551	Α	25321	1	1361	
25184	55552	В	25322	1	2793	
25185	55553	Α	25323	27	255	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25186	55554	A	25324	225	1408	RIIYMHMESOKIWFALSTPMEIR
						NECCLPSHSSPKMYLGACLF\PL
		1				SSSWGIDDRDDLLRTIHRMIDN
1		l				GHAARLAGFYHRWFRYSPCEW
		1				RDYLAELNEOGOAYAOFVAST
						AECCGEGGIKAWDYVRMGFLS
		ĺ				RMGVLNNWLSEEESLWIOSRIH
						LRALRYYSNWRQYFAGYTFGR
						OYWOSPEDDHLPLLREFLAGET
						TDVDIIRRAYLALLPSFHTETDP
						QGFKQLRHAYDDALPIAQSPAK
						SVLOPEEYEWEALLVEMLGLL
		İ				HRIAMVQLSPAALGNDMAAIE
						LRMRELARTIPPTDIQLYYOTLL
						IGRKELPYRTCQLHACTSADTP
						LRKIPRFSGKLHFYAFCPNIYSS
		1				YHSAAKYGGSCOPGSTAHRLG
						YYWRWHFIAGLCHADPHAHSS
25187	55555	Α	25325	230	380	
25188	55556	Α	25326	432	1247	PSQEPSVHGRWMA*KGHSRIV*
		1				WRAYD*TH\FNPVLKKSVSLGS
						NIRHMLAEEATTEELDGT\GPV
						LV*PNRH*PAYWMRAYLNLKK
					1	MSCRSFRRKA*RW*CETQTVV
						HRDRVDQGNNHFDVVARHYH
						LYAFLRKERQLIFFKFKYARIQY
						AG
25189	55557	Α	25327	10	638	SSVPTAGSRYNHLRAPRYSPLF
						ANYSMSDRCCKPFG/LDSSTG*
				ł		WFQ*RSVPLPILLPDTSRHQL*C
				1		SDPTRNGPA\QACQRFFHIVERV
						ARVHHARFAATVTVDHVVIDQ
		1				RFFQICRT/PWCRLHRHHWRSSS
						GTR*TF*SPARHFCLLHNDSSYR
						STARPTCSGTDVPDRRCSDAHL
						CDHWSGSRAHADTDAECWCL
		_				NPQPAPSLLQCRR
25190	55558	Α_	25328	803	1622	
25191	55559	A	25329	498	686	RRPSYSVLQRLPSAVLLPYY*R
						DWYHRTAGRRRDGNA GRQHQ
						NGCYPDPPDRDGRRSAFRNP

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO;	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	-	1		sequence		
		_		L		
25192	55560	Α	25330	I	2063	MKNFMENVLRYLSDDKWKPD
					1	AKASMTVGTNLDTVYFKRHGQ
		l				VTGNSAAFDFHPDFAGISVEHL
		l				SSYGDLDPQEMPLLILNGFEYV
		l				TQVGNDPYAIPLRADTSKPKLT
		1				QQDVTDLIAYLNKGGSVLIMEN
		l				VMSNLKEESASGFVRLLDAAG
		1				LSMALNKSVVNNDPQGYPNRV
		i .	i			RQQRATGIWVYERYPAVDGAL
		l				PYTIDSKTGEVKWKYHVENKP
		l				DDKPKLEVASWLEDVDGNRKR
		l				NFSNDARANGTAAFTDCETQT
						VVHRDRVDQGHNHFDLVARH
		ĺ				YHLYAFRQFDGTSHVSSTEVEL
1		1				RTVAFEERSMTAAFISWTECTL
		ı				QIRTCPQNPTGKVWTCDELEIM
		ı				ADLCERHGVRVISDEIHMDMV
		l				WGEQPHIPWSNVARGDWALLT
		l				SGSKSFNIPALTGAYGHENSSSR
		l				DAYLSALKGRDGLSSPSVLALT
		l				AHIAAYQQGAPWLDALRIYLK
		l				DNLTYIADKMNAAFPELNWQIF
		i .				QSTYLAWLDLRPLNIDDNALQ
1		l				KAL\IDQEKVAIMPGYTYGEEG
		1				RGFVRLNAGCPRSKLEKGVAG
1		ĺ				LINAIRAKKSATMIDTTLPLTDI
		l				HRHLDGNIRPQTILELGRQYNIS
		ı				LPAQSLETLIPHVQVIANEPDLV
		l				SFLTKLDWGVKVLASLDACRR
						VAFENIEDAARHGLHYVELRFS
		1				PGYMAMAHQLPVAGVVEAVID
		1				GVREGCRTFGVQAKLIGIM
25193	55561	Α	2533I	2	696	FLLLLWEIRKSSQQTTPTEMNA
		l				AEMAQLVAGVDEVGRGPLVG
		ł				AVVTAAVILDPARPIAGLNDSK
			İ			KLSEK\RRLALYEEIKEKALSWS
		1				LGRAEPPEIDELNILHATMLAM
		l				QRAVVGLHIAPEYVLIDGNRCP
						KLPMPAMAVVKGDSRVPEISA
		1	1			ASILAKVTRDAEMAALDIVFPQ
		1	1			YGFAQHKGYPTAFHLEKLAEH
	1	1	1			GATEHHRRSFGPVKRA/LGTCV
						LILVSRLSKPESEDVL
25194	55562	Α	25332	2	63	
25195	55563	В	25333	138	182	
25196	55564	А	25334	356	706	ISDICAPNMVSAIHAIPYTATMA
						IIPERKTSFFEIDAGLVLVRIIISA
		1				PVSSINI*ITSTIDSGLPPKDGRRS
1		1				ESAPRRATTAIAPRKIHIASQLL
	l			1		VVIIIRSLVGCRMRRWRVLSD
25197	55565	Α	25335	1746	1873	
$\overline{}$						

fero in	leco in vo		SEQ ID NO:	IN	Nestentide tenetion of last	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
10.	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,			sequence		
		ㄴ				
25198	55566	Α	25336	1998	3626	PKAARMANVPNNTTGTAMVGI
i		1				SVA/RHILQEQIHHQEHQHNGFE
1		1				QRFYHFVNRKLDEWRGVIRVE
		1				NLHS/AAGRMAVIPPVLP*WLS
						RYREHSRRLPA*SPKGEAASNP
1						EVIARTLRKLKNQPELSEDTIKK
		l				AVESLSLELVLTAHPTEITRRTL
1	l	l				IHKMVEVNACLKQLDNKDIAD
		ļ				YEHNQLMRRLRQLIAQSWHTD
						EIRKLRPSPVDEAKWGLCRNGK
						TACGKAYQITWAELNKQLEEK
						PRLQTCPSKFGSGPFYF
25199	55567	Α	25337	243	604	PRFPFPLPPATSSVQTAMTDG*N
		l				ECERICVGYLRYSSHSAPDARR
						QRARTHVPVGKHALPALTKAT
1		1				HPSWWWQCAAMAEDSTDARQ
			İ			LKA*WGVNGFLDLRSATMDGR
						LYPVAMCLLPATK
25200	55568	Α	25338	1	3287	MPITERRSVEKEQLIEIANTIMPF
						GKYKGRRLIDLPEEYLLWFARK
						DEFPAEARYTHIDLHVPAPLLV
ì		l				MFTLDTRQSACDRNPHLPIHVC
		l				SSWTSPKCAPRLWTRALLPRTR
1						TPPYATGTTIGSRASWFVTFPD
İ		1				ASFYRRKAPRQEFHTSLQGRSL
1	1	1				YVRQRSTANPTEITRRTLIHKM
						VEVNACLKQLDNKDIADYEHN
1						QLMRRLRQLIAQSWHTDEIRKL
1						RPSPEAIMTEQEKTSAVVEETR
			<u> </u>			EAVDTTSQPVAT
25201	55569	Α	25339	1	1425	
25202	55570	Α	25340	534	1391	RQKRRLYQTYWYKQQPRYLPP
						EHRQRHRHQSAGVSRPYSGYG
	İ					EVRPLSQYQPEWQCWEPDVEW
		l				VRQPPQDAITDPDFFCFYQPGM
	ľ	1				TFEQFVREFAEWFSQKRPAAM
		1				MIGIRADESYNRFVAIASLNKQ
						RFADDKPWTGGHSWYIYPIYD
		1				WKVADIWTWYANHQSLCNPL
		ı				YNLMYQAGVPLRHMRICEPFG
		1				PEQRQGL\WLYHVIEPDRWAA
			ł			MCAR\VS\GYTTGGLYPGQARG
	1		1			AAV*TEALKPSGLPQVCALNQC
1	1	1	1			LLSVHRYAGHVRQERCDGADG
		L				RPAVHERRQLL
25203	55571	Α	25341	786	1009	HHSHEQQFQWPVGASGVDRW
	1	1	1			AVYLHQICPLTQFQY/WCRARQ
			1			EGIMSSPGQQVGFIA*VTSSFSP
						R*KGRRVSSA
25204	55572	Α	25342	2446	2970	
25205	55573	Α	25343	1	2184	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		İ		sequence		
25206	66674	IA.	25344	706	1293	IHRLLIRRIHOIIDLRIWORTVEI
25206	55574	l <sup>A</sup>	25344	/00	1293	HGAPVRFIOMAAWTHIAVLLT*
		1				
1		1				QLRQLRAGFQRNSWAIFYFFHH
1		1				RKQYIFHFDLRRFPVIMHALFC
i		Į.			1	AVQRCADLMAHRRQKRRFCLA
İ	i	1	l		1	GFFCFRPCLSVFYHQFLQFSCTR
		1				FDLRRQLFAVAIQCMNIAFAAA
		1				LVDFDLPDIDGITLARQLAQQY
						PSLVLIGFSAHVIDETLQ
25207	55575	Α	25345	I	329 I	
25208	55576	Α	25346	882	1019	
25209	55577	Α	25347	1	2265	
25210	55578	A	25348	284	535	CVAASVTGTRVLIPPLLNNRSR
		ı				RSPVRYVSKGNWWGSVCNCAS
		1				NNSNSVSR*SLPPMRSHAWRKV
		l _				RRIMRQLPLERPRPGFTI
25211	55579	Α	25349	13 I	208	LVRWLLSPGW*WKISPIISICLFP
						V
25212	55580	Α	25350	1	3108	MDSQDKYFEATQTVYEWCGV
	1	1	1			ATQLLAAYILLFDEYNEKKASA
		ı				QKDILIKVLDDGITKLNEAQKS
						LLVSSQSFNNASGKLLALDSQL
1	l l		ļ			TNDFSEKSSYFQSQVDKIRKEA
1		1				YAGAAAGVVAGPFGLIISYSIA
1	1		İ			AGVVEGKLIPELKNKLKSVONF
	1	1				FTTLSNTVKQANKDIDAAKLKL
	1					TTEIAAIGEIKTETETTRFYVDY
İ	1	1				DDLMLSLLKEAAKKMINTCNE
						YOKRHGKKTLFETYLTDHPVTF
						RERLQMSIYKIPLPL
25213	55581	A	25351	I	296	I I I I I I I I I I I I I I I I I I I
25214	55582	A	25352	3	164	VGD/NVGTTARWGIFALIIVETL
		1.		ľ.		AWFTVVASLFAQHKQRAENLI
						ORLHLLWSFNP
25215	55583	В	25353	91	990	
25216	55584	A	25354	1146	1881	RCGVQ\WTMYIRAVFVNLTNP
222.0	55501	1.		1		KSIVFLAALFPOFIMPOOPOLM
	į.	1				OYIVLGVTTIVVDIIVMIGYATL
1		1				AQRIALWIKGPKQMKALNKIFG
		1	ŀ	,		SLFMLHNAFAWFYLGAFLLTVI
						AWFLLGNAQKMPOTTLOWGIL
						VFLGVVASGIGYFMWNYGATQ
1						VDAGTLGIMNNMHVSAGLLVN
	l	1	1			LAIWHOOPHWPTFITGALVILA
	1		1			
			1			SLWVHPNKRFRNWLTLLAIAH
	1		1			GGVQSAPQAFAQGFGHHQTLA
		<del>ا</del>		1010	2005	LKTLYYPMR
25217	55585 55586	A	25355 25356	1943	2287 274	
25218	155586	IA.	23336	144	274	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25219	55587	A	25357	876	1400	YRHVRDSPGNDRLFETWRSAG CAARLLRQSGETRLLSRVVRDY GGRWPVSLLDGLPDATWCTEK RGGFCTCATGRAGEKWAQFPEN SLLTNLANPKAIIYFGSVFSLFV GDNVGTTARWGIFALIIVETL WFTVYASLFALPØMRRGYQRL AKWIDGFAGALFAGFGIHLIISR
25220	55588	Α	25358	1	1428	
25221	55589	A	25359	421	797	IIFPFLLFHLCNQLSHLLQYAVV NAPVRRILPIQLLWQQLIQPGEK LKSIRRAIQHIGQTQIIGMFIQMP IMIAYETDRATGDGI/WAAH*T HEYPCHVRQSQFHENHDDVQE NPPHPWKIQTPGH
25222	55590	Α	25360	1	1320	
25223	55591	A	25361	1	1251	MLLSITVAFRNLEGIVKTHASI. AHLAQVEDISFEWIVVDGGSND GTREYLENLNGIFNLRVSEPD NGIYDAMNKGIAMAQGKFALF LNSGDIFHQNAANFVRKLKMQ KDNVMITGDALLDFGDGHKIK RSANRAGLFLIGYGAFRIVEFF RQPDAQFTGAWVQYISMGQILS IPMIVAGTMKQYLELMQKVLD EGTQKNDRTGTGTLSIFGHQMR FNLQOGFPLVTTKRCHLRSIIHE LLWFLQGDTNIAVLHENNYTI NQLKNDPDSRRIIVSAWNVGE LDKMALAPCHAFFGYVPDGK LSQLYQMSCOVFLGLFPNIAS YALLVHMMAQQCDLEVGDFV NTGGDTHLYSNHMDQTHLQLLS REPRILPKLIIKKPESIFDYRFE
25224	55592	A	25362	3	1327	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25225	55593	A	25363		2443	MGLIGFVLTALWIKLIHNFTDH PRMASPELKIFSENGAVVDMD HKKPGSAAASOPKLHYIKQLLS NRMMLGVFFGGYFINTTWFFI TWFPIYLVQEKGMSILKVGLVA SIPALCGFAGGVLGGVFSDYLI KRGLSITLARKLPIVLGMLLAS TIILCNYTNNTTLVVMLMALAF PGKGFGALGWPVISDTAPKEIV GCLGGVFNVFGNVASIVTPLVI GYLVSELHSFNAALVFVGCSAL MTMSARSATGHECVFWCNGKP RRLAMKLIYWCAAAPTGDVVQ KLTGKWALIANSHRAGQPTRN VNEEVGQRLLEEMEWYDNYL NMGKTDRSANPSPGNKKGGLA NVVEKALGSIAKSGKSAIVELS SGQPPTKRGLIYAATPASDFV CGTQVASGITVQVFTTGSFV YGLMAVPSH*NGNWKITASVT SIQPNTMELPNCCMMGVSTANT TSKSSLVICALR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25226	55594	A	25364		2701	TFFLPAGEILPPRLEPQITLPVGS RRISIAVTDLPEPESPHLRSGLG WASLCCFMVICKFPAAEGLIL AAVCDSRGSRYWCMGNRRYG YASDLLVRCGATVMFSEVTEV ROAHLLTPRAVNEEVGRLE EMEWYDNYLNMGKTDRSANP SPGNKKGGLGKRGSSKALWLE LQIQARKQVGLRVYTVACVL RTGTWYDRNGFDWRVPGQLN MGNPAPETGRYRLAHPATPHD PRTTPDHPSHIKPHAPTNQPDT LTPTHHHHITOTRDPSPPPTRTTR PRQSTHITTPPHPTTTTRHTDIHP PHTTPDHPPPTTVLTRQLHHTNRI IPHRTHTTTCRRNHHNQMNTIT PRYNTSIVGTIGGGMVERKVIE ESLQALQERKPRLFHGRMARN GADAVGSDCGGAMSVISVHG MRPRLVLIGGGHVNRAIAQSAA LLGFDIAVADIVRESLNPELPP STTLLHAESFGAAVFALDIRPP STTLLHAESFGAAVFALDIRPP NFVLIATNNQDREALDKLIEQPI AWLGLLASRRKVQLFLRQLE RGVALEHIARLHAPVGVNIGAE TPGEIARVLAEILQWKNNAPGG LMMKPSHPSGIMWNLEVE
						KPTVIRCTVAFAQAVFDGEMT VEGVTARLATSSAEAMKLTER

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	ł	
25227	55595	IA	25365	li .	1262	MGNWHLSPCPAPAPGHSCLFL
23221	33393	<u>۱</u> ^	23303	l'	1202	VGTSPRILAVPGHTGSKAINKA
						ALLLESYMSQALKNLLTLLNLE
	l	ĺ				KIEEGLFRGOSEDLGLROVFAG
						QVGG\QPLYAAKEPVPEERLVH
		ł				
1		1				SFHSYFLRPGDSKKPIIYDVETL
		1	1			RDVAPVLDVAGATPPTIRHQRV
		1				TALVAPKNGSRDVRSCAGKMP
						TDGSIRAVLLPFQVSTIGGVTYF
	1	l				RVGTKDQGPQCPHVQRSSAVR
	1	1				PGPEAAPGDNSYPPYEDRSTCG
		l				MQAPDASYSANPDLSFTWSPCI
		l				SEDALHTSPLYCTTPTSGGEAF
		l				KGLASDLVPHEDKMVLQNGKO
	1	l				FTSPRHTEWAVLRAGHALARG
		l				RNLLDLAAGGMAWVSMSQEC
		1				PGPGTICSRDLQGTECLRMIQIL
	1	1				PPKDPVTRGSTHCNAGTKRELE
						EFSSQVTLTALIQPLMQVSAQF
						RAADGAP
25228	55596	Α	25366	2	176	
25229	55597	Α	25367	ĮI.	1395	MRESLELPRDLLNCCDQNANS
		l				DMDMKSRLRGYQMEIMNLLG
		l				AGVKDFELESDDLVYLVEEISK
		l				QQSIHDVA WLLLVAFVYICEQR
i						NDLKSELIFTREAEHKSLENLEF
						DHVPEELDTSARNAGALTRRRI
1						IRDAATLLRLGLAYGPGGMSLF
1	1	1				EVTAWAQLHDVATLSDVALLK
		1		ļ		RLRNAADWFGILAAQTLAVRA
1		1				AVTGCTSGKRLRLVDGTAISAP
						GGGSAEWRLHMGYDPHTCQFT
		l				DFELTDSRDAERLDRFAQTADE
1		l				IRIADRGFGSRPECIRSLAFGEA
		l				DYIVRVHWRGLRWLTAEGMRI
		l				DMMGFLRGLDCGKNGETTVM
		l				GNSGNKKAGAPFPARLIAVSLP
1		1				PEKALISKTRLLSENRRKGRVV
1		1	1			QAETLEAAGHVLLLTSLPEDEY
1		1				SAEQVADCYRLRWQIELAFKR
		l	1			LKSLLHLDALRAKEPELAKAWI
		l	1			FANLLAAFLIDDII\SHRWISPPE
25230	55598	A	25368	482	765	
122230	122270	l'	20000	702	700	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25231	55599	A	25369	1	1575	MGSVTKSRGPTDSSAFFQINRD
23231	33399	<u>۱</u> ^	23309	1	1373	YSFLDYILGGCOLMFTPWARLL
		l				QSTCCEQCSKKAHDQFLADLA
		l	ĺ			SILPSNTTPLIVSDAGFKVPWYK
		l				SVEKLGWYWLSRVRGKVQYA
		l				DLGAENWKPISNLHDMSSSHSK
		l	İ			TLGYKSLTISNPISGOILLYKSRS
		l				
		l	1			KGRKNQRSTRTHCHHPSPKIYS
		l				ASAKEPWILATNLPVEIRTPKQL
		1	ł			VNIYSKRMQIEETFRDLKSPAY
						GLGLRHSRTSSSERFDIMLLIAL
		l				MLQLTCWLAGVHAQKQAFRF
		l				MRLVDGTAISAPGGGSAEWRL
		l				HMGYDPHTCQFTDFELTDSRD
						AERLDRFAQTADEIRIADRGFG
		l				SRPECIRSLAFGEADYIVRVHW
		l				RGLRWLTAEGMRFDMMGFLR
		l				GLDCGKNGETTVMIGNSGNKK
		l				AGAPFPARLIAVSLPPEKALISK
1		l				TRLLSENRRKGRVVQAETLEA
		l				AGHVLLLTSLPEDEYSAEQVAD
		l				CYRLRWQIELAFKRLKSLLHLD
	ĺ	l				ALRAKEPELAKAWIFANLLAAF
		<u> </u>				LIDDII\SHRWISPPEVPDPKRRT
25232	55600	A	25370	1	1341	MAGGRKFPDGGDRTTLCGLSQ
		l				PGVLAPRSPEKRRAINQRYPSK
		l	[			TGQLPASITDMMRTARHHLSG
		l				NGISVPKGAELAHPSTVLELFAI
		l				SAKPIHPEELDTSARNAGALTR
	ŀ	l	l			RREIRDAATLLRLGLAYGPGG
		l				MSLREVTAWAQLHDVATLSDV
		l				ALLKRLRNAADWFGILAAQTL
			İ			AVRAAVTGCTSGKRLRLVDGT
			ľ			AISAPGGGSAEWRLHMGYDPH
						TCQFTDFELTDSRDAERLDRFA
						QTADEIRIADRGFGSRPECIRSL
						AFGEADYIVRVHWRGLRWLTA
						EGMRFDMMGFLRGLDCGKNG
						ETTVMIGNSGNKKAGAPFPARL
	1	l	1			IAVSLPPEKALISKTRLLSENRR
		l				KGRVVQAETLEAAGHVLLLTS
		l				LPEDEYSAEQVADCYRLRWQIE
						LAFKRLKSLLHLDALRAKEPEL
	1					AKAWIFANLLAAFLIDDII\SHR
		_				WISPPEVPDPKRRT
25233	55601	В	25371	1	1233	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location uf first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25234	55602	A	25372	1	2197	SHSRGSPGKAVDFTLVSHAAW
		1			l	FGLPHFSTPAFNGQAMMLIAPV
ļ		1				AVILVAENLGHLKAVAGMTGR
		1		İ		NMDPYMGRAFVGDGLATMLS
						GSVGGSGVTTYAENIGVMAVT
						KVYSTLVFVAAAVIAMLLGFSP
					1	KFGALIHTIPAAVIGGASIVVFG
		1				LIAVAGARIWVQNRVDLSQNG
		l		l		CNPAYAEHHQHPGYSDKLKTR
		l				VSFSCLRIISTNLRRECRAQFRF
		l			l	HVDASARHGFRLWQIQGVAQP
		l				VFIITIREVEAAMRATAFGTEVG
		l				RNSRCIRRFHQVIQFQALNALG
		1			i	VELAGIDSRDPRLKVLEEMKRT
			-	1		FHWGRQTISKHIKIWLGLMLGR
1		1				AMTPLMLDATSGKLTVWDGA
		1				HAGAAMGILAVTADQNSAELA
1		1			ľ	YYKSGSFRIEDVLWPSAVTDDN
1						IKRNAFAADGSVNSYSVPFSSV
1		1			l	PLLQRQGRIKYAVTLAKYRTNS
l		l		1	-	NEQQESKFAQATLQWGGPWGT
1						TWYGGGQYAEYYRAAMFGLG
		l				FNLGDFGAISFDATQAKSTLAD
						QSEHKGQSYRFLYAKTLNHLG
					ļ	TNFQLMGYRYSTSGFYTLSDT
					ŀ	MYKHMDGYEFNDGDDEDTPM
l					į.	WSRYYNLLYTKRGKLQSLISKT
1						RLLSENRRKGRVVQAETLEAA
		1	1	1		GHVLLLTSLPEDEYSAEQVADC
		l	1	1		YRLRWQIELAFKRLKSLLHLDA
1		l	1	l	1	LRAKEPELAKAWIFANLLAAFL
						IDDII\SHRWISPPERIPSARKWT
25235	55603	A	25373	1	2754	
25236	55604	A	25374	1	652	
25237	55605	A	25375	1	1800	

SEO ID	ICEO IN NO.	Date	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.01	sequence	1.00	09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	· .	1		sequence	' ' '	
		<u> </u>				
25238	55606	A	25376	1	2187	MAGPRYPVSVQGAALVQIKRL
						QTFAFSVRWSDGSDTFVRRSW
						DEFRQLKKTLKETFPVEAGLLR
						RSDRVLPKLLGQASLDAPLLGR
1		1	ŀ			VGRTSRGLARLQLLETYSRRLL
1						ATAERVARSPTITGFFAPQPLDL
						EPALPPGSRVILPTPEEQPLSRA
1					l	AGRLSIHSLEAQSLRCLQPFCTQ
						DTRDRPFQAQAQESLDVLLRHF
	1					SGWWLVENEDRQTAWFPAPYI
1	1					EEAAPGQGREGGPSLGSSGPQF
		l				CASRAYESSRADELSVPAGARV
1		1				RVLETSDRGWWLCRYAGAGPE
		1				ELDTSARNAGALTRRREIRDAA
1						TLLRLGLAYGPGGMSLREVTA
		l				WAQLHDVATLSDVALLKRLRN
İ						AADWFGILAAQTLAVRAAVTG
		1				CTSGKRLRLVDGTAISAPGGGS
1		l		i		AEWRLHMGYDPHTCQFTDFEL
		l				TD\SRDGER\LARFAQPPDEIRIA
1						DGEFVWRPKCIRSLAFGEADYI
		l				VGVHWRGLRWLTAEGMRFDM
1		1				MGFLRGLDCGKNGETTVMIGN
l		l	i			SGNKKSP\GFPFRARFIAVSLPPE
l		1	1			KALISKTRL\LSENRRKGRVVO
		1				AETLEAAGHVLLLTSLPEDEYS
			1		i	AEOVADCYRLRWOIELAFKRL
l		ı	ĺ			KSLLHLDALRAKEPELAKAWIF
ļ		1	l			ANLLAAFLIDDII\SHRWISPPEV
ł					i	PDPKRRTNSLWRITKMVIWSLO
		1				VAIRGTVSLTAPSLCNSACCCC
		ı				VSTNSATTLNDFAFARSVIDLTI
25239	55607	A	25377	2	333	RLGVWQDILSRRASCYHGMEV
		Γ.		ľ		WDKDSFGHISFDDQSMGYSHL
		ĺ				GHIVENSVIHYA\ARLVIGADGV
		l				DSWLRNKADIPLTFWDYQHHA
		1				LVATIRTEEPHDAVARQVFHGE
		l				AFW
25240	55608	A	25378	3	235	VAVLEORVHEPLAANAPPOLR
23240	33008	ľ	23378	ľ	255	VS/ARLGVWODILSRRASCYHG
		1				MEVWDKDSFGHISFDDQSMGY
		1	l	1		MEV WDKDSFGHISFDDQSMG Y SHLGHIVENSVIHYA
25241	55609	A	25379	1	774	SHLURIVENSVIHTA
25241	55610	A	25380	1	1076	
23242	122010	Ι^	43300	11	1076	

			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		<u> </u>				
25243	55611	Α	25381	1138	1737	SVSTEPSVAAFSSIKLRQDPP/H
		1				DNLHHQYN*GDIAFC\FTPYFH
		1				NCLCQS*WARAFQ*RANEF*R
		1				MNCTQLARTSGSHHLIPLTLRF*
			ŀ			QICISSGQLIQYSVVCRFIHPPEH
						RLTIHPLAGQGVNLGFMDAAE
						LIAELKRLHRQGKDIGQYIYLR
		l				RYERSRKHSAALMLAGMQGFR
		l				DLFSGTNPAKKLLRDIGLKLAD
25244	55612	В	25382	1	735	
25245	55613	В	25383	1	1941	
25246	55614	В	25384	847	849	
25247	55615	Α	25385	1	1227	
25248	55616	A	25386	324	1533	EGFMEHQRKLFQQRGYSEDLL
		1				PKTQSQRTWKTFNYFTLWMGS
		1				VHNVPNYVMVGGFFILGLSTFS
						IMLAIILSAFFIAAVMVLNGAAG
			l			SKYGVPFAMILRASYGVRGAL
			ŀ		i	VPGLLRGGIAALMWFGLQRGS
	ĺ					PFYDLIQTALSSPHKVTIEQFYR
		l				EVGVFLGIALIAVVISVLNNFFV
						SHYVFRWRTAMNEYYMANWQ
	ĺ					OLRHIKGRTAFINAIMTLIAFLP
	İ					VLVTLSAHVPELPIIGHIPYGLVI
		1				AAIVWSLMGTGLLAVVGIKLP
				į.		GLEFKNORVEAAYRKELVYGE
		1		ŀ		DDATRATPPTVRELFSAVRKNY
ŀ		l	ł	ŀ		FRLYFHYMYFNIARILYLOVDN
			i	ŀ		VFGLFLLFPSIVAGTITLGLMTO
						ITNVFGOVRGAFOYLINSWTTL
					ŀ	VEL\MSIYKRLRSFEHELDGDKI
		ı				OEVTHTLS
25249	55617	A	25387	1526	1683	20,11100
25250	55618	A	25388	2709	2918	CWCFWHRRSCCGSVRYALSAV
	[	1		Γ	I	PGCQCPET*RRRFPHSAF*RFRS
		1		l	1	SETGQTGAYVSGPDLQPERLQR
						LWC
25251	55619	A	25389	1	1812	· · · · · · · · · · · · · · · · · · ·
25252	55620	Α	25390	134	386	RLKPSAAIRRRVSSSRISTPLNPA
		1		1		STTAFVGTDCA\IPRLRATSGLA
l		1		ŀ	1	GSPLIQNRFCRARQPRWSAPVA
		ı	l	İ		RHAAVYARHRWNQII
					<u> </u>	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
25253	55621	A	25391	181	1630	RIRQFCFYHHCVLTLAICAFIVIT
		ŀ				LTIWVSFRVSVLVFAMADDIKV
1		1				AVVGAMSGPIAQWGDMEFNG
						ARQAIKDINAKGGIKGDKLVGV
		l				EYDDACDPKQAVAVANKIVND
		l				GIKYVIGHLCSSSTQPASDIYED
						EGILMISPGATNPELTQRGYQHI
		l				MRTAGLDSSQGPTAAKYILETV
	i	1				KPQRIAIIHDKQQYGEGLARSV
						QDGLKAANANGVFFDGITAGE
						KDFSALIARLKKENID\FVYYGG
1		l				YYPEMGQMLRQARSVGLKTQF
		ł				MGPEGVGNASLSNIAGDAA\EG
1						MLAPVLITVDQPFVQAGFQPLR
						RLLPAHETGRRTRAYGVGRLT
Ì		l				RQIRRQIATTFRHNAQAAESKD
						FQWYRCDPCQLFHLMNRQHAR
						QHHASNVKMAMIKVNRLFIGR
1		1				RSLHRYVALNMRITLGGVLHH
1		1				GEVGEDQRVGTQLRRHIHGAL
		1				PTGVTVRMRKSVNRDVKFAA
			1			MLMDKTHRFLQFFLGKVKAGE
25254	55622	A	25392	2	505	
25255	55623	Α	25393	1	2038	
25256	55624	Α	25394	188	1771	GKQTSTSPAGWENSLRMRYT\
	1	1				MSFSLIATGLLGVYLTTMPGY
1		l				WGILFVWALFGVTCDMMNWP
		1				VLLKSVSRLGNSEQQGRLFGFF
1		ı				ETGRGIVDTVVAFSALAVFTWF
l		l		i	ł	GSGLLGFKAGIWFYSLIVIAVGI
		1			1	HFFVLNDKEEAPSVEVKKEDG
1						ASKNTSMTSVLKDKTIWLIAFN
l					ł	VFFVYAVYCGLTFFIPFLKNIYL
1		1		l	1	LPVALVGAYGIINQYCLKMIGG
ŀ						PIVLEKVLPPVVSVRVKGTASQ
		1				GOKIPEEFKOFFGDDLPDQPAQ
		ı				PFEGLGSGVIINASKGYVLTNN
				1	Ì	HVINQAQKISIQLNDGREFDAK
1				1		LIGSDDOSDIALLOIONPSKLTOI
		1				AIADSDKLRVGRSGLNLEGLEN
		1		1		FIQTDASINRGNSGGALLNLNG
		1				ENPIDOLKVVGRPHDRIDGPLK
					1	TTGTARYAYEWHEEAPNAAYG
		1				YIVGSAIAKGRLTALDTDAAQK
		1				APGVLAVITASNAGALDKGDK
					1	NTARLLGGPTIEHYHOAIALVV
1		1		l		AETFEOARAAASLVQAHYRRN
		1		1		KGAYSLADEKQTVNQPPEDTP
1	L	1				NGA I SLADEKŲ I VNŲPPED IP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25257	55625	А	25395	356	849	GSACRVKEIPRPASQMP/HTLPA GSRPPGSEAEPGPEAAPPPARRE AHQIPRPRGHLPSSPGPRTHVA AHNIRVVTEAHADSHALLSDLG AAPFVVMSRILRVDGDEDPPHV DESIQPTTENAVYFRPVQLTSAI ETGGKEEPYGLSAASLGRAESS AASLAGRR
25258	55626	А	25396	154	379	LVPRLKLGDLPSEINPLSSCSLV REKDPPTTSCTHT\TNPRNISPIS NPDSTGNRTVQLTW*PLPEPLE LWPKAL
25259	55627	А	25397	4761	5127	LGSGDLPWEINPLSSCSLLREKD PPTTISGPQTITSPRNISPISNPHTR TSKRLNRSGQAFLQNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPLELWPKAL
25260	55628	A	25398	I	753	MGSWLQGLRAMVFALNYMVT RVRNKKDPPTTSGPQTTSPRNI SPISNPRPRETEFICOPKTTAPL MDWEGSLPLMFNHCRDTSLIH PCFQGVRPCRDACLSPSLASP AFLGKGQVPLNPFTLSGKSRF SGGGASTPTFSFHVSTPSLLFW GRGKYPSTPSSPLVASPAFLGK GQVPLNPFTLSGKSRFSGEGA KAPETITDAELRVTLTVEAAVC STIALSLGWEILPRHWGKEEVT KTTYYPVIP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or peptide sequence	deterion, v-possible nucleotide insertion)
25261	55629	Α	25399	174	2238	LRSGDLPWEINPLSSCSLLHEKD
				1		PPTTSGPQT\TSPRNISPISNPRQR
				ļ		RHILSMDPKLRRRSWTWVGSLP
		ŀ				LVFNHCRDASLIIHPGFRGVRPR
						RDVCLGPSPLATITDAELYVTL
						TVEGKSIPFLIDTEATHSTLPSFK
						GPVALASIHVQNVQIKRDKEGH
	İ					YIMVKGSIQQEELTILNMYAPN
					1	TGAPRFIKQVLNDLQRDLDSHT
		l			i	IIMGDFNTPLSTLDRSTRQKVN
						KDIQDLNSALHQADLIDIYRTL
						HTKSTECTFFSAPHRTYSKIDHI
				1		VGSKALLSKCKRTEIINCLSDH
		1				SAIKLELRIKKLTQNHSTTWKL
		1		ì		NNLLLNDYWVHKEMKAEIKM
	i	1		l		FFEINENKNTTYQNLWDTFKAV
	1			ŀ		CRGKFIALNAYKRKQERSKIDT
	1			İ		LTSQLEELEKQEQTRSKASRRE
						EITKIRAELKEIETQKTLQKINES
						RSWFFEKINKIDILLARLIKKKR
	İ					EKNQIDAIKNDKGDIATDPTEIQ
				1		TTIREYYKHLCPNKLENLEEMD
				i		KFLDTYTLPRLNOEEDESLNRPI
				1	ŀ	TGSEIVAIINSLPTKKSPGPDGFT
				1		AKFYORYKEELVPFLOKYKEEL
						VPFLLKLFQSIEKEGILPNSFSEA
	1			1		SIILIPKPGRDTTKKENFRPISLM
			1	1		NIDAKILNKILANQIQQHIKKLI
				l		HHDQVGFIPGMQGWFNIRKSIN
	1	1				VIQHINRTKOKNHMIISIDAEKA
			1	l		FDKIQQPSC
25262	55630	Α	25400	3	267	EKDPLTTSGPQT\TSPRNISPISN
				1	ľ	LRLFAFTWTDPDTHQAQQITW
		1		İ	i .	AVLPQGFTDSPRYFSQAQISSLS
	İ					VTYLSIILIKTHVLSLPIMSD
25263	55631	A	25401	167	408	LGSRTFPWEINPPSSCSLLREKD
	1					PPTTSGPQT\TRPRNISPISNLVS
						GLFLLSSPTSLTIPQPLSSFNLDD
						TLQSLPSLNF
25264	55632	Α	25402	142	441	LRLGDLPWEINPLSSCSLLCEKD
						PPTTSGP\PRNISPISNPVSGLFLL
					İ	SSPTCLTIPQPLSPFNLGATLQSL
	1	1			1	PSLNFNSFHFLVETKETRFIRGP
	1	1	l		I	KTPAP
25265	55633	A	25403	79	381	LGSGDLPWEINPLSSCSLLREKE
	1	Ι		1	I	PPTTSGPQT\TRPRNISPISNPELA
		l	1	1		TLAGNLATGPRNARSPGFLLSH
		l				VLSVWDPTENQTVQLTWQPLP
	1	1	l .	i	I	OPLELWPKAL

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
25266	55634	IA	25404	1	511	MWKGPKGLDMYGKSSVSPKTS
23200	33034	^	23404	l'	311	DILGRDTLLLALKVQTVVLQTA
						CGEGHVAGNCGRPLETEGSLO
1		1				LTATKKLRDSVLQPKSPEFCQQ
				1		FTRAWNRTQVPDETEAPAGTY
1				1		AAQSGDLPWEINPLSSCSLLHE
		1				KDPPTASGPQT\TSPRNISPILNR
		<u> </u>				VSEVSDHAGTPALVLHP
25267	55635	A	25405	570	1182	LGSGDLPWEINPLSSCSLLHEK
l						DPPTTSGPQT\TSPRNTSPISNLH
1						ALKGLKPAITRLLQHGLLKPINS
1		1	1			PYNSPILPVLKPDKPYKLVQDL
l		1				CLINQIVFPIHPVVPNPYTLLSSI
		1				PPSTIHYSVLDLKLAFFTIPLHAS
1		1				SQPLSAFTWADPDTHQVQQIT
						WAVLPQSFTDSPHYFSQAQISS
						LSVTYLSIILIKTHVLSLPIVSD
25268	55636	A	25406	489	615	LRNTWNSPRLMACALHSGSPSC
						TWGPYS*SGLSENLASQRVCPP
ļ						YQNENVGRVRDTEIKEHCYEES
l			i			SYRAATQIQVRKVGIITEPYPFM
1		1	1			ASLRTHCIICETCYEMKISFSKS
1						LNPLEKNKKSQPANCAVKEVS
	ļ.					EQLRRRQAFSVAAGLKGKGSP
						AQSIRKNLQKPYQHFQTLQQLL
	į.					PLOWAPCYGPSNFATHGTHOG
						LWLVLSTVAAQAVPGALIAEA
	1					TALLAWIQGAVS
25269	55637	A	25407	579	715	LGSGDLPWEISPL\SCSLLHEKD
						PPMTSGPQT\TSPRNISPISNLR
25270	55638	Ā	25408	1553	1896	<u> </u>
2527I	55639	Α	25409	964	1332	SCRFIRIYQGACCNLHPGEINSH
1			1			VAHTKPVWWSLHTDTHENCHL
		1				NTAVFFYHWLALEFFLNPLRR/
		1				CSC*HSLPGQFPVSLCLRVLSVD
			i			CAHPWGKPEAPGS*HPGPWQFS
		1				SLPSPLWPLYQHP
25272	55640	В	25410	1	717	
25273	55641	A	25411	590	1142	PNSSWMRGEPKKDPPTTSGPQT
					ļ	TSPRNISPISNPR/PKETRFICGP
1	1		1			KTPAPLMDWEGSLPLMFNHCR
		l				DTSLIIHPCFQGVRPCRDACLSP
		l		1		SPLAASPAFLGKGQVPLNPFFTL
						SGKSRFSGGGASTPTPSFHVSTP
						SLLFWGRGKYPSTPSSPLVASP
				1		AFLGKGQVPLNPFFTLSGKSRF
1				1		SGEGA
		Ь.	L			London.

SEO ID	CEO ID NO.	1444	SEQ ID NO:	Mustentide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1			· ·	scquence		
25274	55642	A	25412	1	790	MGLVHLQRQSYWTVQRSSINH
						FLGCNPHTGKDKTLYMRWTKS
						FRKVEDPPTTSGPQTDQPKKHL
						TKFKSETKETRFIHGPKTPAPV
1						MDWEGSLPLVFNHCRDASLIIH
1						SHFKGVRPRRDACLGPSPLAAS
1						PAFLGKGQVPQPLISLCPDPLFP
						HPNLISLRPNPLCPHPDLVSLCP
1						DPFPAFLEAHKNFQTPEPQQPGI
ł						PPEPPPGACYKC/HEI*PPGQG
1						MPAAQDSS*AMS/LSVRDPTGN
						OTVOLTWOPLPEPLELWPKAL
25275	55643	Α	25413	1	736	MQAMEKWKREAKVETEKDQK
						NOYOQTWLSDSASGYRYTKLP
		l				FYFRHNNLIPALAHLLFLDSLYS
						DLLTAAFFMQFWLSAQMSSDQ
			ŀ			RGLPGYLLWAEEISLLEISELTS
						GKQDSSWPEVKAGLKKEANYL
İ						SSDSARLHPGEINSLVAHTKPV
		l				WWSLHMDTHEIWCRDSNWGD
1						LPWEINPLSSCSLLHEKDPPTTS
						GPQT\TSPRNILPISNPPSSKHQE
1						KPPEAISTLPNAAATAAAAVGS
						LLWSL
25276	55644	Α	25414	1644	2010	LGSGDLPWEINPSSSCSLLREKD
ì						PPTTSGPQT\TSPRNISPISNPHTR
						TSKRLNRSGQAFLQNLLPQELA
				1		TSARNLTTRPRNACSPGFLLSR
			l			VPSVRDPTGNWTVQLTWQPLS
						EPLELWPKAL
25277	55645	Α	25415	1	1035	MGKEYSLDVKKSIKVFKDNRS
						QGNRLQKLGLEDTDREDAMGF
						GSHRAKLTVVAALGACHCPEN
			1			EGQTVLPSSTSGRSDKRERVSA
		1				GYTPPFFVKEGVPSPLFKLHVV
						RCCSIQSHHSRRSQNCAEDVIR
						KTKTDQAVSSMSSAPVTVQQL
		l				NIIPALLVALTCGWAFCLMVSO
						EQYDEASKQAASFSNNAVIPVY
		ŀ				MSHMSKTLYKSEVFPINTYAQK
						ICFIAHTKPVWWSLHMDAHEI
1		1				WCRGRRSTDLPWE\INPLSSCSL
1						LREKDPPMTSGPQT\TSPRNISPI
						LNQELATRAGNLATRPRNACSL
1		1	l			GFLLSRISSVWDPT*KFGLVQLT
1		1				LGKPLPEPLELWPKAL
25278	55646	Α	25416	174	393	LRSGDLPWEINPLSSCSLLHEKD
23270	22040	ľ	22-710	l,	J~~	PPTTSGPQT\TSPRNISPISNPGET
1		1	l			KETRFIRGPKTPAPVMDLGRQP
1		1	l			SLGV
				L	L	3LO 1

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25279	55647	A	25417	2	4574	WDVLGAVIGTECGTIESGLSMV FLKDGERKLCTPSMDTTGYGN
		ļ			LRFYFVMAKWIYIPENVVKGR	
	l	l	:		KEIILVLDFTWCMVHRGICDPG	
					NSHENDIILYAKIEGRKEHITLD	
	l				TLSYSS/L/SSLYWPVMSQILFW	
	ĺ	ĺ			QRTVH*TWL\QL*DGIPDIPNVY	
					F*KLWQFQALLLP*LLLYPWC*	
		İ			SQLWLWCLGQW*GPGFQQRW	
						AASANYIFP*QLTIQNNLRRTTR
						*CKAVWNSVQMVATVSFFPER
						RCMGY**DYHDICA
25280	55648	A	25418	I	363	
25281	55649	A	25419	1	301	
25282	55650	A	25420	2	309	
25283	55651	A	25421	3	512	YIGPSCLKFCSGRGQCTRHGCN
						CEMASQTFPMFISESFGSSRLSS
	1					YHNFYSIRGAEVSFGCGVLASG
						KALVFNKDGRRQLITSFLDSSQ
						SRIISVELPGDAKQFGIQFRWW
	1				ļ	QPYHSSQREDVWAIDEIIMTSV
	1				•	LFNSISLDFTNLVEVTQSLGFYL
						GNVQPYCGHDWTL
25284	55652	A	25422	2	878	
25285	55653	A	25423	1	750	
25286	55654	Α	25424	1	1404	

SEO ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
25287	55655	A	25425	I	2506	GCSRLLVTVDLNLTNAEFIOFY
		1	1			FMYGCLITPNNRNQGVLLEYSV
		l			1	NGGITWNLLMEIFYDQYSKPGF
						VNILLPPDAKEIATRFRWWOPR
						HDGLDQNDWAIDNVLISGSAD
						ORTVMLDTFSSAPVPOHERSPA
						DAGPVGRIAFDMFMEDKTSVN
		ĺ				EHWLFHDDCTVERFCDSPDGV
		1				MLCGSHDGREVYAVTHDLTPT
		1				EGWIMOFKISVGCKVSEKIAON
						QIHVQYSTDFGVSWNYLVPOC
		l				LPADPKCSGSVSQPSVFFPTKG
		l				WKRITYPLPESLVGNPVRFRFY
						QKYSDMQWAIDNFYLGPGCLD
	l				NCRGHGDCLREQCICDPGYSGP	
						NCYLTHTLKTFLKERFDSEEIKP
				l		DLWMSLEGGSTCTECGILAEDT
						ALYFGGSTVROAVTODLDLRG
				l		AKHDYILLPEDALTNTTRLRW
						WQPFVISNGIVVSGVERAQWA
				İ		LDNILIGGAEINPSOLVDTFDDE
				İ		GTSHEENWSFYPNAVRTAGFC
						GNPSFHLYWPNKKKDKTHNAL
						SSRELIIQPGYMMQFKPFGFCRS
						DSWQLVQTQCLPSSSNSIGCSPF
						OFHEATIYNSVNSSSWKRITIOL
						PDHVSSSATOFRWIOKGEETEK
						QSW\AIDHVYIGEACPKLCSGH
						GYCTTGAICICDESFOGDDCSV
						FSHDLPSYIKDNFESARVTEAN
		l				WETIOGGVIGSGCGOLARYAH
						GDSLYFNGCQIKRAATKPL\DL
25288			25126	146	10551	
25288	55656	A	25426	146	10561	GGGGGGGGGMERSGWARQT
						FLLALLLGATLRARAAAGYYP
						RFSPFFFLCTHHGELEGDGEQG
						EVLISLHIAGNPTYYVPGQEYH
						VTISTSTFFDGLLVTGLYTSTSV
						QASQSIGGSSAFGFGIMSDHQF
						GNQFMCSVVASHVSHLPTTNLS
						FIWIAPPAGTGCVNFMATATHR
						GQVIFKDALAQQLCEQGAPTD
						VTVHPHLAEIHSDSIILRDDFDS
						YHQLQLNPNIWVECNNCETGE
						QCGAIMHGNAVTFCEP
25289	55657	Α	25427	1	296	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
25290	55658	A	25428		557	MARSLGVLVALPFPLPVGFNAE EAHNIVKEFSPGKSHPRESLSQQ RETILVQAGAFHWFGWRGKEK LKPKFNTFGRLPNEMLEQWLSP TNQCVDGV/LKGGEDIYNHNNI NQWTASIVEQSL\THLVKLGKA YKYIVTCAVVQKSAYGFHTASS CFWDTTSDGTCTVRL/WENRT
25291	55659	A	25429	178	2270	MMCUNVFCHCLFVL  VRRLFCVOTGGSPVGRGSLHHL WLVFSHVLSLLCSPCLLAPGM GAERALKRWRWQOTQONK ESGLVYTEEBWEREWTELLKL SEPRTHSFNGGTGGGHURD EGKPLHGCSSLLRSGKGGHVK AESSERTHFSNGGTGGGHURD EGKPLHGCSSLLRSGKGGHVK AESSELQQSQAKFPLTSQIRALH PIPSQINEKPGAGHWSAKLHFP YWQLGEAGEEGGSSPDIMRCL LTCLSVPSTAVIPLTDSEHKLLP LHFAVDFGKDWEWGKDDNDN ARLAHLILSLEAKLNLLHSYMN VTWIRIFISTRAPLAQPESPTAS AGEDVGSLADSLDSDRDSVCS KNSNNNGKNGKDKEKEKQRE KDKTRADSVANKLOSFSKTLGI KLKKNMGGLGGLVHGKMGRA KSGKSEESGASASTSPSEKTTIS PTDKAAGASPAEKGGGPRGDA WKYSTDVKLSLNILRAAMOGE RKFIFAGLLLTSHRHQHEEMIG VYLTSAQERSFAEGGGRRDA ATAAAAAAPPPPPRPREPRPRE TEGPPVPERASPGPPTQVLK LERRSFGPAGRAAAAGG TACPGGGRAACERORTSAWPG VRAGRGGAAVRHVPAAEPLA VVAELQPGARRRPAHRQHGRW VAGRGRGGAAVRHVPAAEPLA VVAELQPGARRRPAHRQHGGW GAGRGRGGGGGGGGGAGGGGGGGGGGGGGGGGGGGG

SEQ ID			SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	delction, \=possible nucleotide inscrtion)
25292	55660	Α	25430	404	1116	SLGPLMLSGQKLQTSYTMEYY
						AAIKR/DKIVSLVGTWLELEAIIL
						KKLMQEQKTKYHMFLLDSLSH
						GMQQAERVLIADGTMLLSAQY
						QFENNLLVPILRVSFRKSLQRKE
						EPGRKAKKSQTSGEGIKKRRFW
		l				FEWKEPVALSSQGWYEAKGSE
						RPEKGHLGLLRAESFQDLRTAL
						ISKPYFSVPGKVGPAIKCPETLP
						ELKTYPQYGVTLGEPVRNEQQ
						QASSFPSLSNTHLSKKRNES
25293	55661	A	25432	1571	1782	WLLCRLPPRVPDQL*WCGCQPE
		1	ŀ			KCAGAEFQDGSAMPLPSRTCPH
		l				SPRMCTGWSTTCATTDSATTA
						CPLAL
25294	55662	В	25433	69	1160	
25295	55663	Α	25434	14	437	LQTSHPYPTTSKC/PPP/CEKPSP
						TSL/C*RRSAPHLQPPE
25296	55664	A	25435	782	997	MMLCQLQRPV/CGSHSCSRG/C
						PPAQ/CPSPVPVPSPQSAFPVPQS
		1			1	PSSTCPNPSHPIHPIPMVPSSWSG
						HWDSK
25297	55665	Α	25436	1117	1815	GDAHTEQCLQNLYPRGSRPPLP
						LESHPSSSKHSPKACPTGRS/CG
						PWK/CPGPEVRP*PPPSCTR*DP
		İ				HFRGLLEGLLEPRHVTCLALCG
			l		1	PQRVLYWPVYHERLGEGWDW
					l	CPSSWPGA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25298	55666	A	25437	1261	2757	ALGKDEKSQGPPIQTGGLGPRL
						FRLPSSOGOERRFAAAKAPSSL
	1	1				VPHNGSPLSCWRGLREEGGLSL
		1				ATLWTPCGVGSGVPAAPPSAW
		1				CDLGKLLVCWRGQNRGPRSTQ
		1		1		TDVRRHEARSRORRRKCVAAP
İ	1	1				VAPRSRRWRCPAALAAPAVAV
	1	1				PVVFALIFLLGTVGNGLVLAVL
						LOPGPSAWQEPGSTTDLFILNL
						AVADLCFILCCVPFQATIYTLD
1	ŀ					AWLFGALVCKAVHLLIYLTMY
	į.	1				ASSFTLAAVSVDRCAVPG\HPL
		1				GRAVGAGVGGGVLNVGLVWL
		1				LAALFSAPYLSYYGTVRYGALE
		1				LCVPAWEDARRRALDVATFAA
		1				GYLLPVAVVSLAYGRTLRFLW
		1				AAVGPAGAAAAEARRRATGRA
		1				GRAMLAVAALYALCWGPHHA
		1				LILCFWYGRFAFSPATYACRLA
		1				SHCLAYANSCLNPLVYALASR
						HFRARFRRLWPCGRRRRHRAR
		1				RALRRVRPASSGPPGCPGDARP
1		1				SGRLLAGGGOGPEPREGPVHG
l	i					GEAARGPE
25299	55667	Α	25438	1	1624	MKDKSKTLGLEASIFRNNWKC
						KSIFEGLKGHQEGYFSQMIISYE
		1				KIPSYRKSKSLTPHQRIHNTEKS
1						YVCKECGKACSHGSKLVQHER
						THTAEKHFECKECGKNYLSAY
		1				QLNVHQRFHTGEKPYECKECG
						KTFSWGSSLVKHERIHTGEKPY
						<b>ECKECGKAFSRGYHLTQHQKIH</b>
1		1				TGVKSYKCKECGKAFFWGSSL
	1	1		•		AKHEIIHTGEKPYKCKECGKAF
						SRGYQLTQHQKIHTGKKPYEC
		-				KICGKAFCWGYQLTRHQIFHTG
-				1		EKPYECKECGKAFNCGSSLIQH
		1				ERIHTGEKPYECKECGKAFSRG
		1				YHLSQHQKIHTGEKPFECKECG
						KAFSWGSSLVKHERVHTGEKS
1	1	1		1	1	HECKECGKTFCSGYQLTRHQV
1	1	1		1		FHTGEKPYECKECGKAFNCGSS
1	1	1			1	LVQHERIHTGEKPYE\CKECGK
1		1			1	GFS\GGYHLTOHOKIHTGEKPF
1	1	1				KCKE\CGKAFSWGSSLVKHERV
1	1	1			1	HTNEKSYECKDCGKAFGSGYQ
1		1			1	LSVHQRFHTGEKLYQRKEFGK
1	1	1	1		I	TFTHGSKLVHERTHSNDKPYK
l		İ			I	YNECGEAFLWTTYSNEKIDTDE
	1		1		L	THECOMILENTITISMERIDIDE

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
İ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25300	55668	Α	25439	32	447	VLGGSMMFREGQRGNRQKGP
						KKRRNLALSSALLASTA\PAGG
			İ		l	QPRHWRPG*CCLRQQL*PLQGN
						WAPVSPLQGHRSQLRAGYSISS
i		ı				FLQMFAP*VQGAARAQPAPGA
						AVPRGSGRQGGPRAVDLHGFR
		1				VGWNRLRAASM
25301	55669	Α	25440	1	858	
25302	55670	A	25441	147	1088	SRTTYKGKSSFQTYSDYLRWES
						FLQQQLQALPEGSVLRRGFQTC
		1				EHWKQIFMEIVGVQSALCGLVL
						SLLICVAAVAVFTTHILLLLPVL
	l	1				LSILGIVCLVVTIMYWSGWEMG
		1				AVEAISLSILVGSSVDYCVHLVE
		1				GYLLAGENLPPHQAEDARTQR
		1				QWRTLEAVRHVGVAIVSSALT
		l		l		TVIATVPLFFCIIAPFAKFGKIVA
		l				LNTGVSILYTLTVSTALLGIMAP
	l	l				SSFTRTRTS/CPQGPGCRAAGRG
		l				PGAGCLPRAPAERL*DSPARRG
		l		1		LPIARDGLWTLAPLVPWVGDR
		_				SCFPARLQLAVSPGLGPGRPAG
25303	55671	A	25442	1	1596	MGVSVRVDCGCARASEFLGRP
	1	l	İ			RGAVRGADPGSGLTETCAQSR
		l				TWARARSKGGFRLTLNFYGPR
						YPSEGTSRGQRSEALPFLDIQHP
	i	l				TPLGRPRMLQSRGEMVRSWGP
	i	l				VVEGKLGFCPPLTVFPGGLRGP
		l		ł		HPGLAGERENFARGAKQEACL
						LQGPGDAGLTHPCPATGYFPEA
						SCTSRSIRMFINSQERQLADMSL
		l				FIADSWLCYSGIICWKSLEHQR
		l				GASLSCVYMEGKGGNIWMKAS
		1	l	İ		NVLPLCQMLPTSGHSKSDLFGG
	İ		l			LAVEKQMRQDHHILLHDRSGF
						QLAVTSPLLTRLGKGHIIQVPV
l	i					YVLDAPSRWLGGLRLFRDSSCG
		1	1			LVLSLLICVAAVAVFTTHILLLL
	İ					PVLLSILGIVCLVVTIMYWSGW
	ł	1	1			EMGAVEAISLSILVGSSVDYCV
						HLVEGYLLAGENLPPHQAEDA
				1		RTQRQWRTLEAVRHVGVAIVS
l		l		l		SALTTVIATVPLFFCIIAPFAKFG
l		l	1	l		KIVALNTGVSILYTLTVSTALLG
l				l		IMAPSSFTRTRTS/CPQGPGCRA
	L	_	L	L		AGRGPGAGCLPRAPAERL*DSP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25304	55672	^	25443	1	2355	MDHPGFREFCWKPHEVLKDLP LGSYSYCSPPSSLMTYFFPTERG GKIYYYGGMGQDLADIRGSLEL MTHPEFFWYVDEGLSADNLK SSLRSEILFGAPLPNYYSVDDR WEEQRAKFQSFVYTYVAMLAK GSTSKVQVLYGGTDLEPDYEVR RTFNNDMLLAFISSSCIALLVYI LTSCSYFLSFFGIASIGLSCLVAL FLYHVVFGIQYLGILNGVAAFV IVGIGVDDVFVFINTYRQATHL EDPQLRMHTTVQTAGKATFFTS LTTAAAYAANVFSQIPAVHDFG LEMSLIVSCCULAVLYTMPAA LGLWSLYLAPLESSCQTSCHON CSRKTSLHFPGDVFAAPEQVGG SPAQGPIPYLDDDIPLLEVEEP VSLELGDVSLVSVSPEGLQPAS TNGSRGHLIVQLQELLHWVL WSAVKSRWVIVGLFVSILLISLIV FASRLRSASRAPLLFRPDISLIV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLLFREDTSILV FASRLRSASRAPLFREDTSILV FASR
						HKPPFHGRVCMAPPGCLLSSSP DGPTKGFFFVPSEKVPKARLSA TFGFNPCVNTGCGKPAVRPLVD

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \:-possible nucleotide insertion)
25305	55673	A	25444		1737	MLYAAECLENYMKLQVIPSAL NEALQAQSTWSDLGLASHLS STWCLHGESAAWSQPAVVECG QPRODQLQTHSEAWLCALVATF SQELEQFAVTAQQISDRQGHAV CTAPPRGRPSTLMTINLVCASSA DEGGGGKTETOTAGGRLGRAG TRSRGQLTRLITRTQAAEPRWF LQLLKRSANRSRALTRPPSGLSS DGARRLRISPSAVSSADTKFT VPVSSDSSGRDGGGETRAEAGF GGPHVAQPGVAPPAAAARDF RKPRGLNRQNVSPPGGEGGL GIPPRIORPPSFPGSPADFAS VSHTQGSPPDTGLPGTCQNRLP NPAAVDEGTCTRGSLNCRLS PRVSERRGPEGTFGRAAPPQ CAGTRGLSPPADLGAAIRTPRA VSHTQGSPDTGLPGTGCNRLS PYRPHGQGFGTTGGSLNCRLS PRVSERRGPEGTFGRAAPPQ CAGTRGLSPPADLGAAIRTPRA FCSRTAQPANONTGNHERGLRS VAMFGDRASREATPALSLCESQ GGFEDEKEVFSPEPHVETSDEPL LSTGPAGCWGTDL LSTGPAGCWFINDLTT

SEQ 1D	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
25306	55674	A	25445	2	1642	LLSSISAWFGPPASTPAFTMSIR
		1				VTQKSYKVS\TSCPRAFSTRSYT
	Ì	1				SRPGSRISSSSFSRVGSSNFRGDL
		İ				GGGYGGASG\MGGITAVTVNQ
		1			1	SLLSPLVPEVDPNIQAVRTQEKE
						QIKTLNNKFASFI\DEVGFLEQQ
						NKMLGTKWSLLDQQKTA\RSN
						MDNMFESYINNLRRQLETLGQ
						EKLKLEAELGNMQPLVEDFKN
	l					KYEDEINKRTEMENEFVLIKKD
						ADEASMNKVELGSRLEGLTDEI
						NFLMQLYEEEIRELQSQISDTSV
						VLSMDKSRSLDMDSIIAEFKAQ
		1				YEDIANRSRAEAESMFQIMYEE
						LQSLAGKHGDDLRRTKTEISEM
		1		l		NRNISR\LQAEIEGLKGQR\ASL
		1				GGRPLQDAE\QRGKSWPIK\DA
				i		NAK\LSEAGSPPLQAGPKQDMG
	1	l				R\QLREY\QKLMNVKAGPWTIE\
l						IATYQESCLEGEEEPGWSLGCQ
		ŀ		l		NMSNHT\KTTQRGYAGRPEPPP
						MGGFTSP\GFSYKPGAPGFGSG
		l				AGS\SSFNRHQLSPGAVVVKKIE
						TRDGKLVSES\SNVLPKVKQLR
						QPLPSLPLLRCPRGLGKEAPYP
25307	55675	Α	25446	1	1280	MAYLCNAICMTHMVTLDPVDQ
				l		ALPGATTATSVPGPQCDASCM
						MLFAVVPFNGIALAATQGAQS
						MLPPRVQGSLSSKPSTRRGRDA
						PGLQVSQAPPPRRGFAVGRRYS
						PPALAPGRCAAPHGGGRKELPT
						RRPGHGMAPKFPDSVEELRAA\
						GSESFRNGQYAEASALYGRAL
				l		RVLQAQGSSDPEEESVLYSNRA
						ACHLKDGNCRDCITDCTSALAL
						GPFSIKPLLRRASAYEALEKYP
						MAYVDYKTVLQIDDNVTSAVE
						GINRGPGLKEDTTQKRWNSLPS
						ENHKEMAKSKSKETTATKNRV
		1	1	I		PSAGDVEKARVLKEEGNELVK
		1			1	KGNHKKAIEKYSESLLCSNLES
				[		ATYSNRALCYLVLKQYTEAVK
	1	1		I		DCTEALKLDGKNVKAFYRRAQ
	1	1				AHKALKDYKSSFADISNLLQIEF
L			L	l	l	RNGPAQKLRQEVKQNLH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25308	55676	A	25447	1	1297	MHLLSAYFVPGSMLVGSGYM
						MVNITDVSPPSWSFLCSMLITTT
		1				QGAQSMLPPRVQGSLSSKPSTR
						RGRDAPGLOVSOAPPPRRGFAV
						GRRYSPPALAPGRCAAPHGGG
				1		RKELPTRRPGHGMAPKFPDSVE
		1				ELRAAGNESFRNGQYAEASAL
						YGCALRVLQAQGSSDPEEESVL
						YSNRAACHLKDGNCRDCIKDC
				1		TSALALVPFSIKPLLRRASAYEA
						LEKYPMAYVDYKTVLQIDDNV
		1			l .	TSAVEGINRMTRALMDSL\GPE
				i		W/RALKLPSFPLVPVSAQKRWN
		1		1		FLPSENHKEMAKSKSKETTATK
						NRVPSAGDVEKARVLKEEGNE
			1			LVKKGNHKIAIEKYSESLLCSN
						LESATYSNRALCYLVLKQYTEA
			ĺ	1		VKDCTEALKLDGKNVKAFYRR
	ŀ	i i	ļ	i		AQAHKALKDYKSSFADI\SNLL
			1	1		QIEPR\NGPAQEVAGREVKQNL
25309	55677	Α	25448	3	491	GITFTHSPAATGGGAQRVRRRD
		1	İ	i		PPPGVQLRNMAQETNHSQVPM
		1		1		LCSTGCGFYGNPRTNGMCSVC
		1		1		YKEHLQRQNSSNGRISPPATSV
		i i		1		SSLSESLPVQCTDGSVPEAQSAL
		1	i	1		DSTSSSMQPSPVSNQSLLSESV\
		1				ASSQLGQYICGTKAVPETEDVQ
1	1					ASVSDTAHV
25310	55678	Α	25449	1	860	HLLLLAIDYNLPIAGVLMESQY
		1			1	LGASPKRLVIPNLYAHRKSLAT
	1	l	1	İ	l	LEPYAPRRPMPIARRYAIPYMS
						HHNGYIGDVYYRLTVEEKKSSF
			1			IARRSILTTEFTIRRTKKVPVPSI
		ı		1		NMSSASPLEDESRPSAGVQLRK
ŀ	1	1				GRYRLLRDRYRPGCNSVGESPR
1		1				KSSFSDDIMATESRESIFAEEPR
1		1	i			TGEHSVRGPVSNQSLLSESVAS
				l		SQLDSTSVDKAVPETEDVQDSL
		1				NASPTKQQCG/DVQTVDLYSNN
					1	KELFAQKCYRHRYISRLKKCCL
		1_				CHELVPRDTIKSPESLSVGS
25311	55679	Α	25450	880	1196	SPTTRRGTPGTCLKPTACAGAA
			1	1		*PGCSARRTCASAAPLSTCPPSS
		1	1	1		CAAPPPAPAAVPSTPRPTSPSPW
			l			AAPASPSRRRTQTASTPASTNR
		$\perp$				APSSCWAPTTRPLAP
25312	55680	Α	25451	254	579	IEKISLEPKNRPSPQIPNLVGP/R
		1	1	1		LFLVPGDFQSQVPNFLPFKPSSG
		1	ĺ			PHPAAGKGQPFSFLPAWRSTGP
		1	1			ERATPGPGRPAACSALEAPSLR
i		1	I			GPSGYSAQEPPRRPISARI

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
25313	55681	A	25452	6	1442	RSELIRHSWPRHAQLRGARART
						AVSIRECISVHVGQAGVQIGNA
						CWELFCLEHGIQADGTFDAQAS
						KINDDDSFTTFFSETGNGKHVP
1						RAAMIDLEPTVVDEVRAGTYR
			i		İ	QLFHPEQLITGKEDAANNYAPG
1			ļ			PPTPGGKESIDLV\LDRIRKLTD
						ACSGLQGFLIFHSFGGGTGSGFT
						SLLMERLSLDYGKKSKLEFAIY
i						PAPQVSTA V VEPYNSILTTHTTL
						EHSDCAFMVDNEAIYDICRRNL
		ļ	i		İ	DIERPTYTNLNRLISQIVSSITAS
		1				LRFDGALNVDLTEFQTNLVPYP
l		1				RIHFPLVTYAPIISAEKAYHEOL
						SVAEITSSCFEPNSOMVKCDPR
						HGKYMA\CCMLYRGDVVPKD
						VNVAIAAIKTKRTIOFVDWCPT
1						GF\KVGINYQPPTVVPGGDLAP
ì	ļ.	1			1	VORAVCMLSNTTAIAEAWARL
		1				DHKFDLMYAKRAF\VHWYVGR
l	ŀ	1				GDWKKGEFSEAREDLAALEKD
		i i				YEEVGVDSVEAEAEEGEEY
25314	55682	A	25453	3	618	SSAGREPDPSDLPRRLCFTHRLP
23314	33082	l^	25455	ľ	0.0	AARRWVOLCVHASPEPGGOGV
		1				CPGRSERMVIRVFIASSSGFVAI
1		1				KKKOODVVRFLEANKIEFEEVD
						ITMSEEQROWMYKNVPPDKKP
						TOGNPLPPOIF\NGDRYCGLLVS
1						FSVICIKNPNWHNLFLLIPWSGI
1						NPYCEQDSSFSENVGDEILKNS
						GVPRDFTSILIQKERKSEKVKG
						VDQGHR
25315	55683	A	25454	3	424	SWTMAATIQAMERKIESQAAH
		1		1		LLSLEGQTGMA*S*GTPPCCPG
		1				AAAGSRSSCCAAGSPRSPAASA
1		1				AARTPAAGSPARPTCPPAGSRT
		1				PRLSSRNQPASSRPSRFDLLGKA
						GEQPAIQSSSPWPESWLPSSTK
25316	55684	A	25456	268	445	
25317	55685	Α	25457	3	205	
25318	55686	Α	25458	27	272	AKCSGQGPGRVRAQGERADHE
		1		1		CPGAGAGGGGCNSAASAREES
		1		1		SRLISG\SLQMQNVSLASRRKEE
		1	1	1		EVRAAAAGGAAAGRPRV
25319	55687	Α	25459	1	253	
25320	55688	A	25460	2145	2399	
20020	1-2	100	1			

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	locatinn of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25321	55689	Α	25461	174	1309	HLLCCRAQRRPQTPPAARGLEA
						CSEGALKMPEAPP\LLLAAVLL
		l			1	GLVLLVVLLLLLRHWGWGLCL
		l				IGWNEFILQPIHNLLMGDTKEQ
		l				RI\LNHVLAACGSPGNAQSVLG
		i				GHLTPNCEQKEW/APLNVGDK
		1				KGQDSWDALISREQPALPCLLG
				i		NLGAYFGLLQLLRMAR\LLVNQ
		1				GARLIHHSRFNPDLCPPSPKRM\
						VDFAGVKDKALFQVTL\VCGAS
						PETFHPPSLKKKYDVGHNWTW
		l		1		VFLDHWKDRYL\PDTLLLE\EC
		1			1	G\LLPEGGQLLLAEQRLSSPGAP
		1				\DFL\AHVSREPACFG\CT\HYQI
		1				VPWKYRE\VVDGLGRRPI\YKG
						P\GSEAGALTAPPRPPSRALSPK
		l				PGTEGARPWLLLTLVRLRACVL
						NAKSHARAESLRA
25322	55690	A	25462	2470	3460	SGPCPRCCAECRPYKTRPRSRV
						PGTHGPGPADHGQPPCCMAGA
1						HPPRPQAWMLLQTHSQDCEGK
		l				VGCGGIFCPCYHHCKHTHHHH
		1				ннрининүнүнинини
						ннинничничнын
	İ	l			1	нснин/нининирүрниүнин
		l				RGQDHHPHPHHHH/HHHYHHH
	l	l				НҮНННҮНРНННРННННОРОН
	1	ı				нннонунннунниринр
1	1	1		1		РНННННҮНҮННННННҮ\НРҮ
		1		i		РННҮНННННННРНРНННН/
		1				нннүнниннинүнннн
		1				НННКРНННКНОНРННҮННН
						HPHPCHHHRLHHHHRHHHYHH
		L				TSSVQGPGSQPAGASLPGQACR
25323	55691	Α	25463	1	407	DAERQEALGIVRRIGTDTEAAT
	1	1		1		EPAGATVPAAAAAARIGTVGP
	1	1		1	1	QPPAMPRRKRNAGSSSDGTEDS
		1			1	DFSTDLEHTDSSESDGTSRRSA
1		1				RVTRSSARLSQSSSRISRSCSKS
	1					GSLLALRSLLTLPEE*PVVSSSL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nocleotide insertion)
				sequence		
25324	55692	A	25464	3	2539	RILYIPDGHRAPGASQSGNWEH
23324	33072	<u> </u> ^	2,5404	3	2339	PLLLLEPGNLASSPSMSLAYPHP
		1				CGLTIHQEHRRAHEELAYTPND
						RASSTGHPAFIEDGNPSPVLAFA
l						ASPRPNDSYILKREPPESCEKER
						VFEEATTRGKYGEGAKOETFTF
	İ					
		i				ALTLVFIQCVINAVFAKILIQFF
						DTARVDRTRSWLYAACSISYLG
						AMVSSNSALQFVNYPTQVLGK
						SCKPIPVMLLGVTLLKKKYPLA
						KYLCVLLIVAGVALFMYKPKK
						VVGIEEHTVGYGELLLLLSLTL
						DGLTGVSQDHMRAHYQTGSN
						HMMLNINLWSTLLLGMAVSCP
						DQGPELVPRCPFVQALEKPSWK
						NLHQQDLFATCYWHNEGESCV
1						SCHGKTLSSKTQGGILFTGELW
				ì		EFLSFAERYPAIIYNILLFGLTSA
						LGQSFIFMTVVYFGPLTCSIITTT
l	1					RKFFTILASVILFANPISPMQWV
						GTVLVFLGSTQIILDNLKILNTS
1						AKTLLYKTPLSWQELEGERASS
1						CAHKRSASWGSTDHRKEISKLK
				1		QQLQRTKLSRSGKEKERGSPLL
1						GDH/VSAGSTEGVPS/RASPQGP
1	1					LSCDSAPACT/VSLEGLNQELEE
1						VFVKEQGEEELLRILDIPDGHR
1			i			APAPPOSGSCDHPLLLLEPGNL
		l				ASSPSMSLASPOPCGLASHEEH
1						RGAAEELASTPNDKASSPGHPA
			i			FLEDGSPSPVLAFAASPRPNHSY
						IFKREPPEGCEKVRVFEEATHQ
25325	55693	A	25465	845	1316	LSLGDSAQCLLPHASWCQVAG
23323	33093	<u> </u> ^	23403	043	1310	HPAFLEDGSPSPVLAFAASPRPN
						HSYIFKREPPEGCEKVRVFEEAT
				i		S/RRVLTGPFLTSCPDK\NKVHF
l	1	l		1		
				1		QP\TGSAFCPVNLMKPLFPGMG
		l	l			FIFRNCPSNPGISSSPGQPQATTS
1	l	1		l		EGSGSLQGLPTAIRAMAAHPYH
	l	L_	l	l	1	Q

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25326	55694	A	25466	1077	1506	CDACGRRCRTCRTFCLGLQPAC LDGHHHRHPDCWFWSPRHR+ GMIIDVFSRYSGSEGSTOTLTKC EL, KVLMEKELPGFLQILTNEGE EL, VLYMEKELPGFLQILTNEGE EL, VLYMEKELPGFLQILTNEGE RVNALLKWLLKLGERWQMTE EGIKGQRSGHGPEQAENLGDS RVNALLKWLLKLGERWQMTE EGIKGQRSGHGPEQAENLGDS UPODTERSHVELHCHNEGOFL AGVPKTSVPARPGI PVPALQHA QHOPGCERALHCHNEGOPL SLQGEEQRETHLRGQDWPCTL QMRTLKREVHAL POGRAGGAA REGLGASICETGEHQMTNFQVP RWPPCFPGQAGPVLGTGTRHG LDLLSGRRGTVFKGSSVAME EEVTVTKQSAADLRHTGQGPT CCVLSGGRCGSQAGPKLGT CCVLSGGRCGSQAGPKSLL LGDESEPHGRGPPAAALHHRR NPLNDVMLVGDDAGPAGHFAS VYPPLAWTVTTVTLTVTGFGY RVTDEAGHPVPSQVSGIGRCLQ GMKAPPVTVTVSGEKGSCLCA SCVLCLEHPYFPLVPWLPPVF DSVIPSSTSPGEAVLADVGFRN NVPORAOLKPOKOLLTPF
25327	55695	В	25467	31	783	Quanqua ququum
25328	55696	A	25468	846	1392	PDPAAHRFGHPTLHPGSLRTSS GAGTWYQNPQHHNDHDYYHH HHIJHDDHHVYHHHHIHHHIH HHYHHHHHHHHHHHHHHHH HHQHHHHHHHHYHHHHHH HHHHHHHH
25329	55697	A	25469	181	412	LRSDQQTRKFVSRSSGACSPPTT TELSWPPSLLPSL*FHSPSSQP* MNHSASTTSPLPSFITERESILAT EWDTARN

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25330	55698	Α	25470	1	848	MPSLNTIVSPLGSPHTSLIPPML
						LSANLPFDTTIMIKLQTACSAPI
	l					HNLORPCGENLRTSTFVRRLDR
						NLVKSPOPGGGGOPSROWEAR
	ĺ					GAEPOGRRDPSEVO/RPAGRGF
	ł					GRISRAPRKPSRAPTPTQGLGPP
	l	l				LGAGGOGSLASCRPARKNARPI
						TRAAAHSAHPHSHWHSHARPO
						POSPSAAGOSGDPWPPARVPPP
	ĺ			l		PLLRLPORRTAGRTPVDAPARG
						IFTLSLSSSHSKSSGKHRGARKT
						PEMWPLFRGSLSKLSRRRKVSP
						SAALHWRLRRTOKRLCC
25331	55699	A	25471	92	1083	TMRTHGHRKGNITPWGLSGVG
						GL/ETGRALGEIPNVDEGLMGVI
						AAVAIVLVSLLFVMLRYMYRH
						KGTYHTNEAKGTEFAESADAA
						LQQRERALDSSRDSHLETLGAC
						PGRNGGGLALQEATPRDPGRR
						WPPORPPFAPRRWEKIWAHGPL
						GSAGQHQLTGRKVLVEGLGCI
						CMAHTDLONTSVAKMAINRPN
			ļ			EYAOVSLENDVSCKVKAVOAP
		l				ORLHWPSVDADTGGRGAVHIA
	İ					FPKHVEPETPFAHTIPARNSWT
						KWSSEHILETLSPOKPALPWAP
	l	l				RQQGRPLGLTAPISKRLGPGDG
	ŀ	1				PEGEAGERLAQAHFINTRPPST
		1				GPPGTPAAD
25332	55700	A	25472	73	424	RPGMWSTRSPNSTAWPLSLEPD
						PGMASACTTMHTTTIAEPDPG
	ŀ					MSGWPDGRMETSSPTIMDIVVI
						*CAIAAEAIVLVSLLFVMLRYM
	l					YRHMGTYHTNEAKGTGVADS
						ADACPAGDPA
25333	55701	Α	25473	139	546	RPGMWSTRSPNSTAWPLSLEPD
						PGMASASTTMHNYHHCRSLIPG
						M\SGWPDGRMETSTPTIMDIVVI
						AGVIAAV\AIV\LVSLLFVMVAL
			1			TCNRA/HRGTYHTNEAKG\TEF
		1				AESADAALQG\DPAL\QDAGDS
		1				SRK\EYFI
25334	55702	С	25474	142	408	

SEOID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
i i				sequence		
25335	55703	I.	25475	44	727	ARAGSRSRGLPFCGTAGPPPKA
25555	55/03	l <sup>A</sup>	23473	44	121	
						TLWGGLLRLGSLLSLSCLALSV LLLAOLSDAANNFEDVRCKCIC
		l			1	PPYKENSGHIYNKNISQKDCDC
		l				LHVV\DPMPVPGA\NVEAYCLR
		l				CECKYEE\RSS\STIKVTIIIYLSIL
		l				GLLLLYMVYLTLVEPILKRRLF
		ĺ				GHAQLIQSDDDIGDHQPFGKCT
		l				RCASPLPQFEPTCWNKVEYAQ
		l				QALESFQVQEQRKSV\FDRACC
		_				PQLNLGN
25336	55704	Α	25476	11	1323	VVLLVSVNTEAEESEKAATEQR
		l				/PLEGTDQTLDVEEEQEESKAA
		l				ACGSKKRVVPGIVYLGHIPPHF
		l				QPLHVRNLLSAYG/RSPSHYDL
		l				WNLKYLHHFTWSHHSEHLAFE
						RQVC\HRQHLRVEVTQAKCETI
						FYLQSVEWGQCFLAVDGDLAH
						PDGSWTFAQRPTEQELRARKA
						AQPVGKVLNYYPTQLSLECEVP
						SQPMGTGHSHRGLCQDVKVIN
						VPVSFVWCALVAGLLVVVPPPF
						PQAPEAEVSDISLKRGLQREIEQ
						CRRDIQNFPFPCASEELASQLFP
						LMEVPQGRGTTGFMNAPLTTS
						EVRGLKKELKPLLDDPERVAEQ
						IDQFLGSKLYTWTELMSILGILF
	1					SKEERNMICRAAMGAWERDYP
						AGQNIPAADVTFPARDPQWNN
						NNAAHQKNMRDLQELIIKGIKE
						SAPRPQNLTKAFDEQQEKDEGP
25337	55705	Α	25477	1	490	GTSGTRPLVSVNMEAEESEKA\
						ATEQEPLEGTEQTLYAEEEQEE
1		l				SEEAACGSKKRVVPGIVYLGHI
1		İ		l		PPRFRPLHVRNLLSAYGEVGRV
1		İ	1	1		FFQAEDRFVRRKKKAAAAAGG
1		İ		ĺ		KKRSYTKDYTEGWVEV\RDTR\
	1	l	l	ĺ		IAKRVA\AALLK*PMGARRRSP
		l	ŀ			FRYDLWNLKYLHR
25338	55706	A	25478	2	574	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25339	55707	Α	25479	160	1548	KTSSQTLSLALTMFQRLNKMFV
		1			l	GEVSSSSNQEPEFNEKEDDEWI
						LVDFIDTCTGFSAEEEEEEEDIS
l		1				EESPTEHPSVFSCLPASLECLAD
l		1				TSDSCFLQFESCPMEESWFITPP
l						PCFTAGGLTTIKVETSPMENLLI
		l				EHPSMSVYAVHNSCPGLSEATR
ĺ						GTDELHSPSSPSILPNKMLSVHV
						GTAIHNQAALCQSVESYWQCGI
	1					QLLTQFQSQSKLGQLLAATCKE
						LPGPKESRRTAKDLWEVVVQIC
						SVSSQHKRGNDGRVSLIKQRES
1		1	1			TLGIMYRYVLEPLVLTIILSLFV
1	ĺ	1	1		l	KLHNVREDIVNDITAEHISIWPS
		ļ	1			SIPKKQMSSRTFMSQEETVCRA
						AHTPSLPEEKWVEQLIYALVVA
		1		İ		AARIMAMWGPNAAWLVFLAA
		ı				AGPPPLTPPHSPP/PPPPPPALGR
						WMGPPLRDSASGLPRPPPGRISE
						DSGAWACGPALCPRPAIPSPAP
				ļ		ALRVPEALRLWGTCSV
25340	55708	A	25480	լլ	380	FTSPKTARNWGWLMQVRNQR
						LVLGKAGGKKGSPLEQRGGNG
						HHGGTRLICALV\LVS\MRPLAT
			İ			FAEPQTETCTVAPRERQNCGFP/
			ĺ			GVSRPPQCANKGCCFDDT\VRG VPWCFYPNTIDVPPEEECEF
25341	55709		25481	3	2367	VPWCFYPNTIDVPPEEECEF
25341	55710	A	25482	2	1230	WRRSRRRRPPAPOAGGGDFRA
23342	33/10	<u>۱</u> ^	23402	-	1230	GISPPTGKKSLGLMEPQGNHYR
				l		CRCLOVAGSOAWARCVSMPEL
				l		VVOKVVGHP/LVLLSVVDHFNR
	1		l	l	l	IGKVGIOKCVIGLFWGSWOKK
					1	VLDVLNSFAVPFDEDDKDNSM
1		1	l	l		WFLDHDYLENMYGMFKKVNA
1			l	l		RERIVGWYHTGLKIHKNGITIN
1				l		ELMKRYYPNSVLIIIDVNPKDL
1				l		GLPTEAYISVEEIODDGTPTLKT
1						FEHVTSEIGAESYLEKVATGKL
1	l		l	l		RINHOIIYELODVFNLLPDVSLO
1	i			l	1	EPIKAFYLRTNDOMVVVYLASL
l	1		l	l		IHSVGLTDPFC\VALHNLINNKI
			l			ANODGDKKEGQEKKES/KKDR
ĺ	l			l		KADKGKDKDKEKSDVKKEOK
1				l		NHCLKEKYRFRODSLPDDPRVL
l				l		GLELTPPVARQYSPQDLSEIPRH
				l		ADFRCDPAHFOLWWSQGETPS
		L	L	L		

AGSQAWRAGC VVVHPLVLLSV GROKRWVGVLSV GROKRWVGVLSV GROKRWVGVLSV SNSFAVPFDED HDVLENMYGM GWHTTGRKLH KRYCPNSVLVIID SAYISVEEVHDD TTYSEIGAEEAU KLLDIRSYLEKV INVOLODYSH
AGSQAWRAGC CVVVHPLVLLSV GNQKRVVGVLL SNSFAVPFDED DHDYLENMYGM YGWYHTGPKLH ERYCPNSVLVIID EAYISVEEVHDD TISEIGAEEAEEV KLLDIRSYLEKV
CVVHPLVLLSV GNQKRVVGVLL V'SNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TYSEIGAEEAEEV VTTVGTLSQRITN KLLDIRSYLEKV
CVVHPLVLLSV GNQKRVVGVLL V'SNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TYSEIGAEEAEEV VTTVGTLSQRITN KLLDIRSYLEKV
CVVHPLVLLSV GNQKRVVGVLL V'SNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TYSEIGAEEAEEV VTTVGTLSQRITN KLLDIRSYLEKV
GNQKRVVGVLL /SNSFAVPFDED DHDYLENMYGM /GWYHTGPKLH KRYCPNSVLVIID TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
VSNSFAVPFDED DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD VTSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
DHDYLENMYGM VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD VTSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
VGWYHTGPKLH KRYCPNSVLVIID EAYISVEEVHDD TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
KRYCPNSVLVIID EAYISVEEVHDD TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
EAYISVEEVHDD TSEIGAEEAEEV DTTVGTLSQRITN KLLDIRSYLEKV
TSEIGAEEAEEV OTTVGTLSQRITN KLLDIRSYLEKV
TTVGTLSQRITN KLLDIRSYLEKV
KLLDIRSYLEKV
GFYLKTNDQMV
VALHNLINNKI
QEKEESKKDRK
KSDVKKEEKKE
PLLFLRAMDST
ALNPRESPRSPE
AVQTLANVIRP
LVTMKGETVCT
ELEHPAAWLLRE
DGTAFVVLLTE
KFGLPRPQLR/EA
VGQL/AAAGIN
ETLTLADKYGI
IYLSEVLDTPLL
CQRVYRQELGD.
TGTPALTVVLR
EQAVYHSIDAYF
AGATEMALAK
GPNGPAFLAFAR
ENAGLAVSDVV
NLLMGVGAEGI
TLIVKAOGFRA
VDEIVVAKKSPT
KTKKRPPPVEK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide inscrtion)
l				sequenec		
25345	55713	A	25485	145	1918	PLEYFORSVSGVPOLLFLEHLC
23343	33713	ľ`	25405	143	1710	NPRWPLLSLRAMDSTVPSALEL
						PORLALNPRESPRSPEEEEPHLL
ŀ						SSLAAVQTLASVIRPCYGPHGR
		ļ.				QKFLVTMKGETVCTGCATAILF
		İ				ALELEHPAAWLLREAGQTQAE
ł		ŀ		1		NSGDGTAFVVLLTEALLEQAEQ
			ŀ			LLKAGLPRPQLREAYATATAEN
						LATLPSLAIQSLGPLEDPSWALF
į.		ľ	ŀ			SVMNTHTLSPMDHLTKLVAHA
				ł		CWAIKELDGSFKPERVGVCALF
		ŀ				
İ		ŀ		İ		GGTLEDSCLLPGLAISGKLCGQ MATVLSGARVALFACPFGPAH
				ļ		PNAPATARLSSPADLAQFSKGS
ł						DQLLEKQVGQLAAAGINVAVV
						LGEVDEETLTLADKYGIVVIQA
Į.						RSWMEIIYLSEVLDTPLLPRLLP
						PORPGKCORVYROELGDGLAV
ŀ						VFEWECTGTPALTVVLRGATT
1				i		QGLRSAEQAVYHGIDAYFQLC
						ODPRLIPGAGATEMALAKMLS
		١.				DKGSRLEGPSGPAFLAFAWAL
				l		KYLPKTLAENAGLAVSDVMAE
						MSGVHQGGNLLMGVGTEGIIN VAQEGVWDTLIVKAQGFRAVA
		1		ì		
		1		1		EVVLQLVTVDEIVVAKKSPTHQ EIWNPDSKKAK\KHPPPVETKKI
25346	55714	В	25486	1	642	EIWNPDSKKAKIKHPPPVEIKKI
25346	55715	A	25487	3	395	FLPVNLTHDWOGSSALATLERP
23347	33/13	^	23407	ľ	373	LSQVRLKRFVGTLIAFMVSAIVI
			1	}		LATASMAVASITESVQTAAFID
						NMARNVSNKLLLQQGIDQKIL
ŀ						ALLQSLEAALEYVGEQQDALA FQQQ*NCNWGHKHICIISLPWN
25348	55716	A	25488	3	358	HEPMCGETHQALQGAMEKLW
23348	33710	^	23400	ľ	330	SRFMELMQE/KKVDLKERVEEL
		l				EHCCI*LSGERQTPSGSGKPGHG
		1				KESCTLVRGAPASESCPPAGEYI
		1		1		ALYQSQRAVRKEEECISRLAQD
		1				KGEVKVKLLE
25349	55717	A	25489	I	250	
23349	133/1/	l^	23489	l'	230	VQCGGIPPGQNNKEEMEVLPEP
	l	l				PPPINRKKDKSYATAMGPFLRQ
				1		EALSGELLACLVIQD*QGNWV YKPISFNIYKKLRKSIRG
25350	55718	A	25490	1	702	TAPISENITAALKKSIKG
25350	55719	A	25490	1	252	
25351	55720	A	25492	i	122	LAPLVTYFSSLSLGFFNLKGKL
23332	120	l^	25472	l <sup>*</sup>		APSSWRC*GLNEIIRGKH
25353	55721	A	25493	3	505	
20000		r		I*	545	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
25354	55722	A	25494	li .	3345	MRVGFRDIVGSLSEYSFGCPVN
		1				YEVFHSV WITILCCLMANDRKP
		1				QFLYFFQFFSFHGGRNLMSSFH
		1				PGNGHNDSRRSVFYANEKWEF
		1				LDPTPKDLEESIVOEEKKEPTPE
						GNKVSQRLKNLPHTSLKAKQL
		1			İ	LOTSSTNRGTVITATRLAFDLRT
		1			i	QSTKCSHPASGSSGHSTDFQLE
		1				GEWGLWDLGTKGFKLPYSLSI
						DIDNVKSPHFPHELKTLTVSLGS
		1				NRRMGLEKKECHQKQGALREQ
						LOVHIONVEILVSE
25355	55723	A	25495	296	1350	TLWLQGEQPSTQEIHEKV/LNE
23333	33723	ľ	25495	250	1550	AMGAMMYHTIILTREDLEKFK
		l			l	APRVIVQIGSGYDNVDIKAASE
		l				LGIAVCNIPSAAVEETPDSTICHI
						LNLYORNTWLYOALRGOAVA
		1				VRAKAFGFSVIFYDPYLODGIE
		ı			1	RSLGVORDLLYOSDCVSLHCN
						LNEHNHHLINDFTIKQMRQGAF
		ŀ			1	LVNAPHGGLVDKKALAQALKE
						GRIRGAALYVRESEPFSFAQGP
						LKDAPNLICTPHTAWYSKOASL
						EMREAAATEIRRAITGHIPESLR
					ł	NCVNKEFSVTSAPWSVIDOOAI
						HPELNGATYRYPPGIVGVAPGG
						LPAAVEGIIPGGIPVTHNLPTVA
						HPSQAPSPNQPTKHGDNREHSN
25356	55724	A	25496	694	1185	PKPFKEGTIRGAALDMHESEPF
23330	33724	A	23490	094	1103	SFAOGPLKNAPNLICTPHTAWY
						SEQASLEMREAAATEIRRAITG
		1				CIPESLRNCVNKEFFVTSAPWS
						VIDQQAIHPELNGATYRYPPGV
						VGVAPGGLSAAMEGIIPGGIPV
					İ	THNLPTVAHPSQAPSPNQPTK*
						MK*KOMGEVA*GAARIRGETL
						GLNGFGCTGQA/VAVRAKAFG
						FSVIFYDPYLQDVVERSLGVQR
						VYTLQDLLYQSDCVPLHCNVN
		1		1	l	EHNNHLINDFTIKQMRQGAFLP
		1	l			PKPFKEGTIRGAALDMHESEPF
		l		1		SFAQGPLKNAPNLICTPHTAWY
		1			1	SEQASLEMREAAATEIRRAITG
1		1		1	1	CIPESLRNCVNKEFFVTSAPWS
1		1		1		VIDQQAIHPELNGATYRYPPGV
1		1				VGVAPGGLSAAMEGIIPGGIPV
L					l	THNLPTVAHPSQAPSPNQPTKH

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
<u></u>		_				
25357	55725	Α	25497	290	1251	PFMLYVSISTLYIAFCHILNLYR
						RNTWLYQALWEGTRVQSVEQ
					i	MGEVA*GAARIRGETLGLNGF
		1				GCTGQA/VAVRAKAFGFSVIFY
						DPYLQDVVERSLGVQRVYTLQ
						DLLYQSDCVPLHCNVNEHNNH
					ŀ	LINDFTIKQMRQGAFLVNAARG
i						GLVDEKALAQALKEGTIRGAA
						LDMHESEPFSFAQGPLKNAPNL
					l	ICTPHTAWYSEQASLEMREAA
1					ł	ATEIRRAITGCIPESLRNCVNKE
						FFVTSAPWSVIDQQAIHPELNG
			İ			ATYRYPPGVVGVAPGGLSAAM
						EGIIPGGIPVTHNLPTVAHPSQA
					1	PSPNQPTKHVDNREHPNEQ
25358	55726	I <sub>A</sub>	25498	1	1538	MLLQKTQFEYAFKKKRKLEES
23336	33720	1	25470	l'	1550	KKRGAGPASSDPRWRGSSQTA
1						PHASEVSGAPLGRSCETTRDTG
				1		VGPSPRQWLGAGAGTWQHRA
						RAASTPSSRGLRALOTWGGGE
			Ì			VMNGPLH\PPPPRVALLD/SRNC
		1				TVEMPIPKDLATMAFCDTHSTQ
						EIHEKILHEALGAMRYHTITLA
		1				RADLEKFKALGVIVRIGSGYDN
					1	VNIKAACELEIAVCNIPSAAVEE
						TANSTICHILSLYRRNTWLCQA
	1				l	WARKHVCYSMGQIREVALGG
1	i		:			AHIGGETQG\LIGFGSTGQAVPV
	1					RAEAFGFSVIFYDPYLQDGIERS
1						LGVQRMSQGAFLVNAARGALV
1	1					DEKALAQALNNGKIR/GAALDV
						PQSELFSFAQG\SLEMREAAATE
						IRRTITGCIPESLRNCVNKEFFVT
i						SAPWSVIDQQAIHPELNGATYR
						YLPGFVCVAPGGLPAATEGIIPG
						GIPVTHNLPTVAHPSOAPSPNOP
						TKHGDNPEHPNEQSRECRKVII
						QIHLRPRDSEKLMNSEKTNLTV
				İ		FLADSGHMHY
25359	55727	A	25500	1	2595	
25360	55728	A	25501	561	1023	SGHDAYREQIQEYRVISLLLNP
						N\DHVNKCQSTNDAYPTGFRIA
1		1	l			VYSSLIKLVDAINQLREGFERK
						AVEFQDILKMGRTQLQDAVPM
		1				TLGQEFRAFSILLKEEVKNIQRT
1	l	1		1		AELLLEVNLGATAIGTGLNTPK
		1	1			EYSPLAVKKLALKSLAFVGNLF
25361	55729	١,	25502	2	227	LISI LAVKALALASLAF VUNLF
25362	55730	A	25503	262	428	
23302	22/20	ΙΑ	23303	202	420	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25363	55731	A	25504	389	2310	ATSGPPGRSLGSACTIWVLVWT
25505	33731	^	23304	307	2510	GSIPIYSFHGKVEKYMCFHNMS
						DDTWSAKVFFPLEVFGFLLPMG
						IMGFCCSRSIHILLGRRDHTOD
						WVOOKACIYSIAASLAVFVVSF
		ŀ				LPVHLGFFLQFLVRNSFIVECRA
	ŀ					KOSISFFLOLSMCFSNVNCCLD
						VFCYYFVIKEFRMNIRAHRPSR
						ATEEVSKNLVAMKEILYGTNE
						KEPQTEAVAQLAQELYNSGLLS
1						TLVADLQLIDFEASLGLHGLEQ
l						AVDLALPIAQAQGEVLNNGKC
					j	MDQFPVDVYQGGAGT\YVNMS
						TNEVLANIGLGLMGHQKGEYQ
				1		YLNPNDHVNKCQSTNDAYPTG
						FRIAVYSSLIKLVDAINQLREGF
1		1				ERKAVEFQDILKMGRTQLQDA
l						VPMTLG\QEFRAFSILLKEEVKN
						IQRTAELLLEVNLGATAIGTGL
		l				NTPKEYSPLAVKKLAEVTGFPC
l		l				VPAEDLIEATSDCGAYVMVQG
		l				ALK\RLAVKMSQI\CNDLRLLSS
l					1	GPPG\SSIMPAKVNPVVPEVVN
1		1			İ	QVCFKVIGNDTTVTMAAEAGQ
		1			1	LQLNVMEPVIGQAMFESVHILT
ŀ		l		1		NACYNLLEKCINGITANKEVCE
		1			1	GYVYNSIGIVTYLNPFIGHHNG
		l				DIVGKICAETGKSVREVVLERG
						LLTEAELDDIFSVQNLMHPAYK
25364	55732	Α	25505	133	375	
25365	55733	A	25506	3	505	ARGREGVSRRERPLLSARRLGA
				l		EWDSAGAETASGLQVPRLGGS
						WPQTSVFSAAVKARGCRIATLP
		l		1	1	MDLIGFGYAALVTFGSIFGYKR
		l		1		RGGVPSLIAGLFVGCLAGYGAY
		l		I	Ì	RV\SNDKRECKKCHWFTAFLPG
				l	1	LPSMGVRFKRSKKIM\PAGLVA
		1		1		GL\SLM\MILRLVLLLL
25366	55734	Α	25507	244	696	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
				sequence		
		_				
25367	55735	Α	25508	1	1442	MGQLHQAQASADIATSRLQQT
						SLTDVTRHQQFFSTYNTDDFIQ
						FTATYREQTRTRRQRQYAVNH
	l					VTFFFGKCTFRDRHRHRVIGIVL
						NIGLTFPAHQTQDGIGSTRSQR
l						QSRLVANKVATRNLVKHFDDD
						REANRGIQEAQTEHHHRGVLV
						NESRQRFGCQQHNRHRNHYRR
						HHHRQMVNHPYCSNYRIQRED
						GVKDDNLCDDHPETGIQLYASL
i		l				LLQVFFFAANIYGWYAWSRQT
				1		SQNEAELKIRWLPLPKALSWLA
	į .					VCVVSIGLMTVFINPVFAFLTR
		l				VAVMIMQALG\LQGVMPELQA
		1				DAFPVWDSCMMVLSIVAMILM
1					ŀ	TRKYVENWLLWVIINVISVVIF
1						ALQGVYAMSLEYIILTFIALNGS
		ļ.				RMWINSALIHQVVLDLIQQGIVI
						VWRDHLHMQRLHRLLAYHPC
		1				MYLVHIADFRDFPAHTRLQVQ
l		l				RFPAIPVHLQVIHSRYLSTVATR
1		l				YAESEATPVSGALGLLCPTLPIV
25368	55736	A	25509	133	375	
25369	55737	A	25510	2	471	AFAORETAGRRVGORWCGDCF
		-				RTPGTALGGSWPOTSVFSAAV
1		l		1		KARGCRIATLPMDLIGFGYAAL
						VTFGSIFGYKRRGGVPSLIAGLF
		İ				VGCLAGYGAYRV\SNDKRECK
		i				KCHWFTAFLPGLPSMGVRFKRS
						KKIM\PAGLVAGL\SLM\MILRL
						VLLLL
25370	55738	Α	2551I	3	432	NSRVDDFVAAQDAKGKKVAP
23370	33730	^	23311	٢	132	APAVVKKQEAKKVVNPLFEKR
						PKNFGIGQ\QRLLARAEKKAAG
						KGDVPTKRPPVLRAGVNTVTT
						LVENKKAQLVVIAHDVDPIELV
						VFLPALCRKMGVPYCIIKGKAR
						LGRLVHRKTCTTVAFT
25371	55739	A	25512	59	882	SRLKNASIFVASPSGKKAKGKK
233/1	33/39	Ι^	23312	139	002	VAP/APAVVKKOEVKKVVNPLF
		1				EKRPKNFDIGQDIQPKRDLTSFV
		1				
		1				KWPPLYQRQRAILCKWLKVPP
	1				1	EINOFTQALDHQTAALLLQLAH
	1	1			1	KYRSETKQEKKQRLLALAKKK
		1	1		1	AAGKGGIPTKRPPVLRAGVNTI
1		l			1	TTLLENKKAQPVVIAHDVDPIE
1		1			1	LVVFLPALCHKMRVPYCIIKGE
1		1			I	ARLGRLVHRKTCTTVAFIQVNS
1		l	1		1	EDKGALAKLVGAIRTDYNDRY
		1				NEIRRHWGGNVLGPKSVACIG
1	I	1	I	1		KLEKAKAQELATKLG

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25372	55740	Α	25513	1	833	I GTRPKMPKGKKAKGKKVAPAP
23372	33740	ľ`	23313	ľ	055	AVVKKQEAKKVVNPLFEKRPK
						NFGIGODIOPKRDLTRFVKWPR
				1		YIRLORORAILYKRLKVPPAINQ
1						FTOALDROTATOLLKLAHKYR
1		1				PETKHEKKORLLARAEKKAAG
						KG\DVP\TKRPPV\LRAGVNTFT
		l				PL\VENKKAQLVVIAH\DVDPM
		İ				RGWLSFLPAL\CRKMGVPYCIIK
1				1		GK\ARLGRLV\HRKTCTTV\AFT
		l				
l				1		QVNSESQRRLWAKLVEAIRTN
						YND\RYDEIRRHWGGNDLRPK\
		<u> </u>				SVARI\AKLEKAKAK\ELATKLG
25373	55741	A	25514	1	1176	MEKELVDHTGLFLSAHASEAL
l		1				ALKLMIYSEVAHKLRAVRSQH
1		1				PDMGVSLPLTPANSCPKTIERM
		l				RRSRELEREKDQSIETDHLPWA
	1	1				FGSTFLKTPLSCKTLMKYICYA
1	ļ	i				FIINLSFVKGVSAVTLMMSEES
		l				NMQMQFSVSITSGFGPFKSHIIA
						AIPNAERKESQGEKMAPAPAVI
		ı				KKQEAKEVVNPLFEKRLKNFGI
		1		1		GQDIQPQRDLTRFVKWPHYIRL
		1				QRQRAILS\AHKYRPETKQEKK
İ	İ			1		QRLLAQAKKKATSK/EDIPTKR
		i		1		PPVLRAGVNMVTTLVENKKAQ
	i i	1		1		LVMTAHDVDPIELAVFCLPAPC
1		1		i		CKKGVPYCIIKGKARLGHLVHR
1						KTCTTVVFTKVNSEDKGALAK
						LVEAIRTNYDRYDEIHCHWGG
		_				NVLGLKSVAHIIKLEKAKVKEL
25374	55742	Α	25515	2	524	
25375	55743	Α	25516	144	412	AGSCPFAAGPGPLGSGRCFVLIR
						FILIQNRAGKTRLAKW\YMQFD
	ŀ			l .		DDEKQKLNEEVHAVVTVRDAK
		_				HTNFVGVSGTFKIILPPLWLASN
25376	55744	A	25517	38	476	
25377	55745	A	25518	235	892	RSRVGTNRLFGETYPRASPGPQ
1						STALLTAYKKMTDLVAVWDV
						ALSDGVHKIEFEHGTTSGK/REV
ı		1				VYVDGKEEIRKEWMFKLVGKE
	1	1				TFYVGAAKTKS/ATINIDAISGF
1		1	1			AYEYT\LEINGKSLKK\YMEDRF
	1	1	1			KNPPILWVLHM\DG\ENFRIVLE
			1	1		KDAMDVWCNGKKLETARDFC
	1	1				KMSDTISDDTKVDEQERALSRT
		1		1		PEDKWNFRPAVPMRGERGSPS
1						HCGQAH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25378	55746	ĪA	25519	li .	1233	MOLKFPGROKIHISKKWGFTKF
25510	55710			1		NADEFEDMVAEKRLIPDGCGV
				1		KYIPNRGPLDKCHHGKCVATG
		1				TSYMCKCAEGYGGDLCDNKN
	1	l	1			DSANACSAFKCHHGQCHISDQ
		1	ľ			GEPYCLCOPGFSGEHCOOGLLG
			1			GVREMLRCKVRSNIVTMKAKL
				i	i	SFRICMTLTILANMWPRPILGG
		1				VDQIPIKPKSKVLYLGAASGTT
			1	1		VSHVSDIIGPDGLVYAVEFSHR
		ļ	l .			AGRDLVNVAKKRTNIIPVLEDA
		1				RHP/HQPDQ\ARSVALNAHTFLR
	1				NGGHFLISIKANCIDSTASAEAV	
		1		l		FASEVRKLQQENLKPQEQLTLE
		1				PYERDHAVVDYSSSSATEQRRT
						ENDSDKLTEVGFRKLVINFSKL
1			İ			KEDVRTHHKEVKNLEKRLDEW
						LTRINSVEKTLNDLMEAENHGT
1	i					KKYVTQAQASVAYLIKWKKG
25379	55747	A	25520	78	978	AAGHSAKKSCLSLLPAWSFPLG
		1				STRAQWHVRRLQARISGGGRH
		1		l	ŀ	RCGRRGQ\GKTRRRMGPMVVS
1		1		1		VEPHRHEGVFIYRGAEDALVTL
				ļ		NMVPGQSVYGERRVTVTEGGV
				1		KQEYRTWNPFRSKLAAAILGG
		1	}	1		VDQIHIKPKSKVLYLGAASGTT
		1		i		VSHVSDIIGPDGLVYAVEFSHR
l	1	1		1		AGRDLVNVAKKRTNIIPVLEDA
1		1		ŀ	1	RHPLKYRMLIGMVDVIFADVA
1		1		l		QPDQSRIVALNAHTFLRNGGHF LISIKANCIDSTASA\EAVFASEG
1		1		1		
1		1		ł		EKLQQENLKPQEQLTLEPYERD
		4.	25521	230	314	HACV/VGVYRPLPKSSSK OMPGNNPAFSA*CDAGASYQA
25380	55748	Α	25521	230	314	YVNSAIY
0.000	55749	١.	25522	1360	1848	RFRALV/TEGFSLRELFPVATVL
25381	55/49	A	25522	1360	1848	VASST\VTKRFIFLLAAD\VRLA
		1				LRRSI\THPFVRKQELTVYTLNN
	1			i	-00	ELENLLTNVVNQAQQGGKVMI
	1			1		DSVPVDPNMLNQFQSTMPQVK
1		1	1	1		EQMKAAGKDPVLLVPPQLRPL
						LARYARLFAPGLHVLSYNEVPE
						ELELKIMGALM
t	1		I			ELELKIMOALM

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25382	55750	Α	25523	91	1184	AAACSPPPPARLTYGSETLRGG
		1	i		1	DCSKMAAGCCGVKKQKLSSSP
						PSGSGGGGGASSSSHCSGESQC
l		l		1		RAGELGLGGAGTRLNGLGGLT
i		l			ł	GGGSGSGCTLSPPQGCGGGGG
		l				GIALSPPPSCGVGTL\LSTPAAA
						TSSSPSSSS/APASSSSPGSRK\M
		l				VVSTE\MC\CFCFDVLYCHLYGI
		1				\QQP\RPPRFTNEPYPLFVTWKIG
	İ					RDKRLRGCIGTFSAMNLHSGLR
	į .	1				EYTLTSALKDSRFPPMTRDELP
		1		ŀ		RLFCSVSLLTNFEDVCDYLDWE
				l		VGVH\GIRIEIHQCKKASKR\TA
	1					TYLPEV\AKEQGWDHIQTIDSLL
	1	i				RKGGYKAPITNEFRKTIKLTRY
						RSEKMTLSYAEYLAHRQHHHF
		1				QNGIGDPLPAYNHYS
25383	55751	Α	25524	3	154	
25384	55752	Α	25525	575	1707	TALLLTQSLFGGLFTQTHMKFG
		1				AVTRI*NRKTGNSKKQSTSPPPK
		1				ERSSSPATEKSWMENDFDELRE
	İ	ı				EGFRRSNYSELREDIQTKGKEV
	1	l			ļ	ENFERNLEECITRITNTEKCLKE
1		ı				LMELKTKARELCEECRSLRSRC
		1				DQLEDCLLKKLHSHQANPEFDL
		1				ITEHLTLCIRISIQIKAYLSLSKA
		ı				QSSLSHRPPTYLAYLFNGFRLF
		ı				KNLKAYLHPGEINSFIAHTKPV
		1				wwslhtdaheiwcrdsdlklv
		1				PTLPLIPLEAALRNITHSLSIPPP
						KNFRRPNTSTLFCVIFLINIRRQE
						YQASEPKPSHRIPCDLQRIKYLG
		1				IQLTRDVKDLFKENYKPLRNEI
	i					KEDTNKWKNIPCSWVGRINIVK
	1	ı				MAILPKPLLVIPRQTGSGMDPQ
		İ				QTSGDLQKCLTVLRKTNKQKAI
		1				ASTSRKRMTMQKLHLKEKLINS
	1	1				KDQRTNDKNHMIISIDAEKAFN
	1	1		1		KTEHRFMLKTLNKLEINSRWIK
	i					DLNVKPKTIKTLEENLGNTIQDI
		1				VMDKDFMTKTPKAMATKAKI
1		I				DKWDLIKLKSFCTAKETIIRVY
		1				RQPTERESIFVIYPSDKGLISRIY
	1	1		I	1	KELAIPGKGNSSNVSKDSKMSK
	1	ı	1		1	HQKMQGENKHD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence	1	
25385	55753	A	25526	110	569	TALLLTQSLFGGLFTRTRMKFG
	ł					AMTRIG\DLPWEINPLSSCSLLC
	i	l				EKHPPTTSGPQTDQPKKHLTNF
		ĺ				KSETKETCFIHEPKTLAPVTDW
						EGSLPLVFNHCRDGLSDHSATF
	ŀ					QGCQTMQGCLPWSFTLSGKSR
	İ			1		FSGEGANHHGHRASGNSHSGS
25386	55754	A	25527	2	464	LFGGLFTRRRMKFGAVTRIR\DF
						PWEINPLSSCSLL/CEKDPRTTS
1						GPQTDQPSKHLTNLKSASTPPP
	ł					YNPFITSPPHTRSGLQFRSTSSPP
<b>!</b>	l					APAQQFTLKKVAEAKGIVKVN
				1		APFSLSDLSQISVRLGSFIKYEKS
l		1				SPVHGSFGSNPETLYSPRP
25387	55755	A	25528	162	206	
25388	55756	A	25529	74	446	TAMLLTQSLFGGLFTWTRMKF
ļ		1				GAVTRIG\DLPWEINPLYSCSLL
	1	1				SRFKKIKACYHSPATSWPFKTY
	l					KLSLQLPHFTCPKTRQALQVSS
l		1				GAVPYQPNCFAYPPCGAQPVPS
						FVLNTFLHNSLCRA
25389	55757	A	25530	66	311	FGAVTRIG\DLPWEINPLSSCSLL
						REKEPPTTSGPQTNQAKKHLTN
						FKSGACYTCRKSGHWAKECPQ
						PGIPPKPRPICVGPH
25390	55758	A	25531	728	825	MKFGAVTRIG\DLPWEINPRSSC
						SLLHEKDPPM
25391	55759	A	25532	291	311	TALLLTQSLFGGLFTQTHMKFG
		_				AVTRI*NKKNNTK
25392	55760	A	25533	1	1056	
25393	55761	A	25534	245	487	TALLLTQSLFGGLFTQTRMKFG
		1			1	AVTRIG\DHPWEINPLSSCSLFQ
		1				EKDPPTT/SGPQTDQPKKHLTNF
					L	KSTSFVFSSCIPPP

SEQ ID NO:	SEQ 1D NO: of peptide sequence		SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25394	55762	A	25535	818	2391	TALLLTQSLFGGLFTQTRMKFG AVTRIGOIPWEINPPSSCSLEIP, RIPLLHFFGAGPSTPQFLLJISPS AASPALGQGQDLINLVFKVYN NRKKLQFLASTVTGTATSPAH KNRQTFEPQOPGVPEPPSIGAC YKCQKSGHQAKECPQLRIPHLS QWTGYPEPSIGAC YKCQKSGHQAKECPQLRIPHLS QWTGYPEPSIGAC YKCQKSGHQAKECPQLRIPHLS QWTGYPEPSIGAC GWTGYPEPSIGAC DSSVKLECFALGKIDDSIREKG AIRIKFSSILMRCNLVOSPILVG EGWTGARCQGKSSTANPKLSL KSRTSNKKMKAFMSALQATFE EETLORVNSFHHNVLDNCLLP NGGTCLFETAPPEWEQKIQNTH LSIVDNLLWECKASGRPPWY TWLKNGGRLNFEERIGIENGTLI ITMLNNSDSGYYQCAAENKYQI IVANAELRVLGSQLVHFRENGT ITMLNNSDSGYYQCAAENKYQI IVANAELRVLGSQLVHFRENGT
25395	55763	A	25536	425	749	TSGSQGTTTENQDELQIKFISAR HSQATEGINSTSAKFD IASLLTQSLFGGLFTWTHMKFG AVTRT/RGDLPWEINPLSSCSLL HEKDPPTTSGPQTDQPKKHLTN FKSAQLKASGK/DLQKPYQHFQ TLQQLLPLQWAPCYGPSSVSI

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25396	55764	A	25537	2	2204	I IDMIFTPGPPSTPKHKKSOKGSA
23390	33764	^	23337	<sup>2</sup>	2204	FTFPSQOSPRNEPYVARPSTSEI
		1				EDQSMMGKFVKVERQVQDMG
		1				
		ı				KKLDFLVDMHMQHMERLQVQ
	İ	i .			İ	VTEYYPTKGTSSPAEAEKKEDN
		l				RYSDLKTHCNYSETGPPEPPYSF
		ı			1	HQVTIDKVSPYGFFAHDPVNLP
						RGGPSSGKVQATPPSSATTYVE
		1				RPTVLPILTLLDSRVSCHSQADL
١,						QGPYSDRISPRQRRSITRDSDTP
		1				LSLMSVNHEELERSPSGFSISQD
		1				RDDYVFGPNGGSSWMREKRYL
		1				AEGETDTDTDPFTPSGSMPLSST
		1				GDGISDSTVPLFLSSEILQKQVG
		1				QSITSMLGFLSRGPSMKLCMGL
		1				ACVLSLWNTVSGIKGEAKKEK
						GMTFLPTTDSKKFFSLLSVTSYS
		1				SFAFHKFSVAVYNISNLKTVDP
		1				AKFPTRYCYCLNNRTNDLSDFT
		1				ALLVDIIGNSTSYLTEIFKSTSIL
		1				SVNQSNESDCIFICVMTGKSGR
		1				NLSDFWEIEEKYPIINYTFTSGL
		1				SGVLALLLTQSLFGGLFTRTRM
		1		1		KFGAVTRIG\DLPWEINP/LSSCS
		1		1		LLHEKDPPTTSGPQTDQPKKHL
						TNFKSAARPTFLGQGQVPLNPF
		1				SFTLSGKSCFPRRQEPPNRLFPH
		1				PNLLSLCPNPLFLCPNPFSTFLE
		1				GKNHHPHPFSVSQVFSLGLPPS
		1				LWEHSPMAHRLRVQPRQQPPDI
						HKQVISLQSGHSLLVKSQSWSQ
		<u> </u>				DPIKFQLPHHHKNTASVCINPSV
25397	55765	Α	25538	110	542	TALLLTQSLFGGLFTRTRMKFG
						AMTRIG\DLPWEINPLSSCSLLC
İ						EKHPPTTSGPQTDQPKKHLTNF
						KSETKETCFIHEPKTLAPVTDW
						EGSLPLVFNHCRDGLSDHSATF
						QGCQTMQGCLPWSFTLSGKSR
						FSGEGASCSLPG
25398	55766	Α	25539	1	781	MPLQPLATPFTSPGSPSVAQVT
						TNTGEPGFAQQEYAETPQTTAR
						PPHPHPALRALQASVHQTPRLG
						DCLGSSESATALHGSGEPNKLA
		1				PPGRPTERGGLFKCSVPLRTVR
		l				GCRAGLRGTETVPSSLQRQPAG
		1	l	I		DVGWINNKSTTALDRTPTDTQ
						RTRRPRPPKQKQRGRALKERPR
1		1		I		DSDSAREGPLKAVAGLFGGLFT
1		1	l	1		RTCMKFGAVTRIG\DLPWEINPL
			l			SSCSLLHEKDPPTTSGPQTDQPK
1	1	1	l			KHLTNFKSDLLSLATED

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25399	55767	A	25540	1571	1781	TALLLTQSLFGGLFTRTRMKFG
		1				AVTRIG\DLPWEINPSSSCSLLRE
		1			l	KDPPTTSGPOTDOPKKHLTNFK
		1				SA
25400	55768	A	25541	2150	3195	TVLLLTQSLFGGLFIWTRMKFG
						AVTRIG\DLPWEINPLSSCSLLH
1		1				EKDPPTTSGPQTDQPKEHLTNF
1						KSDED
25401	55769	Α	25542	4688	5149	TAMLLTQSLFGGLFTRTRMKFG
	İ	1				AVTR/IRGTDLPWE\INPLSSCSL
		1				LREKDPPMTSGPQTDQPKKH\L
						TNFKSGACYTCWKSGHWAKER
	i	1				PQPGIPPKPRPICVGPHLKIRTCS
		1				THLGQATPRAPGTLAQGSLTDS
		1				FPDLLGLAAEDSHCLIASEAP
25402	55770	A	25543	1	433	MAAFPAALNRPTRARARRRIS
		1				AHSAASAAAAVVVAGTARGM
1						VPGSEGP\CRA\GDEVADWEIVI
						EGTANLGPYFEGLRKHYLLPAI
		1				EYFNGGPPAETDFGGDYGGTO
		1				YSLVVFNTVDCAPESYVQCHA
						PTSSAYEFVTWLDGIK
25403	55771	Α	25544	1	235	
25404	55772	Α	25545	1	301	
25405	55773	A	25546	2	438	
25406	55774	Α	25547	1058	1494	KSVRLVVN/YLRTQKAVVRVSP
		1				EVPLQNILPVICAKCEVSPEHVV
		ı			İ	LLRDNIAGEELELSKSLNELGIK
		1			İ	ELYAWDNRRVPSAVPMQGPWP
		1			i .	AEHFLQVNEQPPAGSPSPCPSSS
		1				SSSSGLRGGMQTANGPACALTP
		1				TCAQTDCPCPTSH
25407	55775	A	25548	1	3965	RRFQPLPSAALRRCPPPARVGG
						RWVSAEKVNEGGSGGGGGQRL
		1		1		TRRARSTARVPAPGTMDAPRAS
		1				AAKPPTGRKMKARAPPPPGKA
		1	l	}		ATLHVHSDQKPPHDGALGSQQ
			1	1		NLVRMKEALRASTMDVTVVLP
		1	1	1		SGLEKRSVLNGSHAMMDLLVE
			1			LCLQNHLNPSHHALEIRSSETQ
		1	1			<b>OPLSFKPNTLIGTLNVHTVFLKE</b>
1		1	1	i		KVPEEKVKPGPPKVPEKSVRLV
		1	1			VNYLRTQKAVVRVSPEVPLQNI
		1		I		LPVICAKCEVSPEHVVL
25408	55776	A	25549	1	388	
	1	1	- 4 . 7			

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25409	55777	A	25550	1	1748	MVLARVARRPAGSAEAQASLA
23.10	153777	1.	23330	ľ		GKAALPERARKMSSPGIDGDPK
l						PPCLPRNGLVKLPGQPNGLGAA
		l				SITKGTPATKNRPCQPPPPPTLP
l .					1	PPSLAAPLSRAALAGGPCTPAG
1		1				GPASALAPGHPAERPPLATDEK
1		1				ILNGLFWYFSACEK\CVLAOVC
						KAWRRVLYQPKFWAGLTPVLH
		l		l		AKELYNVLPGGEKEFVNLQGF
1		l				TARGFEGFCLVGVSDLDICEFI
1						
ŀ						DNYALSKKGVKAMSLKRSTIT
						DAGLEVMLE\QMQGVVRLELS
		1			1	GCNDF\TEAGLWSSLSARITSLS
l						VSDCINVADDAIAAISQLLPNLA
						ELSLQAYHVTDTALAYFTARQ
						GHSTHTLRLLSCWEITNHGVVN
						VVHSLPNLTALSLSGCSKVTDD
1		1				GVELVAENLRKLRSLDLSWCP
1		1				RITDMALEYVACDLHRLEELVL
		l				DRCVRITDTGLSYLSTMSSLRSL
						YLRWCCQVQDFGLKHLLALGS
						LRLLSLAGETPVSALTLAVTTH PHLVHPPNLPGPCANSHPARTH
1						
						SPGSEAEEEGGAARPSPPEPWA
		1				ARTEPPSDPAAGCPLLTTTGLS
					ŀ	GLVQLQELEELELTNCPGATPE LFKYFSOHLPRCLVIE
25410	55778	١.	25551	1	377	MRRLTRRLVLPVFGVLWI/DGA
25410	33//8	A	25551	1	311	AVLLGNQEEVGGAD/WDLKCR
						PL/EVNVSKSDDTLKINGVEDH
1						KTIFDGDGKTYQNVQQFIDEGN
						YTSGDNHTL/SRPSLR*RQRP*IP
						CIRSQHGNRKRIPRRRIFI
25411	55779	A	25552	222	287	CIRSQUONKKIIIIGGUT
25412	55780	A	25553	2	918	GHCEVNRDWLQPLLHRVKEDY
25412	33780	1	25555	1	/10	TRVVCPVIDIINLDTFTYIESASE
					ł	LRGGFDWSLHFQWEQLSPEQK
		1				ARRLDPTEPIRTPIIAGGLFVIDK
						AWFDYLGKYDMDMDIWGGEN
						FEISFRYWMCGGSLEIVPCSRV
						GHVFRKKHPYVFPDGNANT\YI
1						KNTKRTAEVWMDEYKQYYYA
1		1			1	ARPFALERPFGNVESRLDLRKN
1		1				LRCQSFKWYLENIYPELSIPKES
1		1				SIQKGNIRQRQKCLGISKGRTTK
1		1		1		KPQT*S*A\LCQGQRRRCQSPRV
		1		1		WGLSHYTQADSFQGELVALFSS
	1	1		1		FTFVSLGAPVVSCSFARMGD
	1	1_	L			LILASPOALA ASCSLAKMOD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25413	55781	A	25554	8.4	2804	PRGSWRCRRDLKCRPLSHSDA DWDDLWDQFDERRYLNAKKW RVGDDPYREVCESTGGRVSD AIRAIPDTRHLRKKATSNSLSRQ QLASPLEPRSSYGGYTPGPHAIGP LWTSGSLKTPNHIDTVFAPGLP QPWFHLNYLRAMPSLSSAPKCT LLVYCTDLPPTSIIITFHNEARST LLTHREPRAVSTSQMAMTAAA LTPAPLRTYSVHLSCRAHQLVP MPQRKKYDETWVREHTKHSKI SLFPSCRLHFSCLSRRMAVGS GKFQVMGDLGEPFLRVRWLRI WTLGPDFHGSALNSVLNRIPT HLIREIILVDDFSNDPDDCKQLI KLPKVKCLKNNERGGLVSSRIR GADIAQGTTLTFLDSHCEVNRD WLQPLLHRVKEDYTRVVCPVI DIINLDTFTYJESASELRGGFDW SLHFQWEQLSPEQKARLDPTE PIRTPIIAGGLFVIDKAWFDVLG KYDMDMDIWGGENFEMMTVQ VLQPRRSEALICTWKVHLTRL QSPCPAMLAPEYAPEASVLVCT STALLIALVQAFFTGPQAKKLQ QSPCPAMLAPEYAPEASVLVCT SLTYTTLGSEISFRVWCGG SLEIVPCSRVGHYFRKHPYVF PDGNANTYIKNTKRTAEVWMD ESKLDLRYNLRCSFKWYLENI ESKLDLRYNLRCSKFWYLENI ESKLPTSTALLIALVQAFFTGPQAKKLQ GSPCPAMLAPEYAPEASVLVCT SLTYTTLGSEISFRVWCGG SLEIVPCSRVGHYFRKHPYVF PDGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYVF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYF PGGNANTYIKNTKRTAEVWMCG SLEIVPCSRVGHYFRKKHPYF PGGNANTYIKNTKRTAEVWMCG SCHARGRENGPO SCHAR
						LAWSGEETDNDQLDEGFYVYQ

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25414	55782	A	25555	11	2439	MPLKKKGDEPQMEKYIQERSM
		l				LAPPSCSDHRDTHSRCIPHIQRL
-		1				FQCPLGPWFQGEQRNQARGEG
	Ì	1				GALHPLPVTAGTVALPGAAQPT
		1				PARGNVTESLQGATVKLVCKK
		1				TSFIFIYCQHPAQCLALACDHEC
				ł		IDLCTHVASTSLCLRGYQGMKR
						TIERALTATLAQGTAVPPFPSDV
						PSOKDAAVRGKGDGSEWERTL
		l				TMKRSNLNSEKILPAILLLTEFP
		1			1	RHQSPCSFDKPHHPNTLGCWLP
		1				TVLETRGGTNGQSSGKREATLC
		1				PCPLLGLPISEEDCVPPALLLPPR
						G\LPPGLQLSWAPVPQFPPLGPS
		1				SLGIPA/LPLVLNLGCLPSLVCPP
						TSAHTSEVAPSLKSPAEPSPPAR
		l				LPRSHQPALSREMRHSDYSVSV
		l				HAICWDHDFYTLVTHYMNNTS
						PISSKRSSDKLNPHVLVVQDSM
						TILSLHNHLALAGQDMMVWEP
		1				RKTLQRRQQPDSSSHSPPPALV
						ECHPLEPEPLVAGIMYSFSGLQ
		1		1		GVGLRDRAVDETNKRNEKRTL
	1					EMSRVEALSSFENSEFGCPPSIN
		1				TREITGNSLEGNVKKGVSVPNC
		l				TAPGKRTEKKYSKIHEMVKHS
		l				GNCKRTDGIWEEYGWSWRLH
	ļ	l				MKKVFPGFMLVKGGEDAAPGT
		l				KEIKSVSGIFQRGKKKPRGRKE
		l				KNRKKRGFAFSKETNFVYLLIL
		l				VCLIGKVVVWLTSACAEKPKP
		乚				HGEATCRHSGPSAPLNFQPTRV
25415	55783	Α	25556	2	1178	AKCVEVCGKREPPSMSPLNQSA
	İ	1				EGLPQEASNRSLNATETSEAWD
	1	1				PRTLQALKISLAVVLSVITLATV
		l				LSNAFVLTTILLTRKLHTPANYL
		İ				IGSLATTDLLVSILVMPISIAYTI
						THTWNFGQILCDIWLSSDITCCT
		ı				ASILHLCVIALDRYWAITDALE
		İ			1	YSKRRTAGHAATMIAIVWAISI
		1				CISIPPLFWRQAKAQEEMSDCL
		I			i	VNTSQISYTIYSTCGAFYIPSVLL
		ł				IILYGRIYRAARNRILNPPSLYG
		1		l	1	KRFTTAHLITGSAGSSLCSLNSS
		1		1	1	LHEGHSHSAGSPLFFNH\VKIKL
		1		1	1	VTVALKRKEDSAARERKATKIL
						GIILGAFIICWLPFFVVSLVLPIC
		1			1	RDSWWIHPALFDFFTWVGYLN
						SLINPIIYTVFNEEFRQAFQKIVP
		Ļ	L	ļ		FRKAS
25416	55784	Α	25557	3	146	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25417	55785	A	25558	45	592	PSPPPPARAPSARTRRAPIPAAG
23417	33703	Γ.	22550	1.5		OGRARPPRTVSRCGSAAMATKI
		1		1	\	DKEACRAAYNLVRDDGSAVIW
	l					VTIKYDGSTIVPGEOGAEYOHFI
		1		}		QQCTDDVRLFAFVRFTTGDAM
		1		ł		SKRSKFALITWIGENVSELORA
						KTGTDETLVKEVVQNFANEYVI
l		1				SDRKELEEEFIKS\ELKKAVGAN
		1				YDAQTE
25418	55786	A	25559	249	1808	INGGTLTVTLSVTNOGAETLPF
230	33,00	١.	20000	1 '		GTGWHPYFPLSPOTRIOAOASG
1	1	1				YWLEREQWLAGEFCEQLPQEL
		1		1		DFNQPAPLPRQWVNNGFAGWN
		1		1		GOARIEOPOEGYAIIMETTPPAP
	l					CYFIFVSDPAFDKGYAFDFFCLE
İ		1				PMSHAPDDHHRPEGGDLIALAP
				1		GESTTSEMSLRAYNDTNRRSDK
				1		AFTPHPTCFPSNQNNSASPPTIT
1				İ		PDTATIAPVSHKAFAGNALRSII
						SDGKLTAGSVINNASAGAVPIP
						ASIIVCTIGISAAVGMTNKHPAT
						AIDTTHIMLLSTAPSAWGNNQT
				1		RAAPNTSLLAAYRFLIDSRDTE
		1		İ		TDSRLDGLSDAFSVFRCHSIMN
		1				CVSVCPKGLNPTRAIGHIKSML
		1		1	ŀ	LQLPPNVEKFAGAYLIQFALFQ
		1		1	ł	PLTHNRLMFFGAFADFLHADQ
	1	1		1		TFPGQITAAVKGQFVRRRLRFF
		1		1		AIISPSRTLS/YHTP*PRR*PR*SN
		1				FVTGRDAGRGLYNRQ*KTS/PS
		1		l		SICSA*GANPVVHHAMTVKFA*
		1			l	WQPIMKISSTSFPSMRPLSHMK
1						TINGLTTFVAW
25419	55787	В	25560	1	567	
25420	55788	Α	25561	1	741	MLILISPAKTLDYQSPLTTTRYT
		1				LPELLDNSQQLIHEARKLTPPQI
			1	1		STLMRISDKLAGINAARFHDWQ
1		1		1		PDFTPANARQAILAFKGDVYTG
		1		1		LQAETFSEDDFDFAQQHLRMLS
				1		/GLPYRLEMGIRLENA\RGKDLY
						QFWGDIITNKLNEALAAQGDN
						VVINLASDEYFKSVKPKKLNAE
				1		IIKPVFLDEKNGKFKIISFYAKK
	1		1	1		ARGLMSRFIIENRLTKPEQLTGF
						NSEGYFFDEDSSSNGELVFKRY
		L	L			EQR
25421	55789	Α	25562	3	320	IGLVLPISVRKRHAASARCLVN
				1	1	RRPMPRLHGLPGIPMRPPSLPRV
	1	1	1	1	1	RHAGTVFRRHRKRGSPMAY*Y
	1	1	1	1	1	GHSDVVKHREALVADLCHKAA
		1			L	FQLCRGQRHCRPALWRHR

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25422	55790	IA	25563	1600	1908	
25423	55791	A	25564	142	326	TRRAPSAISSRCCCNSHOTSKSS
25425	33771		23301	1''-	520	LVRTSSSLRSSSHLRTIA*CSSV
		1				HLPISCMQIRPSQAR
25424	55792	A	25565	1	1599	TIET ISCMOTO SOAR
25425	55793	Ā	25566	393	611	HSRAVCRFYPAKTSPFPVRRCR
23423	33793	l^	23300	1393	011	YROFVPR*HONE*AGRE*OPCSI
		1		1		ATVLPYRALPSLAHPRLSADOL
				1		PAAHL
25426	55794	A	25567	971	1628	TAKIL
25427	55795	Ā	25568	3	1895	
25428	55796	c	25569	1	2505	
25429	55797	Ā	25570	1	3345	
25429	55798	A	25571	457	790	PSFRRRYRQVVVISVRKRHAAS
25430	22/98	l <sup>A</sup>	255/1	437	790	ARCLVNRRPMPRLHGLPGIPMR
1					i	
1		1				PPSLPRVRHAGTVFRRHRKRGS
1						PMAY*YGHSDVVKHREALVAD
						LCHKAAFQLCRGQRHCRPALW
		_				RHR
25431	55799	Α	25572	1662	1767	
25432	55800	Α	25573	3	603	RLRSLFFLPDKMKLKDCVMIKK
						IFALPVIEQISPVLSRRKLDELDL
1						IVVDHPQPPSGDYTLHPLPPIIR
				1		ANRPNRFRINAGCTRTFTLSTPI
						NVFRHKILRTQEFPSLTHHAYSP
						LLVVINKAKFDGLSPEFQQALV
1						SSAQEAGNYQRKLVAED/LAK
					l	NHRRHERSGRGS/LSPISTAKPL
						ATHWGIRFATCLLKMCRRELIC
25433	55801	Α	25574	2271	2519	HRQLVIVFQQPLVSGFHEAELS
	i				l	LDDAKWVLHP\ARMLAFMYSM
					l	LMAVLFLRGCCFKVLTLPGRSA
					1	ISQSTSTSASSSRCGAPW
25434	55802	Α	25575	931	1213	
25435	55803	Α	25576	1	2767	MIAILSGLRCSIVANYIYAENNL
						FWLRLNNPKAIWCLRICTFATV
					1	IGGTLLSLPLMWQLADIIMACM
						AITNLTAILLLSPVVHTIASDYL
					i	RQRKLGVRPVFDPLRYPDIGRQ
					I	LSPDAPLTTTRYTLPELLDNSQ
						OLIHEARKLTPPOISTLMRISDK
						LAGINAARFHDWQPDFTPANA
	1	1		1	I	ROAILAFKGDVYTGLQAETFSE
	1		1		1	DDFDFAOOHLRMLSGLYGVLR
		1				PLDLMQPYRLEMGIRLENARG
1		1			1	KDLY\QF\WGDII
25436	55804	A	25577	395	467	
25437	55805	A	25578	1	675	
25438	55806	A	25579	<del> </del>	4014	
-5455	122000	٠.		J	Little	L

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
i	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
25 420	55007	<del> -</del>	25580	1802	2385	I RKISAPALIKSRTG*EMASLPTS/
25439	55807	A	23380	1802	2383	
						HDKQIEQALADVDVPIVGVGGS
						YHLAESYPPVHYIATDNYALVE
						SAFLHLKEKGVNRFAFYGLPES
						SGKRWATEREYAFRQLVAEEK
						YRGVVYQGLETAPENWQHAQ
1						NRLADWLQTLPPQTGIIAVTDA
l		i		1		RARHILQVCEHLHIPVPEKLCVI
		ـــ				GVMNRRTVRSPFRESLKISP
25440	55808	Α	25581	1	1568	MVKQLKLVSFLLRPGDSKQGY
İ		1				DKHSSLQVGLMIPVCSCIRFRKF
		ł				SEQSFKFEEGTDAAFHGFWLW
		1				PCTMLNVTPIKGMMTVIYEFPV
1						DSETTLQNYDIYFTNEELTDEQ
l						KSLIEWYRDVFRPEDLRLVESV
		ŀ				QKGLKSRGYRGQGRIMADSSG
		1				SGISEHAWCMSRGAQGRQFCK
		1				GAKMSQVLITGATGLVGGHLL
		1				RMLINEPKVNAIAAPTRRPLGD
		1				MPGVFNPHDPQLSDALAQVTD
ļ.		ı				PIDIVFCCLGTTRREAGSKEAFI
					i	HADYTLVVDTALTGRRLGAQH
		1				MLVVSAMGANAHSPFFYNRVK
						GEMEEALIAQNWPKLTIARPSM
		1				LLGDRSKQRMNETLFAP\LFRL
						LPGIILLEELNWKTWAERWNS
1		1				MLGPRAVKVFFSLAFLPGTLEP
	ł	ı				AQILFPTQRQGKKAALLLGLW
1		1				KLEIYSDNRRSPEVSTAWNSPP
		1				TGKLDNKQYMIMIPRKRETNTT
		1				TRGASNARLDPPSRKGYKGHY
1		1				ETIGHALEHDKOSOGSYNVEHT
		1				IKROTPRVRRCTSIIAGIYQELG
25441	55809	В	25582	I	1560	
25442	55810	Α	25583	1	2115	
25443	5581I	A	25584	3036	3957	RIYDAVSEPAEPVDCPRNPVCR
						FY*QYRDHRGKTVYDVASGDA
					l .	LFISELG/PLPENVTWLSPEGEFQ
1		1				KWN/GTAWVKDTEAEKLFRIRE
1						AEETKNNLMQVASEHIAPLQD
1		1				AADLEIATEEEISLLEAWKKYR
1						VLNSRAMALILTPDLIRSNTACE
	1				l	CSSFVLAGOTAKAAADDGLFPF
		1	l			IFARVNKAGSPVAGLIIVGILMT
	1	1	l		I	IFQLSSISPNATKEFGLVSSVSVI
	1	1	1		I	FTLVPYLYTCAALLLLGHGHFG
	1	1	l		I	KARPAYLAVTTIAFLYCIWAVV
	1	1	l		I	GSGAKEVMWSFVTLMVITAMY
		1	1		1	ALNYNRLHKNPYPLDAPISKD
25444	55012	+	25505	ļ, —	2490	MEN LINKLININY TYLDAPISKU
25444	55812	A	25585	1	2490	

SEO ID	SEQ ID NO:	111.4	SEO ID NO:	Nuclcotide	Nortestide Innetion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25445	55813	Α	25586	368	761	LYCEACIMAFRMSEQPRTIKIY
						NLLAGTNEFIGEGDAYIPPHTGL
			l		i	PANSTDIAPPDIPAGFVAVFNSD
i			ŀ			ESSWHLVEDHRGKTVYDVASG
	l				i	DALFISELGPLPENVTWLSPEGE
		l				FQKCSGTTRVKNAKA*TLF
25446	55814	A	25587	1	809	MPVSSYERGHAEKRVVQECCG
					\	INLTSSANTILSDCERVNGYCVL
					l	CHTTRALVTGNHHRNAVYAET
						PSNSRINYIVSSHNAFRMSEQPR
						TIKVYNLLAGTNEFIGEGDAYIP
					i .	PHTGLPANSTDIAPPDIPAGFVA
ļ						VFNSDESSWHLVEDHRGKTVY
						DVASGNALFISELGSLPENVTW
						LSPEGEFOKWNGTAWVKDTEA
						EKLFRIREAEETKNNLMQVASE
				1		HIAPL\QDAADLEIATEEEISLLE
						AWKKYRVLLNRVDTSTAODIE
						WPALP
25447	55815	A	25588	1	2301	
25448	55816	Α	25589	718	1131	
25449	55817	Α	25590	279	513	CRRIDTWQPIYQTCGRLMAVEL
						LTVVTHPLNPSQRLPPDRYFTEI
						TV/SHRMEVVKEQIDLLAQKAF
						SLAYLSPCESGL
25450	55818	A	25591	1	407	PQDNAKKLRPHQLSSDEGHTG
1	İ					MGGTAKDVGFVSMRTYSWISS
1						ALPKRLGGGVMPIGATIATEEV
1	ŀ	l				FSVLLGNPFLHTTTFGGNPLAC
l						AAALATINVLL\GRTYRLRLSK
l						KAICCWTVSVNWRGNIPIWYR
1						KRVVKGC
25451	55819	Α	25592	1	2079	
25452	55820	В	25593	1	700	
25453	55821	Α	25594	1427	1845	ACISGFSTETSASGRVSVITDAS
1	1		l			LFRVLPRVCGMAVAATKRSGRI
						TTSEALCCANQLRRRPCVSPTR
1			1			STPSWLSCAV*ICTSGTT*MKR
l						VPNARHCWICSSLIPHSGLHPQP
1			1			ITAKFAPIALSSSVTSPFSSVTFG
		L				*IN
25454	55822	A	25595	2	295	
25455	55823	Α	25596	1	900	
25456	55824	A	25597	1	1422	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	i	1		sequence		
25457	55825	A	25598	2	535	I IYGNREORAVSSHTNTWVNRAL
				Ī		ARGWSSLGYRWWVSAWTPSR
	1			ŀ		RFISOLMSRPVDASAAKVKRSA
	l	l				SVPCGSIPFGNCFSVRLRILSASC
	i	1		İ		GCIILPVRFSSSSGSEIPSTISSGSI
	l	ı				TLPLDLDIFWPSSSRIRPVM*TV
		1		l		WNGTCGLPFSSLMKCMVIMIM
						RAIOKKMMSKPDTITLVGWN
25458	55826	A	25599	442	1368	RRTMAAFACGVVRDASEVIRPS
		ľ.				STLVPLVGEKHAKGLFGTIVDN
		l				FYLVALIFAMGTSLGLATPLVT
	i	l				ECMOWLFGIPHTLLGFI/LYNAI
		l				CVACGLQKGVRIASDVRSYLSF
	l					LMLGWVF\IVSGASFIMNYFTD
İ				i		SVGMLLMYLPRMLFYTDPIAK
						GGFPQGWTVFYWAWWVIYAI
		1				OMSIFLARISRGRTVRELCWIL
	ì	l				WTVLGSNTLLLIDKNIINIPNLIE
1	i .					OYGVARAIIETWAALALNNGN
		1				MWGFFILWFIGPGTLVNAWON
1	i	ļ	i	Ì		RAQFVHHILRRNGIADGFRHLA
		1	i		1	ALTIHGKAVGOYLTIRRFTLHR
25459	55827	Α	25600	2468	3907	
25460	55828	Α	2560 I	3	3738	YKTNYTDNSEYYANVGFNVKP
		l				VKRDGKMSVMSDPDTAIYPFPP
		l				KPTPLSIDEKAYYREKIKRLLTE
						RNAVMVAHYYTDPEIQQLAEE
		l				TGGCISDSLAMARFGAKDPASN
		l				LLVAGGGTCRSVVINAVFSYVT
		1				NVWGWAFEWYMVVMLFGWF
						WLVFGPYAKKRLGNEPPEFSTA
		1				SWIFMMFASCTSAAVLFWGSIE
					l	IYYYISTPPFGLEPNSTGAKELG
		1	[			LAYSLFHWGPLPWATYSFLSV
l	I			l		AFAYFFFVRKMEVIRPS
25461	55829	Α	25602	1331	1456	
25462	55830	Α	25603	549	588	
25463	5583 I	Α	25604	19	1629	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
					L	
25464	55832	Α	25605	1	1995	MVGVRFALGLMWLTLIVAETIS
						ANSGIGYLAMNAREFLQTDVV
	l	l	1			VVAIILYALLGKLADVSAQLLE
		ı				RLWLRWNPAYHLKEATLSAEQ
		ı				AARIREMTVITSSLMMSLTVDE
		1				SDLSVHLVGRKINKREWAGNA
		l				SAWHDTPAVARDLSHGLSFAE
		l				QVVSEAHSAIVILDSRGNIQRFN
		1				RLCEDYTGLKEHDVIGQSVFKL
		l				FMSRREAAASRRNNRVFFRSGN
						AYEVENVPDPGVEQADDIILRIT
		1			1	ATAICGSDLHLYRGKIPOVKHG
		ı				DIFGHEFMGEVVETGKDVKNL
		l				OKGDRVVIPFVIACGDCFFCRL
		1				QQYAACENTNAGKGAALNKK
		l				QIPAPAALFGYSHLYGGVPGGQ
		l				AEYVRVLKGMWGRLNDAOPG
		l				FRSSRPLRYGAGIMTLLNISGLS
		1			1	HHYAHGGFNGKHQHQAVLNN
		l				VSLTLKSGETVALLGRSGCGKS
		l				TLARLLVGLESPAQGNISWRGE
		l	1			PLAKLNRAQRKAFRRDIQMVF
		l	i		ł	ODSIST\VNPOPNRLHIV/RFPLT
		l				
		l	i			RLNQYQPSFSTDLYHGTLKPAS
		l				LTMSGVVLLGRM/PRKTSQQV
	1	l				QWA\CIARTDKASMPTVYSESL
		l				FVEPLERVLYVAVILTQIIRGLR
		l			1	DTEIETINPDIAVHFALCFHGLG
		l				SIPTKGAEKSPFLTIHKVRVKPD
		l				IPSPVSIMAPCRAHPTCEALFNN
		ᆫ				STALHSPWFCDSL
25465	55833	A	25606	179	371	CVLQYTHWPACSTVA\HSRRW*
		l				NRRRLRLAVTKTGSLFSHRCAG
						ARLAFSKKLRCRDALPASRS
25466	55834	Α	25607	544	983	SVQNPRVNWIHAALQRTGRGR
		l				RRHEQHGEDHFVNGAAGVHQ
		1				AANGLVNPPRHQVFGAHQAKG
		ı			l	DGENHRQRGAPDGDLQRDGHF
		1	ļ			GEVILPLAEIGREEVGGERRHV
		1				AAVFDQ/S*AGPFPRPATRRPTR
		1				RVQRPSSEARTSCAWVGRW
25467	55835	В	25608	1	1746	
25468	55836	Α	25609	1	858	
25469	55837	Α	25610	98	288	LCRNNGEPLARSGAAMGALLD
ļ		1				REHSRHP\PDLEG\GSQQQVCDS
	i	l				GGSVTAANTSGGQQVKAQLEL
	L	Ь			·	

SEQ ID	SEO ID NO	Mes	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
25470	55838	Α	25611	1934	2812	RPQTYSDAQPGFRSSRPLRYGA
		1				GIMTLLNISGLSHHYAHGGFNG
					1	KHQHQAGLNNVSLTLKSGETV
		1				ALLGRSGCGKSTLSRVLVGLES
						PAQGNISWRGEPLAKLNRAQR
		1			i i	KAFRRDIQMVFQDSISAVNPRK
		1				TVREILREPMRHLLSLKKSEQL
		1				ARASEMLKAVDLDDSVLDKRP
		l				PQLSGGQLQRVCLARALAVEP
		l				KLLILDEAVSNLDLVLQAGVIR
						LLKKLQQQFGT\ASLFITHDLRL
		l				VERFCQRVMVMDNGQIVETQV
						VGEKLTFSSDAGRVLQNAVLP
		l				AFPVRRRTTEKV
25471	55839	Α	25612	1	515	MLAVECRSLPFPPLVQPVRYTD
		1				VTVKDDYNPETEQYTLTISQRT
						PATPDQAEKQPLHIPFAIELYDN
						EGKVIPLQKGGHPVNSVLNVTQ
						AEQTFVFDNVYFQPVPALLCEF
						SAPVKLEYKWSDQQLTFLMRH
		l				ARNDFSRWDAAQSLLA/ILHQA
		<u> </u>				ERRASSARSAAVSAGACG
25472	55840	Α	25613	1	1053	
25473	55841	Α	25614	1	1521	
25474	55842	A	25615	430	1120	QTASTFLKRGKCASRQSKLCGN
	İ	1		1		RRRKRRQRISSYCLLRGTACSP
		1				AHQPDAFHQKRGNAGRHYAEC
1		Į.				VLQYSSCSTRYS\PGR\TQLINLF
		1				EVADGKRLVDLPGYGYAEVPE
		1				EMKRKWQRALGEYLEKRQSLQ
1						GLVVLMDIRHPLKDLDQQMIE
1						WAVDSNIAVLVLLTKADKLAS
						GARKAQLNMVREAVLAFNGD
l .						VQVETFSSLKKQGVDKLRQKL
		<del> </del> —		ļ		DTWFSEMQPVEETQDGE
25475	55843	Α	25616	407	1176	AYSTSLRVKICRKTSTLLLRSRV
						TQIRSNTKSTKRAAHCSLTASC
						PPRCSIHATTVTSTTPCLWRRIA
			İ			TMLRALARLLLRICFSGRTLKIA
					l	CLLLLVAGATILIADR/AALYHA
						GKVKWLLVSGDNGRKNYDEA
						SGMQQALIAKGVPAKVIFCDY
					I	AGFSTLDSVVRAKKVFGENHIT
					1	IISQEFHNQRAIWLAKQYGIDAI
		1				GFNAPDLNMKHGFYTQLREKL
				1		VIAKGHGSLLTDLPVAKAGTM
		L				WAIEIDDVARHSRSHL
25476	55844	A	25617	3	168	NPFYSAMR\KSAGIRHILARHVE
		l				GASHMAEGYTRATAGNIGVCL
						GTSGRCCFRLCW
25477	55845	В	25618	169	1227	

SEQ ID SEQ ID NO: NO: of peptide h					Amino acid sequence ( X=Unknown,
sequence	lou	in USSN	location of first	codon fur last amino acid	*=Stop cudun, /=possible nucleotide
		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			sequence		
25478   55846   /	۸.	25619	489	740	AIARSCADYHPANFRHHRAAA
					RAGDDYLSRRAERQPGAKAGG
					SRLRAGKRPCSAFRYW*CAAG
			ļ		E*SVGEKIMAGDVISPKRRL
25479 55847 A		25620	146	475	
25480 55848 E		25621 25622	662	191 4568	
25481 55849 A 25482 55850 A		25622	20	2661	AGHIHRPRYOHGVGTESTSIMS
25482 55850 7	٩.	25623	20	2001	VASRSAERVFLTKFESWKNFPI
					NRGRNKMAKMRAVDAAMYV
					LKKEGI\TPAFG\VPGAA\INPFY
1 1 1					
					SPMRKHG\GIRHILARHVEGAS
					HMAEGYTRATAGNIGVCLGTS
					GPAGTDMITALYSASADSIPILC
					ITGQAPRARLHKEDFQAVDIEA
					AKPVSKMAVTVREAALVPRVL
					QQAFHLMRSGRPGPVLVDLPF
1 1 1					DVQVAEIEFDPDMYEPLPVYKP
					AASRMQIEKAVEMLIQAERPVI
					VAGGGVINADAAALLQQFAEL
					TSVPVIPTLMGWGCIPDDHELM
					AGMVGLQTGHRYEKYTEGRKI
					VHIDIEPTQIGRVLCPDLGIVSD
					AKAALTLLVEVAQEMQKAGRL
			l		PCRKEWVADCQQRKRTLLRKT
					HFDNVPVKPQRVYEEMNKAFG
			l		RDVCYVTTIGLSQIAAAQMLHV
			l		FKDRHWINCGQAGPLGWTIPA
			l		ALGVCAADPKRNVVAISGDFD
l.			1		FQFLIEELAVGAQFNIPYIHVLV
			1		NRPAANGAQGSCHPDAPAVFR
					SSIFIRKSEEKLVVTMNELSASR
					ALPEETMPGRFELKPTLEKVLH
				1	APDNFLFMDPLPPMHRRGIIIAA
			l		IVLAVGFLLPSDDTPNAPVVTR
					EAQLDIQSQSQPPTEEQLRAQL
					VTPQNDPDQNLYRKASQKSSR
					KLPKRDLPHILTPFRAPMASVC
					AKRKGQVLHQQYSLKKYRYK
25483 55851 A		25624	1	570	
25484 55852	4	25625	312	873	APRSRVQAKIAASNTGELNALQ
			l		QLGFS\LVEGEVDLAL\PVNNA\
1 1 1					SDSGAVVA\QETDIPA*RQLASA
1 1 1			1		AFAQSRFRAPWYAPDASSRFYA
			1		QWIENAVRGTFDHQCLILRAAS
			l		GDIRGYVSLRELNATDARIGLL
					AGRGAGAELMQTALNWAYAR
					GKTTLRVATQMGNTAALKRYI
			l		QSGANVESTAYWLYR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25485	55853	A	25626	2	922	FSPPGLHDAGEAVFWRVNKSA
25405	33033	ľ.	25020	[		NYGVLDKLARGYADLSKAESO
					•	WDEMMRTAGSLKLGTIHASINS
					1	LFENITAAPADPILGLADLFRAD
						ERPGKINLGIGENPSCCRTSSSP
						VFDAAIWPAPVNNASDSGAVV
	İ				l	AQETDIPALRQLASAAFAQSRF
				ł		RAPWYAPDASSRFYAQWIENA
				ł		VRGTFDHQCLILRAASGDIRGY
					1	VSLRELNATDARIGLLAGRGAG
				•	1	AELMOTALNWAYARGDHMI/R
1						I*RTAGGGNRTRLYAVGNG*RQ
						TVWRWRFYPSLPAVAGATFWO
						RQSVTDAVLHRFAGDGGAAAR
						YPAWR
25486	55854	Α	25627	911	1441	AIPSISCFLLAIKALILSAIWLNA
				i		TPSRSKLEPSSKWIRSLRCPSPN
	l	l			1	RCAAASSFNISCQWFLSEYGPP
						NQVASGKTSPFVIVFKQPRYRA
						VTKPNCRLMMRNGCSTLARML
						PVMYAMLMPVLFLRGCCFKVL
						TLPGRSAISQSTSTSASSSRCGA
						PW*PASAETNCSSPCSRLPS
25487	55855	Α	25628	I	1247	MERVLDNLLNNALRYCHSTVE
						TSLLLSGNRATLIVEDDGPGIAP
						ENREHIFEPFVRLDPSRDRSTGG
						CGLGLAIVHSIALAMGVNAQA
						DFMKLTGADEQIAAYCFKMPF
						VFHLIEEVSRNFGYALCLINIDH
				l	1	KAALNITQRTAANILLDGQMQ
						HAVDQAFTQRTARQGSTFVQY
				l		ARLARKLATANICWSYFVPVR
1				l		ASIEPLTWENAFFGVNSAIVRIT
		i				SEAPLLTPDALAPWSRVQAKIA
				l		ASNTGELDALQQLGFSLVEGEV
1						DLALPVNNASDSG\AVVAQETD
		1				IPALRQLASAAFAQSRFRAPWY
				i		APDASSRFYAQWIENAVRGTFD
			1			HQCLILRAASGDIRGYVSLREL
		1	l	I		NATDARIGLLAGRGAGAELMQ
l						TALNWAYARGKTTLRVATQM
		1	1	1		GYTAALKRYIQSGANVESTAY
L		L.		l.	100.5	WLYR
25488	55856	A	25629	1	1925	
25489	55857	A	25630	402	664	TARRLLFFRD/RTARVAVPNAA
		1	1	l		VVLPFPLPVKTMIPRSLGRRRS
						GGICRPLGYLVAMDAIDGLQN
L				l	L	ADNSNGESRIATSSFRSRSARR

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nuelcotide insertion)
25490	55858	Α	25631	920	1237	IARPGCHLSHCHSEPSGRLSK*P
						FSCNSLKTGDF*PI*GLIQTQIFS
					İ	PFAFRRIIPSGSGKVSGSHSKS
		1				HHWKAFIQKQSKWKTCSGRLR
		l				SAIPSIKLFTVASS
25491	55859	Α	25632	1	1341	MVHRFGIRVRFVALGFYQDVIL
						PVRAHRHEWGHYVHLCASIQR
					1	QIDVSFARDATSHSSCPVTGVR
			1			FWGYPFAANKVVIAGFELEGET
						MTRPGLICAEGGLLVMIVSLRS
		ļ				ELYDSYHEFTRQRVTEIVEKAA
		l				NHLPAVVEMMTLHRCAINRHN
		l				FVRRVGPAGISTFFASSPDGVN
		l				AGFSTFRVVFTCQRSRPLQRHS
						HADVQTATLLLNTVNLEQKQA
		1				NAILSGLSDMIPNSSPESAPEIQL
		l				LQSRMILGKTIAELNLRDIVEQK
		l				YFPIVGRGWARLTKEKPGELAI
		l			1	SWMHIP*TLSKNRPTPFS/DGLS
		l				DMIPNSSPESAPEIQLLQSRMIL
		1				GKTIAELNLRDIVEQKYFPIVGR
		1				GWARLTKEKPGELAISWMHIP
		1				QLNGQDQQLTLTVGENGHYTL
		ļ				EGEEFTVNGMVGQRLEKDGVA
						LTIADIKAKPGTQFVLSQRTELE
		1				AINALQETFTVSERSKESGMLE
		1				LTMTGDDPQLITRILNSIANNYL
		l		1		QQNIARQAAQDSQSLEFLQRQL
	1	l		1		PEVRSELDQRKKNSTFIASSAIR
25492	55860	Α	25633	170	935	LTQEDTRINLIPMAVESLHLPTQ
		l				MLINGGETYA WRNWKRGGQY
						KSATLNTGQPHVRARELVDSD
					į.	TLASDAARLTCRHGLALPALFT
	1	1			1	LIAVVTSLLSPQFIRQILWSRLT
	1	1			l	KTR*AGDQLDAYSTTEWSGSA
	1				I	TDTHGWGKRPLYTGR*RVHRQ
					1	WYGRPASGKRWRCADYRGH*
						GQTRNTVCPEPA YRTGSD
25493	55861	В	25634	42	755	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of loca	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
	1	<u> </u>				
25494	55862	Α	25635	793	2127	RYCKGTVMDQIRLTHLRQLEA
		1				ESIHIIREVAAEYSNPVMLYSIG
						KDSSVMLHLARKAYYPGTLPFF
						LLHVDTGWKFREMYEFRDRTA
1						KAYGCELLVHKNPEGVAMGIN
	1					PFVHGSAKHTDIMKTEGLKQA
	1					LNK/YTTSRAKERIYSFRDRFHR
						WDPKNQRPELWHNYNGQIN\K
				i		GESIRVFPLSNWTEQDIWQYIW
	i					LENIDIVPLYLAAERPVLERDG
	1			ľ		MLMMIDDNRIDLQPGEVIKKR
	ì	1				MVRFRTLGCWPLTGAVESNAQ
		1				TLPEIIEEMLVSTTSERQGRVID
		1				RDQAGSMELKKRQLIELIINVH
	į.	i				NLLKNGFGFQVKVNRIALLAIN
	ľ		ì			VEFFFRLVQLAAHFSSGTLAQD
						KLCSWFGLNVRDSQRNAIFFQT
		1				LADHTIDGELFTFQCIVAVFPNL
		1				PIYSYATIYVSSSSIPISSEESPSIR
1	1					FACSQTSRQPPVSDSRFCVSQV
25495	55863	Α	25636	360	566	GAETMGDLLWVVGILLMCSLS
1		1				TLVLVWLDPRLKS*RT*A*CGA
		1		ŀ		LTSHQAINNGRNEKRKPIRESDF
		1				LKA
25496	55864	Α	25637	1	312	LLRKSVSVIIKGTIKTIIGFMLLQ
		1				AGSGILTSTFKPVVAKMSEVYG
		1				INGAISDTYVMQDG*APELGLS
		1		1		PGRFLRHDTDFVLQLGIVMVRL
		1				AGDGSLNINAQANN
25497	55865	Α	25638	517	796	PTARFGWVKGVDLPAD/CNRQ
	1			1		DRFAIDVRVQGS*\WGCVLPLF
1	1	1				RVLLFVSCALLLVSVSCVLRLL
	1					FCCSS\LSLFLSGLGGGRSPKAG
				l		DVFRDRR
25498	55866	Α	25639	47	411	AIKVRELSIKLKMC/YSLIKTLH
	1					G*KYRNFMVIGSMVFGKKAITH
						VAGVKRRTAVVVGFKVFDIQR
1						SQFRIVVTGDLAQLLYRVIKVIT
				1		CGHFVRQHGIVLCAGVLHVGD
		_				RYQAHVKTLGGLI
25499	55867	Α	25640	I	1488	
25500	55868	Α	25641	2	298	CCICL/YSYAPIDVW/WG/WNTA
		1		1		GQVQAA*TLKAASSSIVTIPLRN
		1				TFIFNYSLSGLRRRRLIIRSRRHS
	1	1		1		THASNITLIAASTASRIGWFASA
		_				YHTRSNHGR
25501	55869	С	25642	I	2064	
25502	55870	В	25643	1	1116	1

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25503	55871	Α	25644	312	620	SACRCCLVVVPLFVCL/GSSLSL
						APTFPLLASFSSSRASRVVAFGL
						GSLRAGSALCLPCAAVVLALRS
						AGTCLEWWWWHSVVLPPETK
						RLPSTSLIPYPASVSI
25504	55872	Α	25645	2	2237	
25505	55873	Α	25646	692	6383	RMSRSSDYDQYRSRNALIRRHI
		1				EKMDASLHVGTKEFDISKVSEV
	1	1				DSVDDLLIDNAARYLLKDWKG
1		1				VGELVNGVEVALEYTAERGIAL
		1				LKQNPELYWQILAEAASIAQVG
		1				GEVWIAPKFERNGLRLLANSEI
		1				GAASQLQTYHRVDPGRPCKLD
	1					LSGGMSQRVMIAMAIACRPKL
l						LIADEPTTALDVTIQAQIIELLLE
l						LQQKENMALVLITHDLALVAE
						AAHKIIVMYAGQVVETGDAHA
1				l		IFHAPRHPYTQALLRA
25506	55874	Α	25647	856	1467	
25507	55875	Α	25648	1823	2014	SQEIALMQFRPRLTGASGSP*RP
1		1				PHRTLLRSDQNAATIPQKRASA
						LIPLMRILPVRYGHLLLC
25508	55876	Α	25649	1	218	
25509	55877	A	25650	2740	3293	IFA VNLILQCHVGGTHHQRFLL
		1				FAGNGDAGNQIRERFPNAGG/E
		İ				LQSPDVALLLRPAFWRRPQSSA
						AAAHGE*SRGSVPEAPYTRRQF
						ALPAPPIKCAPLPERQRPSVPSR
	1					HLRLPACPGYKNRASSAKPSYS
	1		l			FLAQRQHLQRLSPLPQNQNLPQ
			1			RRRDQRQRAGAMSARVPDLISS
						SRSMRRTS
25510	55878	В	25651	I	1875	
25511	55879	В	25652	1	2981	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25512	55880	Α	25653	I	1649	MTFRNCVAVDLGASSGRVMLA
		l				RYERECRSLTLREIHRFNNGLH
		1				SQNGYVTWDVDSLESAIRLGL
		1				NKVCEEGIRIDSIGIDTWGVDFV
		1				LLDQQGQRVGLPVAYRDSRTN
		1				GLMAQAQQQLGKRDIYQRSGI
		İ				QFLPFNTLYQLRALTEQQPELIP
		l				HIAHALLMPDYFSYRLTGKMN
		ĺ				WEYTNATTTQLVNINSDDWDE
		l				SLLAWSGGQQSLVWVAEASGE
1						WGVLACTLFAWNRNYFVLLFV
						GVFLSSFGSTANPQMFALAREH
						ADKTGREAVMFSSFLRAQVSL
						AWVIGPPLAYALAMGFSFTVM
		1				YLSAAVAFIVCGVMVWLFLPS
		1			i	MRKELPLATGTIEAPRRNRRDT
						LLLFVICTLMWGSNSLYIINMPL
		l				FIINELHLPEKLAGVMMGTAAG
						LEIPTMLIAGYFRQTSGPTAYGR
		l				SVGRIRRSRRIRQSCYYQRIFSL
		1	]			LACELANALERPENFCGMHFFN
		1				PVHRMPLVEIIRGEKSSDETIAK
1						VVAWASKMGKTPIVVNDCPGF
						FVNRVLFPYFAGFSQLLR/ERRG
		1				FPQDRQSDGKTVWLADGPGIS
						AGRCGH
25513	55881	A	25654	1590	2855	RNLLGEAADPVSGPHSAIYRPD
120010		ľ.		1.070		WPKSGDCACQGPIKGSANRPA
		1				VVPHVHGP\SEDLEVFLNVFGE
		ı				LPOPLIDTOILAAFCGRPMSWG
i		l				FASMVEEYSGVTLDKSESRTD
		l				WLARPLPERQWEYASPNVWY
		l				LLPITAKLMVETEASGWLPAAL
		l				DECRLMQMRRQEVVAPEDAW
		l				RDITNAWQLRTRQLACLQLLA
ŀ		l				DWRLRKARERDLAVNFVVREE
						HLWSVARYMPGSLGELDSLGL
		l				
						SGSEIRFHGKTLLALVEKAQTL
		1		1		PEDALPQPMLNLMDMPGYRKA
		1		l		FKAIKSLITDVSETHKISAELLAS
1		l		l		RRQINQLLNWHWKLKPQNNLP
1			l	1		ELISGWRGISAVKSSEAGLGAL
1		Ì	l	l		SATSGFGKLQIQHQAFTLRTRT
1		l	1	l		TDQHTLLAGTLFIAKILIPMVSF
		I		l		TFQYCCFAVPQATYCHRIAPIL
L		L	l	L		GNGAMKPGRKIS

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25514	55882	Α	25655	I	3315	MDELRLVLMTIIHIKLPPIRRAD
						GSFGNDLTTGAGFNDRKTVPR
	l l	1				YARVHVYRCRKVICIFTKRIPFC
		1				LDVPAHRALVVMKGTLYGMP
	ŀ	l				VVAAAFEFAFMGGSMGSVVGA
				l		RFVRAVEQALEDNCPLICFSAS
	1					GGARMQEALMSLMQMAKTSA
						ALAKMQERGLPYISVLTDPTM
	1					GGVSASFAMLGDLNIAEPKALI
		ĺ				GFAGPRVIEQTVREKLPPGFQR
		ŀ				SEFLIEKGAIDMIVRRPEMRLKL
						ASILAKLMNLPAPNPEA
25515	55883	Α	25656	246	422	RHADTDLRR*ISDRFSPAPPADP
İ	1					ANGGR*TPRHAAKRRDPGTPV
				1		QPARKPSKPTRLLR
25516	55884	Α	25657	884	1276	LVTRQLSPGNRCNVFAFSSAVE
						TSLTCQGWLSPVCAVCQAISSS
		l		l		HNASIQVRSPAASCGSPFCSKRP
	1					SALWWTSVSPFLSPRRRTSGAN
						AESVSAT*SKRRSSARRSASARS
						TLSGAALRSRTASNEWRS
25517	55885	Α	25658	649	1427	LPLLGWSMSPRMTAQLACDAL
						QMALWRRKRPRNVIVHTDRGG
		1				QSVQQFRALKRHITASRETERF
	1	1				YLDVQKQFPKVTAQKVIVSEA
		1				GASVYSASELAAQEFPDLDVSL
	1	l				RGAVSIARRLQDPLAELVKIDP
		l				KSIGVGQYQHDVSQTQLARKL
		l				DAVVEDCVNAVGVDLNTASVP
						LLTRVAGLTRMMAQNIVAWR
1		l				DENGQFQNRQQLLKVSRLGPK
İ		l				AFEQCAGFLRINHGDNPLDAST
		l				VHPEAYPVVERILAATQQALKD
		l				LMGNSSELRNLKASFLDNEEN
		l				WPLLLDALIPVANTCEMILMPA
		1				CFGLADDKLWRWLNEKLPCSL
		l				MLLPTLPPSVLGIRLQNQLQRQ
		I				FVRQGGVWIECGDGGDTTTITI
		l				TQR**PAGRVYRSPGSLSGGGT
		L				HSGSNTAGTERSDG
25518	55886	A	25659	I	1878	
25519	55887	A	25660	1	4329	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25520	55888	A	25661	2514	4173	PISCLPDDYYGHCRGVSAHF GASVSCVELLSACARPLWRHL GLALLRVWCRTFILLSALASVF CPCSVVWGRLLFSASLSVVVW GGYFLSPLGSLSPRGTARLGAA CRSREDJRRR*WRGIFTSRTIFAS AVPASVNDBYCAZPAACIRFTS TSAY*VGCSDRNA/DAEASGEG WRRAFGDATLSTGQFGGEAREE VILGLIGSQAKTGGNTPKASAV RKITLVAWPALETGLTMLSM** IG*ETRYSEVEPSSKSIVPSASPDSL IVFA*QPPSKLNTPSSSQCSSSP RIRRRGSVERVLPVPSFRNT ATSPPSTLAEQCIEAJPSAVFA APVRVAASMISGFCALASIRS ASTRRPSASVFITSTFLPLR*VMI SPSLNALPLIRLSAQQRNSFTRL SPRVMANBASPVTVAAPPMS DFIESINAVCLMQARVHWRFI ASWVVIQPSPLENNLRVSLC AAPGTLCLTTFVSSSGDR*NAL CNRCNRPAPCFRSSAIRFATVLA ARRHDWVWIPSPLIPRISS

SEQ ID	SEQ ID NO:	IMa-	SEQ ID NO:	Nueleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25521	55889	A	25662	2221	4400	I IRGCVVSGKSSCSKTNLPSDDKR
20021	33003	ľ	25002	1222		TGASCPLRDLFLRYLRAHALVT
						AEQLAHEFSLGIAIVEEOLOOLE
						EQGLVMNLQQDIWVSDEVFRR
	1	1				LRLRSLQAAREATRPVAATTYA
		1				RLLLEROGVLPATDGSPALFAS
		1				TSPGVYEGVDGVMRVIEQLAA
		1				SAINASLWESOEFVYGKPVYAV
1						GENYSQGQYYLASFANKIWLSI
						OGVVDLHGFATNGLYYKSLLD
						KLKVSTHVFRVGTYKSAVEPFI
		1				RDDMSPAAREADSRWIGELWQ
		i				NYLNTVAANRQIPAEQVFPGA
		1		1		OGLLEGLTKTGGDTAKYALEN
1		1				KLVDALASSAEIEKALTKEFGW
1		1				SKTDKNYRAISYYDYALKTPA
		1				DTGDSIGVVFANGAIMDGEETC
1						GNVGGDTTAAQIRDARLDPKV
1		1				KAIVLRVNSPGGSVTASEVIRA
		1	l			ELAAARAAGKPVVVSMGGMA
						ASGGYWISTPANYIVANPSTLT
1		1				GSIGIFGVITTVENSLDSIGVHTD
				i	1	GVSTSPLADVSITRALPPEAQL
İ						MMQLSIENGYKRFITLVADARH
						STPEQ/IDKIAQGHVWT/GLGDF
						DDAVAKAAELAKVKQWHLEY
		1	ĺ			YVDEPTFFDKVMDNMSGSVRA
	1					MLPDAFQAMLPAPLASYQVRS
	1	1				PCLTYILLLFRYHSYQYHAKEIN
		1				LRCLHGRDHRDAAFRAGLYTG
		1				VRSSTTPTGADAGIPSPGDARF
		1				AIHEYIPRNGSSRFNPGKLAPHA
25522	55890	A	25663	1	1665	AME I I I COSSIG I G CIESTI III
25523	55891	A	25664	475	1182	
25524	55892	Α	25665	242	3059	
25525	55893	Α	25666	1761	1970	
25526	55894	Α	25667	455	I137	GTKPRDIDHILGTFITPGMPKGG
				İ		KLDVYAAPELPLKLLGRPTEGE
					ŀ	YNEEF/SLLPVVNYLKDKLSNP
				ĺ		V/RLDGVDVAEGEL/VVLENVR
						FNKGEKKDDE/HRAQASTHGIG
						K/FADVACAGPLLA/AVLDSLSK
						/IADQLIVGGGIANTFI/AAQGHD
		1	l		I	VGKSLYEADLV/DEAKRLLTTC
		1				NIPVPSD/VRVATEFSETAPATL
		1	1		I	KSVRHSDKISYISTGGGAFLEL
						WKVKYLPAVAMLEERG
25527	55895	Α	25668	1108	1932	
25528	55896	Α	25669	1496	1631	
25529	55897	Α	25670	462	1152	
25530	55898	A	25671	545	598	l

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		1		scquence		
0.550.1	55899	+-	0.000	I	1761	MACURINIDADO A DOCUMENTO
25531	33899	A	25672	1	1701	MRGHNWIDMDQARQQSTPHT
		1				DRKICHKNDRPRTTPLRKIDAH
		1				PHTLIILPAESTLSTTKYKLRAL
1		1				LVENTNKDKSAVSVVFRGSVL
		i				HQQAANFPNLMLCFQLKNGVN
		1				ACNDFIMLFVDDNAAGSIERAA
		1				SPCINEKQHAFSESVPAIAAVRO
		1				LGSMIAVEFNDPQTGEPSAAIA
		1				QKIQQRALAQGLLLLTCGAYG
		1				NACKRRIDYVCRIKHSRRIRQV
		1				VLLNFAKSGAFSTTRGTDDKLT
		1				PVIQPRASGEYNEEFSLLPVVN
		1				YLKDKLSNPVRLVKDYLDGVD
		ı				VAEGELVVLENVRFNKGEKKD
		ı				DETLSKKYAALCDVFVMDAFG
						TAHLRAGFLLTGI\GKLRCSLRC
		1				AGPLLAAELDALGKALKEPARI
			1		1	MVAIVGGSKVSTKLTVLDSLSK
		1				IADQLIVGGGIANTFIAAQGHD
						VGKSLYEADLVDEAKRLLTTC
						NIPVPSDVRVATEFSETAPANL
						KSVNDVKADEQILDIVRDLDAA
						NVVINAVFSYVTNVWGWAFE
		1				WYMVVMLFGWFWLVFGPYAK
		1				KRLGNEPPEFSTASWIFMMFAL
		1	1			LYVCCRTVRLGREIHRRAQIVH
						IDIEPTQIGRVLCRISVLSLMLKR
25532	55900	A	25673	1	984	
25533	55901	A	25674	1	1181	MMAVSAPYVGDNIDDGGIYTQ
		1				SETHTISSDCVLDTAAMWTPLS
		1				AVIGCTTNPAQYPANAAEVYN
		1				KDGNKLDLYGKVDGLHYFSDN
1						KDVDGDQTYMRLGFKGETQV1
						DQLTGYGQWEYQIQGNSAENE
						NNSWTRVAFAGLKFQDVGSFD
						YGRNYGVVYDVTSWTDVLPEF
-	1		l			GGDTYGSDNFMQQRGNGFATY
						RNTDFFGLVDGLNFAVQYQGK
1						NGNPSGESFTSGVTNNGRDALR
1	1					QNGDGVGGSITYDYEGFGIG\Y
				•		TQTYNATRVGSLGWANKAQNF
1		1	l		1	EAVAQYQFDFGLRPSLAYLQSK
		1			I	GKNLGRGYDDEDILQICCMSDP
		1	1		1	TQNRQASAKLALPCQVALLSSA
		1		1	l	SPHHAFTPSTSIIQPAHIIIHSSPP
		1			1	PWASSHSISTHQQHTQCSSSSNT
		1		ŀ	1	LAVH
25534	55902	Α	25675	1	147	

SEO ID	SEO ID NO:	Mat	SEQ ID NO:	Nueleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25535	55903	A	25676	683	947	QVRDSLQQGRERRIALSIGWLV
12333	33703		23070	003	j	WREGCODOCELEAGGASALTR
						RGSCRELDPAPFATMLLFCPGC
	1					GNGLIVEDG\QRCHASTDAVPP
25536	55904	A	25677	12	393	RGSCRELEPAEFETMLLFCPGC
23330	33704	,,	23077	1.2	177	GNGLIVEEGORCH/RAVACNT\
	Į.	1		l	i	CPYVHNITPQGNTIWKYPKLKE
1				ĺ		CGSDVLGGAAAWENVDSTAE
				l		SC\PKCEHPRAYFMQLOTRSAD
				l		EPMTTFYKCC\NAQCGHRWRD
25537	55905	A	25678	234	567	YVDETDDCFENNRCGOPVNGA
25557	33703	^	230.0		100	YSPAGLSRVAADASLTTPHAK*
		1				TLRSLTLHQHDKTRTELLNDVA
1		1		i		GALALDDKLGRSTNQLSGGEW
1		1				TPSLARPFLLLGPRKMRLLPLH
						I.PP
25538	55906	A	25679	1	794	HCDGKHFTGVGKIMSIGMQLQ
20000	33700	ļ.,	20017	ľ		DVAESTRLGPLSGEVRAGEILH
		1				LVGPNGAGKESLTGREWPEMP
		i				TVKGTIOFPGHPLEAWSAKK\L
1		i .				ALLRAYL\SOOOTPPFPPPVWH
1						YLTLHQPDKTRPELLNDVAGA
1						LALDDKLGRSTNQLSGGEWOR
						VRLAAVVLOITPOANPAGOLLL
		1				LDEPMNSLDVAQOSALDKILSA
	1	ı				LCQQGLAIVMSSHDLNHTLRH
						AHRAWLLKGGKMLASGRREE
		1				VLTPPNLAQAYGMNFRRLDIEG
		1				HRMLISTI
25539	55907	Α	25680	12	414	RAAPSRNLPPRMPIPIAAPIAAR
-		1				PIITAAAMYSRSIFRFSMTVSSLF
		1				QLKRSSVGKLMFFRRHRQIDDR
		1	1	1		QNHEDEGLQRNDQDVENGPRH
		İ				IQDPL*PPRQETSNQNEDQLSGV
		1				HVTEQSQTEGSWFGQHAYPF
25540	55908	Α	25681	568	724	RFSLGTVLDGIYPHQYDGYSR
						WSAKRYL*WRNL*SGTHRSC*
1		1	1	l		VNNFTRSNKK
		_			1	

SEO ID	ICEO ID NO:	Met	SEQ ID NO:	Nuelcotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25541	55909	ĪA.	25682	1	974	MNGKLQSSDVKNETPYNIPLLI
23341	33909	l^	23082	1'	274	NENVISSGISLISLWHTYADEHY
	i .	1		1		RVIWPRDKKKPLIANSWVAVY
	1	1				TVTGCGNSDRLNNIRTLRA\MA
	1	1		1		
		1		ì		REFSIDVLDEMLQQFRVVTPDR
	1			1		PEHKQLPQHELAERQEKISTWL
	1		l	l		ELMKADGINPEELLGN\SSAAA
	l			1		PR\AGKKRQPGSAKYLFT\DVN
	ŀ					GETKTWTGQGRTPKPIAQALAE
		1	ł			DCHGKPEYGSAVHGCRCDDGS
		1				AGNLCFDLNRHCGLGVRLRPR
		1	1	!		KINGDYRSRFCHAGETGVCAG
		1		1		AETTQMAESGVSGAGLAVRGE
		1				RDGKRSPLQIAIMMNGSSGQAI
		_				SSNVIILQLFLVEVIKSLRMLYM
25542	55910	A	25683	1	1359	
25543	55911	Α	25684		918	DADVACALICRI CI UDOCCIIOED
25544	55912	Α	25685	72	690	PAPVAGAHCPLGLHRSSEHQEP
		1				QLRHVARWPSS*SWLCHGTFR
1		1				KLLPGKKRRGGNKKF*GRRAR
		1				GVGCVVSRVWCGPACACSLRR
	1					WLAHTVHWVFTEAQSIKSHSS
1	İ	1	ł	1		DMWPDGLALSPGCAMGPSGSC
1	İ	1				SRGKNVGGATKNFRGVHNIYC
1		1		1		HKPIPTTQHESKYARQTTTEEC
1	1	1	ł			TQTSSHDFRTTFSAVMQQRLQI
		1		1		ARNLVTHPKLVFMDEPTGGLD
	i	1		1		VSVQARLLDLLRGLVVELNLA
	1	1				VVIVTHDLGVARLLADRLLVM
		1		1		KQGQVVESGLTDRVLDDPHHP
l .						YTQLLVSSVLQN
25545	55913	Α	25686	1334	1545	RSQSRLERSCSVTGSM*RVSPA
1		1				RSFRRITKRVLAAARLAT*LPAS
		1				GRRTGVGVSVDSEFPSELLSSSF
1	i	L	L	l		TD
25546	55914	Α	25687	1784	2125	WLQHIHPQLLRCPVLRAQNVW
		1				IRTLYDRH/RFVTRGTLGWIETG
1	1	1	1	1		DF/DKVPPDLRFFAGGDRSI/RG
1	1	1	1	1		YKYKSIAPKYANGLDIGKSPAA
1		1				GAISPCLTFVMSARRGGHRGQS
		1		1		ASGCRA
25547	55915	A	25688	931	1213	NLHPAPAKRRAPARPQSRLAHR
		1				QRGRMRGAPRPFRQRQIKLCY
1		1	1	1		ARCTPTICPTKVKSRSNTVTSG*
1		1	1	I		TWSPRQRAKWWKSAKPPSAGL
			1			TSSARHP
25548	55916	A	25689	999	1243	VDPVPWLPMALDITSTAPARQF
1	1	1	1	1		RKRIIASLMPT/WGTSLRRYSVP
1		1	1	1		PRRSGWKRWRFPPTGSTTCRPP
		1	1	1		FPAVCSSVCRLPATW
					L	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25549	55917	A	25690	1225	2341	ARTERLSNEGGSTRARGVYWD
						PNSDLCPTLDFSYKMPLLKNPL
		l				EQYYLVQGGFKRTDLNDTESD
1		1			ŀ	STTLVASRYWDLSSGWQRAIN
		1				LRWSLDHFTQGEITNTTMLFYP
						GVMISRTRSRGGLMPTWGDSO
						RYSIDYSNTAWGSDVDFSVFQA
		1				ONVWIRTLYDRHRFVTRGTLG
1						WIETGDFDKVPPDLRFFAGGDR
		1				SIRGYQY\KSIGPKLPNGD\LKG
						ASKLITGSLEYQYNVTGKCTK
						WOFGEWLAPGEVRLAPGATLA
		ı				TPELVASCSTEGLNGLAANFHA
		l			1	ELRARLPWHGGAMKPRPVHLN
1		l				TWEGFYFDLQPDKVKALATAA
					1	AALGVERFVLDDGWFNARHH
						DRAGLGDWWPDATKFPQGLG
						ELVAHVNPFYA
25550	55918	Α	25691	45	233	SSYPRWWAAWWASTTARPSTR
						WRSSPR*SATTWASSPSPTSP*I
1		1				HDRPGIGATHSSRFIPLK
25551	55919	В	25692	1	558	
25552	55920	Α	25693	324	657	
25553	55921	Α	25694	831	1244	WQPGGR*WSRQRSADGTGPDD
		1				LAAAYFPGDRFYRN*PSERC*H
		Ļ				RRG
25554	55922	A	25695	1	1215 840	
25555		A	25696	1	1365	MPQNRGGFLDKKNPGAPLEGA
25556	55924	A	23097	'	1303	VYVNCFTRFPGIGYEGRTAVFC
						GAAKVPPGLNYRGIGAFPGGNF
	l					ASKRSRGRNLAGARCLRFCPK\
						WO\NYSETASVOOON*SVLARA
						IERGINAPLA\SSCGRFFDAVPA
1						ALGCAPATLSYKGEAACALEA
l		İ				LAASCHGVTHPVTMPRVDNQL
1	l					DLATFWQQWLNWQAPVNQRA
1						WAFHDALAQGFAALMREQAT
						MRGITTLHPEGLERMSAGHES
						WLERRNGELGEGKGSKAYPTG
		1				DHKGADLYDDSNFLIQNIFVED
		1				TRGLLRQGREDLIERYKDPLNE
	1	1		1		NPKRCVEQLANWHKELEEYKK
				1	1	ASRIDIKPSREYASTIMNAIWTG
				1	1	EPSVIYGNVRNDGLIDNLPQGC
		1				CVEVACLVDANGIOPTKVGTLP
		1				SHLAAMMQTNINVQTLLTEAIL
						TENRORVYHAAMMOPHTAAV
					1	LGIDEIYALVDDLIAAHGDWLP
L	1	1			l	LOUDE LIVE ADDRESS HIS MAN

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amine acid	*=Stop codon, /=possible nucleotide
ĺ	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25557	55925	Α	25698	1	950	MPDEENRFNALKAVFSQLMTD
		1				ATLTPLFNYHYRISAPPGVNGL
		1				SMKRAVVVFSGGQDSTTCLVQ
					1	ALQQYDEVHCVTFDYGQRHRA
	1	1	İ			EIDVARELALKLGARAHKVLD
						VTLLNELAVSSLTRDSIPVPDYE
		l				PEADGIPNTFVPGRNILFLTLAA
						IYAYOVKAEAVITGVCETDFSG
					1	YPDCRDEFVKALNHAHKEKLD
1		1				EDCKRRMYTNPLRVLDSKNPE
		l				VQALLNDAPALGDYLDEESRE
						HFAGLCKLLESAGIAYTVNORL
	1	1				AVNPEFKADPVVDIYLVASGA
	ì					DTQSAAMALAERLRDELPGVK
			İ			LMTNHGGGNFKKQFARADKW
	Į.	l				GARVAVVLGESEVANGTAVVK
1		ı				DLRSGEQTAVAQDSVAAHLRT
İ		1				KEKDSVEIYENENDQVEAVKRI
		1			1	FAENGKALAVGVILGVGALIG
	1					WRYWNSHOVDSARSASLAYO
						NAVTAVSEGKPDSIPAAEKFAA
İ		1				ENKNTYGALASLELAQOFVDK
		1		1		NELEKAAAQLQQGLADTSDEN
		1	ļ			LKAVINLRLARVQVQLKQADA
		1				ALKTL*IPD*RPDAGLRCKRSPR
	1	1				SPAVCTDRONAHEIPRPDSHLM
1		1				PERR*EAPALPDFLNPARAAG
25558	55926	A	25699	1	3314	MKISRLGEAPDYRFSLANERTF
1		1				LAWIRTALGFLAAGVGLDQLA
						PDFATPVIRELLALLLCLFSGGL
						AMYGYLRWLRNEKAMRLKED
		i				LPYTNSLLIISLILMVVAVIVMG
		i				LRAMLMAMEPIWESDFHTLSY
						GFRPERSVHHAIRTVKLOLTDC
					ŀ	GETRGRWVIEGDLSSYFDTVHH
1						RLLMKAVRRRISDARFMTLLW
						KTIKAGHIDVEDKRAASEGVPQ
1						NKIISPLLSNIMLNEFDOYLHER
		1				YLSGKARKDRWYWNN
25559	55927	A	25700	997	1716	PYLTASSSAFQQLHLSGENHRD
		1			1	DGCAGYSRRTLAAQLQCHCEC
		1				DHNLPPDTPRLPRSGVVLPARF
		1				PRPLHTLISALHRRVLTRHARH
						ESSTLNPQRLPPAHRFFACQSRY
		1	1			VPGPAEYSYAVRSTDESG*A*W
			1			LRVPPNLIALTVQRSLPDLALPA
		1	1			ONCPPCRSMLEPAPYILLGMLA
				1		TWPACPG\HEVG*SHSAHPDEP
		1	1	1		ETLOTVSR*YRRFGRPVH*SVH
		1	1	1	1 .	VVGRYPHQACQCYLSSTAE
25560	55928	A	25701	1	769	
	1	1			.t	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25561	55929	A	25702	1	3707	I MVRSAVVAGIAQAALPQSVVA
23301	33929	<u>۱</u> ^	23702	1'	3707	WEYLVEDYDRIRNDIEAVLPEF
				l	i	ADYNORIRHPGGFHLINAAAER
				l		RWMTPSGKANFITSKGLLEDPS
						SAFNSKLVMATVRSHDQYNTTI
				l		YGMDDRYRGVFGQRDGYRDN
			l	l		CEEIAOLAEDCGNLFAVTVFRC
				l		PAGANLQGNRNVHCIDDLGKD
		l				RFNDIRNVOAAELLAEMAISSA
				l	ļ	QRRMRAAKKVVRKKLTSGPAL
				l		PGKLADCTAQDLNRTELFLWK
			1			GEQNALLRGFPAVRLHSLL
25562	55930	A	25703	1	369	LPSHGAGLGTCSLPCLSLPPTP
25502	33930	<u> </u> ^	23703	l'	309	WAPVOPEPPRRAPPPAPWRPVP
			İ			LTTQGLRN/DEHRVQDWQAAP
1						PAAPLKVCKYTNQHPVFSTRFV
			İ			NAPIDTLYLAALVRTWRTFMSS
					ŀ	SRIVNTPIGTLYLAQ
25563	55931	Ā	25704	1	444	MRLHSSALGRSMGLGAVEOGA
25505	33931	<u>۱</u> ^	23704	l'		ALVGEAPAAQEPTEAGEGSGM
	i					AGCSPKACPAGRQLRPGPA\AA
				ŀ		PSAGPPSPRPPGTPAGPOAPRAA
	İ					PVPARASPSTPPCKLRERAAAF
						A/EPRKGLPQCSGGLKGSSSAA
						KVGAQAEEAPRASESCEDC
25564	55932	A	25705	1767	2130	YTGQRLRRVYWVPQQCQPTCA
		1.		1,,,,		ALDFSPSLSCLPA/AAGLRTYSQ
						PCLSLPPTPWAPVOPEPPO*APP
						PAPRRP\AHRPPKG*GVQAHGA
						G\RQAAPPAAPVRDPLG\KPAGL
						LSLVGTWRTFMS
25565	55933	Α	25706	654	832	RRCARFLAGP*LPSHGAGLGTC
						SPPCLSLPPTPWAPVRPEPPRRA
				l		PPPAPRRPVLCVFS
25566	55934	В	25707	1	537	
25567	55935	Α	25708	1	455	HCGSVIGGFLVSLTLRTKLRTL
			İ			AVSVTALTVVCLEFIPSDVRMR
			İ			SVSSFWWVRSLAGSRVKLQTF
						AVTVTALKAASLELFVPPGGLV
1						VSLASGVKLQTAAAGK/RCLPV
			1			LRHAPALLSPWVVDGTGHRGA
1						GGGAHRGGSGRPGAHGGGGRL
25568	55936	Α	25709	1	314	SACREVWRERHEREPGLRGAL
		l		1		AGQLEFRVGVGLVRPALGGAG
		l				QPGAALDFSPGLSCLPA/AAGL
		İ				GTCSPPCLSLPPPPWAPVQPEPP
						RRAPPPVHGAQSHRPPKG
				<u> </u>		

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25569	55937	A	25710	144	519	HPGQRLRRVYWVPQQCQPIGA ELDFSPSLSCLPA/AAGLGTCSP PCLSLPPPPWAPVQPEPPQRAPP PAPW/WLSPIDHPRAEECECTA QDWQAALPAAPVWDPLEMSG LFDRAEKRYIRSFARKDSM
25570	55938	A	25711	271	743	ARTWNVPKVCVRIKANSHSIFT GLSCLPAGQGSGPAARIIA*ASD PLRGLLCGPSLLDE/PPPPAPWR PVPSTTYGLRSAGEQRGTGRQL HLSAAPVRDPRGEAIWAPESGR SAASILKPARPPAHREERTTPDA PP*EL*HSPRRSAASLREDPWLH S
25571	55939	A	25712	1043	1348	GPARNRAQRRRAGTAGGPITPS AAAGPGAKPLIARRRQGWPAA PSAGPAKPTPTRISSWPAS\QPA AAVPARASPSTTLFKLREWAPA LASPERGSHSATVG
25572	55940	A	25713	22	226	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKAVDTQ RH
25573	55941	A	25714	166	714	
25574	55942	Α	25715	1	462	

Sociation of peptide sequence   Sociation of first sequence   Sociation of first sequence   Sociation of first sequence   Sociation of the s	SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
25575 55943 A 25716 I 924 MFAIISYSLAAVLLTATLTA IIISFPVALCLVIGANLGSGLL LINSAANAARRVALGSIL LINSAANAARRVALGSIL LIVGSLIILPFVHILAETMGKI PKAELVIYPHVFNLVRCLV PPVDPMARFCKTIRDEPELI LRPKHLDVSALDTPTLALAN RETCALATPWTDDGRKYAY ASGGRRSATKVMVVVTDG DGSMLKAVIDGCHNDNIR, AVLGYLNRNALDTKNLIKEI IASIPTERYFTNVSDEAALLE GTLGEQIFSIEDMDLGDEVY GRPHIPMIDPTLRNOLIADLG PQVRVLLLDVVIGGFATADD SLVSAWQKACAARLDNOP, IATVTGTERDPQCRSQQIATI AGIAVYSSLPEATLLAAALII SPAAQQHTPSLLENVAVINIG SFALELQSASKPVVHYQWSI AQQGK WLANPELLEADADA AAVIDILABIKEPILCAPND DARPLSAVQGEKIDEVFIGSG TNIGHFRAAGKLLDAHKGQ RLWAPPTRANDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPFRIR GANVFLASAELAAVAALIGI TPEEYQTTYVAQVDKTAVDT YLNFNQLSGYPTYAQVDKTAVDT YLNFNQLSGYPTYAQVDKTAVDT YLNFNQLSGYPTYAGVTFG YWQSFEDDHLPLAFFLARN PMKNCWKILDIEETTDVDIII YLALLPSFHPETDPOFFGKQL AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEF PSAWQRFIGQLYYCSMEGID RWSLCTIAMNTAHLSFECV AERIRWLQEGRIGTEDDPGFKGL RWSLCTIAMNTAHLSFECV AERIRWLQEGRIGTELDPGFRGCUPIL RRPDICTTONNORSRCEGYQI DKRGHQHGGITALVQCON DKRGHQHGGGITALVQCON							
25575 55943 A 25716 I 924 MFAIISYSSLAAVLLTATLTA IIISFPVALCLVIGANLGSGLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSAANAAARRVALGSLL LUNSALDTETLALAAN RETCALATPWTDDGRKYAY ASGGRRSATKWVVVTOG DGSMLKAVIDOCHDNILRI AVLGYLNRNALDTKNLIKEI IASIFIERYFFNNSDEAALLE GTLGEGIFSIEDMDLGDEVY GRPHPMIDPTLROLIADLG PQVRVLLLDVVIGFGATADF SLVSAWGRACAARLDNQFL IATVTGTERDPCCRSQQIATI AGIAVVSLIPEATLLAAALH SPAAQQHTPSLLENVAVINI SFALELQSASKPVVHYQWSI AGQGKWLANFELLEADAD/ AAVIDIDLADIKEPILCAPND DARPLSAVQGEKIDEVFIGS TNIGHFRAAGKLDAHKGQ RLWVAPPTRMDAAQLTEGG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTINFPRIRI GANFFLASALLAAVAALIGF TPEEFYGTYVAQVDKTAVDT YLNFNQLSQYTEKADGLLK RPWGRKILDTLATTHEOHRI GPGRERLRRMALPMEDEAL TPEEFYGTYVAQVDKTAVDT YLNFNQLSQYTEKADGLK RPWGRKILDTLATTHEOHRI GPGRERLRRMALPMEDEAL TYLLIPSFHPETPOOFFGQL AYEEALRIAGSPAKSWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYGSMEGID RWSLCTIANNTAHLSFECV AERLRWLQSGROTGEIDEEL RYALAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQSGROTGEIDEEL LLYALAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQSGROTGEIDEEL LLYALAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQSGROTGEIDEEL LLYALAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQGGROTGLOGGEG DKRGHQHGGGITALVQCGN		sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
IIISPPVALCL/IIGANLGSGLL LINNSAANAAARRVALGSLL LINSSALIP.PVILLAETIMGKI PKAEL/IYPHYPYNLVRCLV PPVPPMARRCKTIRDEPELL LRPKHLDVSALDTPTLALAN RETCALATPWTDDGRKYAY ASGGRRSATK/MVVVTDGE DGSMLKAVIDQCHIDNILRI AVLGYLIRNALDTKNLIKEI IASIPTERYFINVSDEAALLE GTLGEGIFSIEDMLDGBVY GRPHPMIDTTLRNQLIADLG PQVRVLLLDVVIGGGATAD SLVSAWQKACAARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVVSSLPEATLLAAALI SPAAQQHTPSLLEWAVININ SFALELGASKPVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCARND DARPLSAVQGEKIDEVFIGS TINIGHRAAGKILDAHKGQ RLWVAPPTRNDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEYOTYVAQVDKTAVDT VLNFNQLSQYTEKADGLIK RPWRKLDTLATYHEQHRI GPGRELRRMALPHEDEAL 25576 55944 A 25717 I 417 MGVLNNIWLSEEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLRFLARY PMKNCWKILDIEETIDVDIII YLALLPSFHETETPOPOFRGL AYEEALRIAGSPAKSWWQPE EVAEHEILLAFRALLASDSE PSAWQRTIQQLNYGSMEEID RWSLCTIAMNTAHLSFECV AERLRWLQSPRIGGITALYQCGN DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN					sequence		
IIISPPVALCLVIGANLGSGLL LNNSAANAARRVALGSLL LVGSLILIPVHLLAETINGKI PKAELVIYPHVFYNLVRCLV PFVVPMARFCKTIRDEPELL LRPKHLDVSALDTPTLALAN RETCALATPWTDDGRKYAY ASGGRRSATKVMVVTOTGE DGSMLKAVIDQCHIDNILRI AVLGYLNRALDTKNLIKEI IASIPTERYFFNVSDEAALLE GTLGEGIFSIEDMLDGBVY GRPHPMIDTIRNQLIADLG PQVRVLLLDVVIGGGATAD SLVSAWQKACAARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVVSSLPEATLLAAALI SPAAQQHTPSLLEWAVNINI SFALELGASKPVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCARND DARPLSAVQGEKIDEVFIGS TINIGHRAAGKLDAHKGQ RLWVAPPTRNDAAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEYOTYVAQVDKTAVDT VLNFNQLSQYTEKADGLIK RPWRKILDTLATYHEQHRI GPGRELLRRMALPHEDEAL 25576 55944 A 25717 I 417 MGVLNNWLSEEESLWIQSR RALRYYSNWRQYFAGYTEG YWQSPEDDHLPLLRFLARY PMKNCWKILDIEETIDVDIII YLALLPSFHIPETDPQDFRGLU AYEEALRIAGSPAKSWWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYGSMEEID RWSLCTTAMNTAHLSFECV AERLRWLQERDTGVCSMEEU RWSLCTTAMNTAHLSFECV AERLRWLQEROTGCIPLIHLP RRYDICTIANNTAHLSFECV AERLRWLQEROTGCIPLIHLP RRYDICTIANNTAHLSFECV AERLRWLQEROTGCIPLIHLP RRYDICTIANNTAHLSFECV	25575	65042		25716	1	1024	MEANEWEST A AVILLEATING A
LINNSAANAAARRVALGSLL LVGSLIILPFVHLLAETMGKI PKABLVIYHHYFYNLVRCUV PFVDPMARFCKTIIRDEPELL LRPKHLDVSALDTPTALAAN RETCALATPWTDDGRKYAY ASGGRRSATKVMVVVTDGI DGSMLKAVIDQCNHDNILRI AVLGYLNRNALDTKNLIKEI IASIPTERYFFNSDEAALLE GTLGEGIFSIEDMDLGDEVY GRPHPMIDPTLRNQLIADLG PQVRVLLLDVVIGFGATADD SLVSAWQKACAARLDNQP, IATVTGTERBPCCRSQQIATI AGIAVVSSLPEATLAAALIP SPAAQHTPSLLENVAVINIC SFALELQSASKPVVHYQWSI AGQGKWLANPELLEADADA AAVIDILAABIKEPILCAPND DARPLSAVQGEKIDEVFIGSC TNIGHFRAGKLLDAHKGQ RLWVAPPTRMDAAQLTEEG SVFCKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVFLASAELAAVAALIG TPEEYQTYVAQVDKTAVDT YLNRNQLSYTEKADGLIK RPWQRKILDTLATYHEOHRI GPGRERLRRMALPMEDEAL 25576 35944 A 25717 I 417 MGVLNNWLSEESLWIQSR RALRYSNWRQYFAGYTFG YWQSPEDDHLPLLRFLARS PMKNCWKILDIEETTDVDIII YLALLSFHEFETDPOGFKGL AYEEALRIAGSPASSWWQPE EVAEHELLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEGRITGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV AERLRWLQEGRITGLIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTIANNTAHLSFECV	23373	33943	^	23710	11	924	
LVGSLILIPFVHLLAETMGKI PKAELVIYHHVFYNLVRCLV PKAELVIYHVFYNLVRCLV PFVDPMARFCKTIRGDEELL LRPKHLDVSALDTPTLALAN RETCALATPWTDGRKYAY ASGGRSATKVMVVVTDG DGSMLKAVIDQCNHDNILRI AVLGYLNRNALDTKNLIKEI IASIPTERYFFNVSDEAALLE GTLGEQFISIEDMDLGDEVY GRPHIPMIDPTLRNQLIADLG PQVRVLLLDVVIGFGATAD SLVSAWQKACAARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVVSSLPSATLLAAALII SPAAQQHTPSLLENVAVINI SFALELQSASKYVHYQWSI AQQGKWLANPELLEADAD/ AAVIDIDADIKEPILCAPND DARPLSAVQGEKIDEVPIGSS TINIGHFRAAGKLLDAHKQQ RLWAPPTRAMDAQLTEEG SVFGKSGARVSSIPCAVPCV* RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIGG TPEEYQTYVAQVDKTAVDT YLNFNQLSQYTFKADGLIK, RPWQRKILDTLATYHEQHRI QPGRENLRRMALPMEDEAL. PKARLAYYSNWRQYFAGYTFG YWQSFEDDHLPLRFFLARN PMKNCWKILDIEETTDVDIIR YLALLPSHIPETDPODFKGLI AYEEARLAQSPAKSVWQPE EVAEHEILLAFRALLASDSEI PSAWQRFIQCINYCSMEEDI RWSLCTIAMNTAHLSFECV AERIRWLQEGRITGIDEELE FLYAIAKGNVFNFQTILHLPY RRPDICTOHNOGSRCEGVGII DKRCHQHGGGITALVQCON DKRCHQHGGGITALVQCON DKRCHQHGGGITALVQCON							
PKABLVYFHYFYNLVRCLV PFVDPMARFCKTIRIDEPELI LRYKHLDVSALDTFTLALAM RETCALATPWTDDGRKYAY ASGGRRSATKWVVVTDG DGSMLKAVIDQCHHDNILRI AVLGYLNRNALDTKNLIKEI IASIFTERYFHNSDEAALLE GTLGEGIFSIEDMDLGDEVY GRPHPMIDFTLRNQLIADLG PQVRVLLLDVVIGFGATADF SLVSAWQKACAARLDNQFL IATVTGTERDPCCRSQQIATI AGIAVVSLIPEATLLAAALIF SPAAQQHTPSLLENVAVINIK SFALELQSASKPVVHYQWSI AQQKWLANFELLEADAD/ AAVIDILADIKEPILCAPND DARPLSAVQGEKIDEVFIGS TNIGHFRAAGKLLDAHKGQ RLWVAPPTRMDAAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRIPFPRIR GANVFLASAELAAVAALIGF TPEEFYGTYVAQVDKTAVDT YLNFNQLSQYTEKADGLLK RPWRKILDTLATTHEOHRI GPGRERLRRMALPMEDEAL THEOHYD TYLNFNQLSQYTEKADGLK RPWRKILDTLATTHEOHRI GPGRERLRRMALPMEDEAL TYLLSFHEIFETDPOGFKGL AYEEALRIAGSPAKSWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIAMNTAHLSFECV AERLRWLQSPRIGCHGEIDE RWSLCTIAMNTAHLSFECV AERLRWLQSPRIGCELIFILH PR RRPDICTIAMNTAHLSFECV AERLRWLQSPRIGCELIFILH PR RRPDICTIAMNTAHLSFECV AERLRWLQSPRIGCELIFILH PR RRPDICTIAMNTAHLSFECV AERLRWLQSERIFICELIFILH PR RRPDICTIAMNTAHLSFELT ACREATION TO THE TR RRPDICTIAMNTAHL	1						
PFVDPMARFCKTIIRDEPELL LRPKHLDVSALDTPILALAN RETCALATPWTDDGRKYAY ASGGRSATKVMVVVTDG DGSMLKAVIDGCHNDNIRI AALGYLNRNALDTKNLIKEI IASIPTERYFFNVSDEAALLE GTLGEQIFSIEDMDLGDEVY GRPHIPMIDPTLRNOLIADLG PQVRVLLLDVVIGGFATAD SLVSAWQKACAARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVYSSLPEATLLAAALII SPAAQQHTPSLLENVAVINIG SFALELQSASKPVVHYQWSI AQQGKWLANPELLEADADA AAVIDILABIKEPILCAPND DARPLSAVQGEKIDEVFIGSG TINIGHFRAAGKLLDAHKGQ RLWAPPTRMDAAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVPLASAELAAVAALIGI TPEEYTYVAQVDKTAVDT YLNFNQLSGYTEKADGLLK RPWRKILDTLATYHEQHRI GPGRERLRRMALPMEDEAL STANDAYSNWRQYFAGYTG YWQSFEDDHLPLAFFLARN PMKNCWKILDIEETTDVDIII YLALLPSFHPETDPODFKGL AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEF PSAWQRFIQGLYNCSMEEDI RWSLCTIAMNTAHLSFECV AERIRWLQEGRIGTELHPU RRPDICTTOHNDQSRGCGYQII DKRGHQHGGITALVQCGN DKRGHQHGGGITALVQCGN							
ILRPKHLDVSALDTPTLALAN RETCALATPWTDGRKYAY ASGGRRSATKVMVVVTDG DGSMLKAVIDQCHHDNILRI AVLGYLINRALDTKNILKEI IASIPTERYFFNVSDEAALLE GTLGEGIFSIEDMLDGEVY GRPHPMIDPTLRNQLIADLG PQVRVLLLDVVIGFGATADE SLVSAWQKACARL DNQP, IATVTGTERDPQCRSQQIATI AGIAVVSSLPEATLLAAALII SPAAQQHTPSLLENVAVNIKI SFALELGASKPVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILGAND DARPLSAVQGEKIDEVFIGSC TINIGHFRAAGKLDAHKGQ RLWVAPPTRMDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEETYOTYVAQVBTAVDT VLNFNQLSQYTEKADGLIK. RPWQRKILDTLATYHEQHRI GPGREILRRMALPMEDEAL 25576 55944 A 25717 I 417 MGVLNNIWLSEEESLWIQSR RALRYYSNWQYSAGVTEG YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIIR YLALLPSFHPETPOPQFKGLU AYEEALRIAQSPAKSWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIAMNTAHLSFECV AERIRWLQERDTGEDTEIL FLYAIAKGNVFNFOTILHLP RRPDICTHNNDQSRCEGGYQI DKRGHQHGGITALVQCGN					1		
RETCALATPWTDOGRKYAN ASSGRRSATKVMVVVTDGE DGSMLKAVIDQCNHDMILER AVLGYLNRNALDTKNLKEI IASIPTERYFINYSDEAALLE GTLGEGIFSIEDMDLGDEVY GRPHPMIDPTLRNQLIADLG PQVRVLLLDVVIGFGATADF SLVSAWQKACAARLDNQP, IATVTGTERBPQCRSQQIATI AGIAVVSLIPEATLLAAALIF SPAAQHTPSLLENVAVINIK SFALELQSASKPVVHYQWSI AGQGKWLANPELLEADADA AAVIDILAAIMEPTLCAPDD DARPLSAVQGEKIDEVFIGSC TNIGHFRAGKLLDAHKGQ RLWVAPPTRMDAAQLTEEGE SVFCKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVFLASAELAAVAALIG TPEEYQTYVAQVDKTAVDT YLNRNQLSYTEKADGLIK RPWQRKILDTLATYHEQHRI GPGRERLRRMALPMEDEAL 25576 55944 A 25717 I 417 MGVLNNWLSEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSPEDDHLJLRFLARX PMKNCWKILDIEETTDVDIII YLALLPSFHEETDPOGFFGQL AYEEALRIAGSPASSWQPE EVAEHELLAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEGENTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTHNNDQSRGEGGYQI DKRGHQHGGITALYQCGN							
ASGGRS-ATKVMVVVTOGE DGSMLKA-VIDQCNHDNILRI AVLGYLNRNALDTKNILKEII IASIPTERYFFNVSDEAALLE GTLGEQFISIEDMJCDEVY GRPHIPMIDPTLROLIADLG PQVRVLLLDV/GFGATAD SLVSAWQKACA-ARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVVSSLPS-ATLLAAALII SPAAQQHTPSLLENVAVINIK SFALELQSASKYVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCAPND DARPLSAVQGEKIDEVPIGSX TINIGHFRAAGKLLDAHKQQ RLWAPPTRADAQA(TEEE SVFGKSG-ARVSSIPCA-VPC-V- RVADGATVVSTSTRNFPNRI GANVFLASAELAAVA-ALIGI TPEEYQTYVAQVDKTAVDT YLNFNQLSQYTFKADGLIK, RPWQRKILDTLATYHEQHRI GPGRELRRMALPMEDEAL. 25576 \$5944 A 25717 1 417 MGVLNNWLSEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSFEDDHLPLRFFLARN PMKNCWKILDIEETTDVDIIK YLALLPSHIPETDPOGFKGLU AYEEARIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEI PSAWQRFIQCINYCSMEEDI RWSLCTIAMNTAHLSFECV AERIRWLQEGRIYGSCHYGIII RWSLCTIAMNTAHLSFECV AERIRWLQEGRIYGSCHYGIII RWSLCTIAMNTAHLSFECV AERIRWLQEGRIYGSCHYGIII RRPDICTOHNDQSRCEGYQII DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHGGGGGITAL-VQCON DKRGHQHGGGITAL-VQCON DKRGHGHGGGGITAL-VQCON DKRGHGHGGGITAL-VQCON DKRGHGHGGGGITAL-VQCON DKRGHGHGGGGITAL-VQCON DKRGHGGGGGITAL-VQCON DKRGGGGGGGITAL-VQCON	ļ.			ţ			
DOSMIKAVIDOCNIHDNILRI AVLGYLNRNALDTKNLIKEI IASIPTERYFINYSDEAALLE GTLGEGIFSIEDMDLGDEVY GRPHPMIDDTLRNQLADLG PQVRVLLIDVVIGFGATADE SLVSAWQKACAARLDNQFL IATVICTERDPQCRSQQIATI AGIAVVSSLPEATLLAAALII SPAAQQHTPSLLEWAVININ SFALELQSASKPVVHYOWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCEADAD/ DARPLSAVQGEKIDEVFIGSC TNIGHFRAAGKLDAHKGQ RLWVAPPTRMDAAQLTEEG SVFGKSGARVSSIPGAVPCV' RVADCATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEFYOTYVAQVDKTAVDT YLNFNQLSQYTEKADGLIK RPWRKILDTLATTHEOHRI GPGRERLRRAMLPMEDEAL 25576 55944 A 25717 I 417 MGVLNINWLSEEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLRFLARX PMKNCWKILDIEETITOVDIIB YLALLPSHPETPOPOFFGQL AYEEALRAQSPASSWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQSENTGEIDEVICHIP RRYDICTIANNTAHLSFECV AERLRWLQSENTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTINNDQSRCEGGYQI DKRGHQHGGITALYQCGN		}					
ANLGYLNRNALDTIKNLIKEI IASIPTERYFINVSDEAALLE GTLGEQIFISIEMMDLGDEVY GRPHIPMIDPTLRNOLIADLG PQVRVLLLDVVIGGATADD SLVSAWQKACAARLDNOP, IATVTGTERDPQCRSQQIATI AGIAVYSSLPEATILAAALIE SPAAQQHTPSLLENVAVINIG SFALELQSASKPVVHYQWSI AGQGK WLANPELLEADADA AAVIDILADIKPELCAPDD DARPLSAVGGEKIDEVFIGSG TINIGHFRAAGKLIDAHKGQ RLWAPPTRANDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVFLASAELAAVAALIGI TIPESYGTYYAQVDKTAVDT YLNPNQLSGYTFKADGLIK, RPWRKILDTLATYHEQHRI GPGREILRRMALPMEDEAL. 25576 55944 A 25717 I 417 MGVLNNWLSEESLWIQSRI RALRYYSNWRQYFAGYTFG YWQSFEDDHLPLLRFLARN PMKNCWKILDIEETTDVDIII YLALLPSFHPETDPODFKGL AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEI PSAWQRFIGQLNYCSMEEDI RWSLCTIAMNTAHLSFECV AERLRWLQEGRIGTELHPL RRPDICTTGHNDQSRGCGYQII DKRGHQHGGITALYQCGN DKRGHQHGGGITALYQCGN							
IASIPTERYFFNYSDEAALLE							
GTLGEGIFSIEDMDLGDEVY GRPHPMIDPTLRNQLIADLG PQVRVLLLDVYIGFGATADP SLVSAWQKACAARLDNQP, IATVTOTERBPQCRSQQIATI AGIAVVSLIPEATLLAAALIP SPAAQHTPSLLENVAVINIG SFALELQSASKPVVHYQWSI AGQGKWLANPELLEADADA AAVIDILABIKPEILCAPND DARPLSAVQGEKIDEVFIGSG TNIGHFRAAGKLLDAHKGQ RLWAPPTRMDAAQLTEEGE SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVFLASAELAAVAALIGI TPEEYQTYVAQVDKTAVDT YLNRNQLSYTEKADGLIK RPWQRKILDTLATYHEOHRI GPGRERLRRMALPMEDEAL STOPPHENSTON FOR			l				
GRPHFMIDPTLRNOLIADLO PQVRVLLLDVVIGFGATADF SLVSAWQRACAARIDNQPI IATVICTERDPQCRSQQIATI AGIAVVSSLPSATILAAALIH SPAAQQHTPSLLENVAVINIG SFALELQSASRVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCAPND DARPLSAVQGEKIDEVPIGSS TINIGHFRAAGKLLDAHKOQ RLWAPPTRNDAAQLTEEG SVFGKSGARVSSIPCAVPCV' RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEYQTYVAQVDKTAVDT YLNFNQLSQYTFKADGLIK, RPWQRKILDTLATYHEQHRI GPGRELRRAALPMEDEAL STOPPONTON THE		}					
POVENULLDWVIGEGATADE SLVSAWQKACA ARLDNQPL IATVICTERDPQCRSQQIATI AGIAVVSSLPEATLLAAALI SPAAQQHTPSLLEWAVINI SPALELQSASKPVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCEADAD/ AAVIDIDLADIKEPILCEADAD/ BARPLSAVQGEKIDEVPIGSC TNIGHFRAAGKLDAHKGQ RLWWAPPTRMDAQLTEEG SVFGKSGARVSSIPCAVPCV' RVADCATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEFYOTYVAQVDKTAVDT YLNFNQLSQYTEKADGLIK, RPWRKILDTLATTHEOHRI GPGRERLRRAMLPMEDEAL STOPPONTON STENSON STEN							
SLVSAWQKACAARLDNQPL IATVTGTERDPQCRSQQIATI AGIAVYSSLPEATILAAALII SPAAQQHTPSLLENVAVINIG SFALELQSASRYVHYQWSI AQQGKWLANPELLEADADA AAVIDILABIKEPILCAPND DARPLSAVQGEKIDEVFIGSG TINIGHFRAAGKLLDAHKQQ RLWAPPTRANDAAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVFLASAELAAVAALIGI TIPESYQTYYAQVDKTAVDT YLNPNQLSQYTEKADGLLK RPWRKILDILATVHEQHRI QPGRERLRRMALPMEDEAL STANDAY PMKNCWKILDIESTTDVDIII YLALLPSFHPETDPQDFKQL AYEGALRAQSPAKSVWQPE EVAEHEILLAFRALLASDSEI PSAWQRFIQOLNYCSMEEDI RWSLCTIAMNTAHLSPECV AERLRWLQSEDTGHICHPL RRPDICTOHNDQSRGEGYQII DKRGHQHGGITALVQCGN DKRGHQHGGGITALVQCGN DKRGHQHGGGITALVQCGN				ŀ			
ATVTGTERDPQCRSQIATI		}	1				PQVRVLLLDVVIGFGATADPAA
AGIAVVSSLPEATLLAAALIB SPAAQQHTPSLLENVAVINIG SFALELQSASKPVVHYQWSI AQQGKWLANPELLEADADA AAVIDIDLABIKEPILCAPND DARPLSAVQGEKIDEVFIGSG TNIGHFRAAGKLLDAHKOQ RLWVAPPTRMDAAQLTEEG SVFCKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRIII GANVFLASAELAAVAALIGI TPEEYQTYVAQVDKTAVDT YLNRVQLSYTEKADGLLKI RPWQRKILDTLATYHEOHRI GPGRERLRRMALPMEDEAL SST06 SST04 A 25717 I 417 MGVLNNWLSEESLWIQSRI RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLRFFLARS PMKNCWKILDIEETTDVDIII YLALLPSFHEETDPODFKGL AYEEALRIAQSPAKSVWQPE EVAEHELLAFRALLASDSEI PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSPECV AERLRWLQSERITGEIDELE LYAIAKGNVFNFOTILHLP RRPDICTHNNDQSRCEGYQI DKRGHQHGGITALVQCGN							
SPAAQQHTPSLLENVAVINIC SFALELQASSKPVVHYQWSI AGQGKWLANPELLEADADA AAVIDIDLADIKEPILCAPND DARPLSAVQGEKIDEVPIGSS TNIGHFRAAGKLLDAHKOQ RL WVAPPTRMDAAQLTEEG SVFGKSGARVSSIFCAVPCV' RVADOATVVSTSTRNFPNRI GANVFLASAELAAVAALIGH TPEEYQTYVAQVDKTAVDTI YLNFNQLSQYTEKADGLLK: RPWQRKLDTLATYHEQHRI GPGRERLRRMALPMEDEAL: WGPGRERLRMALPMEDEAL: PMKNCWKILDIEETIDVDIIR YLALLSFHIPETDPQDFKQLI AYEEALRIAQSPAKSWQPE EVAFHELLAFRALLASDSEP PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERILRWLQSRCGYQII DKRGHQHGGGTALVQCGN DKRGHQHGGGTALVQCGN							IATVTGTERDPQCRSQQIATLED
SFALELQSASKPVVHYQWSI AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCAPND DARPLSAVQGEKIDEVPIGSC TNIGHFRAAGKLIDAHKQQ RLWVAPPTRMDAQLTEEG SVFGKSGARVSSIPCAVPCV' RVADCATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEETYOTYVAQVDKTAVDT YLNFNQLSQYTEKADGLIK, RPWRKILDTLATYHEGHRI GPGRERLRRMALPMEDEAL  25576 55944 A 25717 I 417 MGVLNNWLSEEESLWIQSR RALRYYSNWRYFAGYTET YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIIR YLALLPSFHETETPOPOFRQLI AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTTIANNTAHLSFECV AERLRWLQSERNTGEIDEEL LYALAKGWVPNFOTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGITALYQCGN							
AGQGKWLANPELLEADAD/ AAVIDIDLADIKEPILCAPNO DARPLSAVQGEKIDEVFIGSK TINIGHFRAAGKLLDAHKGQ RLWAPPTRANDAQI-TEEG SVFGKSGARVSSIFCAVPCV RVADGATVVSTSTRYFPRII GANVFLASAELAAVAALIGI TPEEYQTTYVAQVDKTAVDT YLNPNQLSGYPTKAADGLK, RPWRKILDITLATYHEQHRI GPGRELRRMALPMEDEAL, GPGRELRRMALPMEDEAL, TALLPSFHPETDPODFKGL AYESALKAVAVAUGH EVAEHELLAFRALLASDSEF PSAWQRFIGQLIVSCMSEDID RWSLCTIAMNTAHLSFECV AERLRWLQSEDTIONTOMINGSMSTEEL FLYAIAKGNVFNFOTILHLP RRPDICTOMINGSMSTEEL FLYAIAKGNVFNFOTILHLP RRPDICTOMINGSMEGGIYGI DKRCHQHGGITALVQCON DKRCHQHGGGITALVQCON			1				SPAAQQHTPSLLENVAVINIGLR
AAVIDIDLADIKEPILCAPND DARPLSAVGEKIDEVFIGSG TTNIGHFRAAGKLLDAHKGQ RLWVAPPTRMDAAQLTEEG SVFGKSGARVSSIFCAVPCVV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIGI TPEEPYOTYVAQVDKTAVDTI YLNFNQLSQYTEKADGLLK. RPWQKLIDLTATYHEQHRI GPGRERLRRMALPMEDEAL GPGRERLRRMALPMEDEAL AUSTING RALRYYSNWRQYFAGVTFG YWQSPEDDHLPLLREFLARN PMKNCWKLIDJEETITOVDIR YLALLPSFHPETDPQDFKGLL AYEEALRIAQSPAKSWQPE EVAFHELLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIAMNTAHLSFECV AERLRWLQSENTGEHEEL FLYAIAKGRVFNFOTILHLP RRPDGTOTHNDQSRCEGYQI DKRGHQHGGGTALVQCGN							SFALELQSASKPVVHYQWSPV
DARPLSAVQGEKIDEVFIGSK TNIGHFRAAGKLLDAHKOQ RLWVAPFTRMDAAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTNFPPRII GANVFLASAELAAVAALIGI TPEEYQTYVAQVDKTAVDT YLNFNQLSYTEKADGLLKI RPWQRKILDTLATYHEOHRI GPGRERLRRMALPMEDEAL 25576 55944 A 25717 I 417 MGVLNNWLSEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLRFLARS PMKNCWKILDIEETTDVDII YLALLPSFHPETDPOFFGCL AYEEALRIAQSPAKSVWQPE EVAEHELLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQSERITGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTYHNDQSRCEGYQI DKRGHQHGGGTALVQCGN							
TIMIGHERAAGKLIDAHKOQ RLWVAPPTRMDAQLITEG SVFGKSGARVSSIPGAVPCV' RVADOATVVSTSTRNFPNRI GANVPLASAELAAVAALIGI TPEEYQTYVAQVDKTAVDT YLNFNQLSQYTEKADGLIK. RPWQRKILDTLATYHEQHRI GPGRERLRRMALPMEDEAL: MGVLNNNWLSEEESLWIQSRI RALRYYSNWRQVFAGVTFG YWQSPEDDHLPLLREFLARN PMKNCWKILDIEETTDVDIIR YLALLSFHIPETDPQDFKQLI AYEEALRIAQSPAKSVWQPE EVAFHELLARFALLASDSEP PSAWQRIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEROTGEIDEEL FLYAIAKGNVFNFQTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGITALYQCGN			ı				AAVIDIDLADIKEPILCAPNDPD
RLWVAPPTRMDAQLTEEG SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEYOTYVAQVDKTAVDT YLNFRQLSQYTEKADGLIK. RPWQRKILDTLATYHEQHRI GPGREILRRMALPMEDBAL. 25576 55944 A 25717 I 417 MGVLNNWLSEEESLWIQSR RALRYYSNWRQYFAGVTEG YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIIR YLALLPSFHETDPOPFRGL AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEROTGEIDEEL LYAIAKGWVFNFOTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGITALYQCGN			1	ļ		i	DARPLSAVQGEKIDEVFIGSCM
SVFGKSGARVSSIPCAVPCV RVADGATVVSTSTRNFPNRI GANVFLASAELAAVAALIG TPEEYQTYVAQVDKTAVDT YLNFNQLSQYFKADGLIK. RPWQRKILDTLATYHEQHRI GPGRELRRMALPMEDEAL. 25576 55944 A 25717 I 417 MCVLNNWLSEESLWIQSR RALRYYSNWRQYFAGYTFG YWQSFEDDHLPLLRFFLARY PMKNCWKILDIEETTDVDIIR YLALLPSHIPETDPODFKGLI A YEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSE PSAWQRFIQCLNYCSMEEDID RWSLCTIAMNTAHLSFECV AERLRWLQSEDTGENTGEIDEEL FLYAIAKGNVFNFQTILHLPV RRFDICTOHNDQSRCEGYQII DKRGHQHGGGITALYQCGN DKRGHQHGGGITALYQCGN				1			TNIGHFRAAGKLLDAHKGQLPT
RYADOA TYVSTSTRYPPRII GANYFLASAELAAVAALIGI TPEEYQTYVAQVDKTAVDT YLNFNQLSQYTEKADGLLK. RPWQRKLIDTLATYHEQHRI GPGRERLRRMALPMEDEAL  25576 55944 A 25717 I 417 MGVLNNWLSEEESLWIQSRI RALRYYSNWRQYFAGYTEC YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIIR YLALLISFHPETDPQDFKQLL AYEEALRIAQSPAKSWQPE EVAHEILLAFRALLASDSEP PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECVA AERLRWLQEROTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGTALYQCGN							
GANVFLASAELAAVAALIGI TPEEYQTYVAQVDKTAVDT YLNRVQLSQYTEKADGLIK. RPWQRKILDTLATYHEOHRI GPGRERLRRMALPMEDEAL. 25576 55944 A 25717 I 417 MGVLNNWLSEESLWIQSRI RALRYYSNWRQYFAGYTFG YWQSFEDDHLPLLRFLARN PMKNCWKILDIEETTDVDIII YLALLPSFHETDPODFKQL AYEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQSEDFTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTQHNDQSRGEGYQI DKRGHQHGGITALVQCGN	1		ŀ	l			
TPEEYOTYVAQVDKTAVDT YLNFNQLSQYTEKABGLKI RPWQRKLIDTLATHEQHRI GPGRERLRRMALPMEDEAL  25576 55944 A 25717 I 417 MGVLNNWLSEESLWIQSR RALRYYSNWQVFAGYTEG YWQSPEDHLPLLREFLARI PMKNCWLIDIBETTDVDIB YLALLPSFHPETDPQDFKQLI AYEEALRIAQSPAKSVWQPE EVAFHELLARFALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEENTGEIDEEL FLYAIAKGNVFNFQTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGTALYQCGN				1			
25576 55944 A 25717 I 417 MGVLNNWLSEEESLWIQSR RALRYYSNWAQYFACHTOF YWQSPEDDHLPLLREFLARY PMKNCWLIDIEATHOUTH YLALLSFHEETHOUTH YLALLSFHEETHOUTH YLALLSFHEETHOUTH RYALLASDEF PSAWQRTQQLNYCSMEED RWSLCTIANNTAHLSFECV AERLRUQCSPACSUCCHEEL FLYALAKGWYPNOTHLHLP RRPDICTQHNQSRCEGYQI DKRCHQHGGITALYQCSN							GANVFLASAELAAVAALIGKLP
RPWQRKILDTLATYHEQHRI GPGRERLRRMALPMEDEAL 25576 55944 A 25717 I 417 MGVLNNWLSEEESLWIQSRI RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIBI YLALLPSFHPETDPODPKQLI A YEEALRIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIAMNTAHLSFECVV AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFGTILHLPY RRPDICTQHNDQSRCEGYQII DKRGHQHGGGTALYQCGN							TPEEYQTYVAQVDKTAVDTYR
GPGRERLRRMALPMEDEAL 25576 55944 A 25717 I 417 MGVLINIWLSEEESLWIQSRI RALRYYSNWAQYFAGYTFG YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIIR YLALLISFHPETDPQDFKQLI AYEEALRIAQSPAKSVWQPE EVAHEILLARFALLASDSEP PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQSENTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGTALYQCGN							YLNFNQLSQYTEKADGLLKPRF
25776 55944 A 25717 I 417 MGVLNNWLSEESSLWIQSR RALRYYSNWRQYFAGYTFG YWQSFEDDHLPLLRFLARN PMKNCWKILDIEETTDVDIIB YLALLPSFIPETDPODFKGL AYEEALRIAQSPAKSVWQPE EVAHEILLAFRALLASDSEI PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEENTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDICTOHNDQSRCEGYQII DKRCHQHGGITALYQCON							
RALRYYSNWRQYFAGYTFG YWQSPEDDHLPLLREFLARY PMKNCWKILDIEETTDVDIBI YLALLPSFHPETDPQDFKQLI AYEALRIAQSPAKSWWQPF EVAFHEILLARALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIAMNTAHLSFECVY AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPY RRPDICTQHNDQSRCEGYQII DKRGHQHGGGTALYQCGN			_			_	GPGRERLRRMALPMEDEALVL
YWQSPEDHLPLLREFLARY PMKNCWKILDIEETTDVDIIR YLALLSFHPETDPQDFKQLI AYEEALRIAQSPAKSVWQPE EVAHEILLAFRALLASDSE PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECVA AERLRWLQEENTGEIDEEL FLYAIAKGNVFNFOTILHLPY RRPDICTQHNDQSRCEGYQII DKRGHQHGGGTALYQCGN	25576	55944	Α	25717	I	417	MGVLNNWLSEEESLWIQSRIHL
PMKNCWKILDIEETTDVDIIR YLALLISFHPETDPOPFRQLI AYPEALRIAQSPAKSTWOPP EVAEHEILLAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIAMTAHLSFECY AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPY RRPDICTQHNDQSRCEGYQII DKRCHQHGGGTALYQCGN							RALRYYSNWRQYFAGYTFGRQ
YLALLPSFHPETDPODFKQLI A YEEARIAQSPAKSVWQPE EVAEHEILLAFRALLASDSEI PSAWQRFIQQLNYCSMEEID R WSLCTIAMNTAHLSFECVY AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPY RRPDICTQHNDQSRCEGYQII DKRGHQHGGGTALYQCGN							YWQSPEDDHLPLLREFLARYER
AYEEALRIAQSPAKSVWQPE EVAEHEILAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV AERLRWLQEENTGEIDEEL FLYAIAKGNVFNFOTILHLP RRPDCTYDHNDQSRCEGYQI DKRCHQHGGITALYQCON							PMKNCWKILDIEETTDVDIIRRA
EVAEHEILLAFRALLASDSEF PSAWQRFIQQLNYCSMEEID RWSLCTIAMTAHLSFECV AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPV RRPDICTQHNDQSRCEGYQII DKRCHQHGGGTALYQCSN			1				YLALLPSFHPETDPQDFKQLRQ
PSAWQRFIQQLNYCSMEEID RWSLCTIANNTAHLSFECV\ AERLRWLQEENTGEIDEEL FLYAIAKGNVFNFQTILHLP\ RRPDICTQHNDQSRCEGYQII DKRGHQHGGITALYQCS\			l				AYEEALRIAQSPAKSVWQPEEY
RWSLCTIAMNTAHLSFECVV AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLPV RRPDICTQHNDQSRCEGVQII DKRGHQHGGGITALYQCGN							EVAEHEILLAFRALLASDSERFL
AERLRWLQEENTGEIDEEEL FLYAIAKGNVFNFQTILHLP/ RRPDICTQHNDQSRCEGYQII DKRCHQHGGITALYQCS							PSAWQRFIQQLNYCSMEEIDEL
FLYAIAKGNVFNFOTILHLP RRPDICTQHNDQSRCEGYQI DKRGHQHGGGTALYQCSN							RWSLCTIAMNTAHLSFECVVLL
RRPDICTQHNDQSRCEGYQII DKRGHQHGGGITALYQCGN							AERLRWLQEENTGEIDEEELGS
DKRGHQHGGGITALYQCGN							FLYAIAKGNVFNFQTILHLPVA
							RRPDICTQHNDQSRCEGYQILS
PRAKGERLFFDAPA*CASSAI							DKRGHQHGGGITALYQCGNAD
							PRAKGERLFFDAPA*CASSARV
CVLSLAGASKKSRSPFARGS.							CVLSLAGASKKSRSPFARGSAL
PHWYRAVMPPPCW							PHWYRAVMPPPCW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino seid	*=Stop endnn, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25577	55945	Α	25718	1680	2058	YRAYAPAFLPLSPSCPPLWRHC
						GSGRGENRRRDSSAHGPYAPRR
						QPDMPAHRQS*SFV/PASCSAC
						MDEPHKRLTVTAGTECGTSASS
		l				AALRAILKPCSSVCSSFFLLLLL
						PPPPPSSSSSSFFFLF
25578	55946	Α	25719	1115	3549	NPDRLLQLNLILETSK*QQMGD
						TRKKRS/NLTVAPIISPLKRYEQ
						HTELSRHINVVNLGDRNRRQQL
						ILDQGKSSQRNIYLSHVAQKIPG
						RATYALSHSVDMITIQLGTLLR
						CAPPHRRRYAGRFFCRSAGNFL
		l				NVQGFDAVLVAVKIIDLLLCLT
İ				ļ		IAPSLIVCTRLRSPWCGALRRCS
		1			-	TDGRSDLASSGVMFSIDTESAL
						TRWCLSLPHGALGKIIAEGLLS
1						VIASKASAIVTTVAVVPVTRRSS
		1				LVNWHSGGSGLWRCNRTDERD
						QQASQGTTRMGRTQRNYSPTR
						QAIHKTGSPTMATTSNTEQPPH
						EKPNTLTQHPRNPDRTIHPKAT
						HNELTQDTPQRDAKQNGEKTQ
						RKKNCLSELNDAEDQAERFQD
						RLMLKLQVTTKPCSMTRLRDC
						AGIWSAANRWSGIGIDRMIMLF
		l				TNSHTIATLFSSRRCAHRNKFH
						LMNEAVRRLLRSSFRKSVLRRD
						ASFHDNQRVHSLQLLKERKKSL
						IHGRICAAKASLFQTRRYRWQK
1						APLFSAQFRGRNRAVTHNRWV
						TTTTAIERTRARGLRPNSGRGF
						HSSPAWQLRHRKCRRCARRYH
		1				TVYWIKRRRSVARASTVVSGRI
		1				TSRRGENRRRDSSAIAHMLHAA
						KQTCLRIAVMIIRAASCSACMD
						EPPSDLTVTAGTDAGLAPAGYA
1						LNERROLLHALTKSTALRTAHR
						GPNRTGWLNRRIVRFVMTALF
25579	55947	A	25720	606	1562	
25580	55948	A	25721	688	762	OV DOCUMENT BERNALLY AGAINSTAN
25581	55949	Α	25722	492	737	SLPSGATLPPPALLLASAPDTA*
	l			I	1	WRCRER*YHLPAYAALSPAVA
	l					HRASLYSTLPSSVPWRRQCAGF
L	L				l	RARRSPEQAWAYPAR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25582	55950	A	25723	335	903	WVHDLPARKGSSARNIMLKSA PLRGHTRTRRKKMNIEANVAT PDARVAITIARFNNFINDSLLEG AIDALKRIGGVKDENITVVWVP GAYELPLAAGALAKTGKYDAG IALGTGIRGGTAHFEYVAGGAS NGLAHVGODSEIPVAFGVLTT ESI/EQAIERAGTKVGNKGAEA ALTALEMINVLKAIKA
25583	55951	A	25724	3644	4545	SEAWPWRTAGTCLLCLNTT/AH VDKAIESRTVVADVLAKENAL TGKLLTVSFQAHEAVIHGHIPA PEENLQVLAALRLQVLQGDYT LHAAIPPLEEVYSLQRLKARISQ KIKTFTPCERLEKRRISFLEGTL RRSFRTGSVVRQKVEEEQMLD MWIKEEVSSARASIIDK WRKFQ GMNQEQAMAKYMALIKEWPG YGSTLFDVECKEGGPPQELWL GVSADAVSVKRGEGRPLEVF QYEHILSFGAPLANTYKIVVDE RELLFETSEVVDVAKLMKAYIS MIVKRKPSTRSASSOGSSIR
25584	55952	A	25725	1	735	
25585	55953	A	25726	147	504	STCPASAPPRPSAGPRILSGSSAS GSPLGSSSASSPAVHKG*RFWL TG*CGP*VSAGNKULFERWDGS VQSIIPLQILESQGSKNLEVFFRG WMVAMDNRFVGLKGDSQQLS GQRIFKLG
25586	55954	Α	25727	1	639	
25587	55955	Α	25728	I	1247	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25588	55956	Α	25729	1	2376	MAEVEEKKQRIFRKFTYRGVD
ļ						LGQLLDMSFEQLRQLYGARQL
						RRLNHGLWRNAEAQAAFAAE
				l		APMLGQEGGADHREAGSGEDA
Ì						PAGYDHPSQDGGQQGGRLQRQ
						DLQPGGDQAGDDRPRPGRVLH
						HLQAQRGKKPM/ISTVTFGQ*P
						DPPLRAGQRL*RC/RLLIYGRGK
						CWALSGNP/RSGKTTLLKSISAR
						LTPQQGEIHYENRSLYAMSEAD
						RRRLLRTEWGVVHQHPLDGLR
l		l				RQVSAGGNIGERLMATGARHY
				1		GDIRATAQKWLEEVEIPANRID
					ŀ	DLPTTFLRATHTVKMFSIPGYSS
						PGQLLDPETNINIGTSYLQYVY
						QQFGNNRIFSSAAYNAGPGRVA
						TAIVLTLYIIYMVGFFATSGELT
			İ			YEVWIGFFASAFTKVFTLLALF
						SILIHAWIGMWQVLTDYVKPLA
	ļ	l				LRLMLQLVIVVALVVYVIYGFV
		l				VVWGMRAALQISQSGQTCALL
1		1				SKVFPTRSHTVSAQGGITVALG
1						NTHEDNWEWHMYDTVKGSDY
						IDAGRKRQEEGDWNSGVGDPS
		1				DAGDRKHQLKAAQLRPEAIKQ
		l				RRIANRLKRRTQFPRHLKGFVN
		l				TLKPIHGGCSVGTKCPQMASLP
	1	l				EGLHHPVKLVFLGKPGCLLTDR
Į.	}	l				PLKGPNTAKPVAVDLNASATAI
		l		l		TSYSLYGGSMILLFLASTLYHAI
1	į	l		1		PHQRAKMWLKKFDHCAIYLLI
		l				AGTYTPFLLVGLDSPLARGLMI
25589	55957	Α	25730	219	652	SASWREAICLSRCRLPRSATAR
		l				GAGRGGCGLADRRASRQGKNL
		1				EAESAQEONGHOHRIHESOHPC
		l				QGGAPVSHHQAAVRLRESQIQ
		1				GAAEKR*PTGDVIHPGQPVSGG
		1				/LK*YPSIPTCLLTTRTASLLKPP
						GVRTSVCWQQLPR
25590	55958	A	25731	1902	2100	RKFFSSSSGRS*PVRCSKL*SSID
						A*PLERIKRSRSYOVGSVGLCL
						RKSFHSTSAISAMPIGAPG
25591	55959	A	25732	3223	3669	
20071	33737	1,,	20102		5007	L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
25592	55960	Α	25733	1	4325	MPEPPTHSMGSCAAGASLTSTA
		1				PCSTAPSPIDHLRAKECERTAQ
		l			1	DWQAAPPAALVRDPLAALVRT
		1				WRTFMSSSRIVNTPIGTLCLAQ
	ľ	1				GFQWFSVLSQVHASTDQEIQE
						MHDEQANPQNAVGTLDVGLID
					1	SVCASDSPDRPNSFVIITANRVL
						HCNADTPEEMHHWITLLQRSK
						GDTRVEGQEFIVRGWLHKEVK
						NSPKMSSLKLKKRWFVLTHIPG
						LLQEFREDALNWGPDEKIFKET
						ELVNDMDKINGRIERAE
25593	55961	A	25734	501	2871	TGCCCLRKTDCRRRESARGVH
				į.		AVYRRICARSMLLYRESVRPKA
		1				VTARVAVEAGIADYWYKYVG
						LNGAIVGMTTFGESAPAELLFE
				ì		EFGFTVDNPLASRAVRLRLPFN
1						NDQVEAAVGWKLAVERHNGP
		1				TALILSRQNLAQVERTPDQVKE
						IARGGYVLKDSGGKPDIILIATG
						SEMEITLQAAEKLAGEGRNVR
						VVSLPSTDIFDAQDEEYRESVLF
						SNVAARVAVEAGIADYWYKY
						VGLKGAIVGMTGYGESAPADK
						LFPFFGFTAENIVAKAHKVLGV
						KAGSHIPRKKYDVPGKKSFSPV
						KYSTIGSPSPERPVSITTIPNSFVI
l		1				ITANRVLHCNADTPEEMHHWIT
1		i				LLQRSKGDTRVEGQEFIVVEKL
		1				IRGLAMEDSRNMFALFEYNGH
						VDKAIESRTVVADVLAKFEKEP
l	1	1				VGKHLPTYDGQIAMGLESTAS
ŀ		1				VTRKHSSPSSLQNALSCETATSL
ĺ		ı				IERRVRMALGTGDRRGLNTWL
						ARLPMEAKEKDEWRYWQADL
						LLERGREAEAKEILHQLMQQR
						GFYPMVAAQRIGEEYELKIDKA
						PQNVDSALTQGPEMARVRELM
		1				YWNLDNTARSEWAN\LLKNKS
	1	1		1		KPDRAHLPGYASTTQWWILSV
l		1	1	1		QATT\AGNLGDHLKERFPLANN
		1		1		DLSKRYTSGKKIPQSYAMAIAR
		1				QKSAWNPKVKSPVGASGLMQI
ĺ		1		1	1	MPGTATHTVKMFSIPGYSSPGQ
25594	55962	A	25735	1	1195	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
25595	55963	A	25736	1931	2676	FCGNTHQTYLGWVGGVANSEA *GEKWGTPDLVG/AERTETIQR
l		1				LLGVCPEQGEGKIYIDGKQVDI
		1				RNCQQAIAQGIAMVPEDRKRD
						GIVPVMAVGKNITLAALNKFTG
	l	1				GISQLDDAAEQKCILESIQQLKV
						KTSSPDLAIGRLSGGNQQKAIL
						ARCLLLNPRILILDEPTRGIDIGA
	1					KYEIYKLINQLVQQGIAVIVISS
	1					ELPEVLGLSDRVLVMHEGKLK
						ANLINHNLTQEQVMEAALRSE
	L	_				HHVEKQSV
25596	55964	A	25737	1491	1667	TNGQWRAFYC*MRSGRNIRRR
						GEDISGGAGVSPRESPE*REVPE
		_				MGPGGAANRGTKRV
25597	55965	Α	25738	419	823	VTLVAITRPIHVNRLRQYLVAIS
						LNETFGPSCKPSRSPCSSLSTCC
	l					WNAGVMHKK*VQGGRLCSYR
	l	ļ		1		N*SICLVVISPVVMGKRCIS*RC
		1				TAVLAALTVTVPSGVVAAHSV
		_				MLPRLPMKRSSIVPLPSNWRTS
25598	55966	A	25739	591	968	VKQCKQADEH*EQSLIPLERRR
				İ		TTPLSVPQL/GKALTTVSFCASG
ļ		1				GTSVNSLSHTS*ECMASAVAVK
						FTFPNLAVNFCTAAMAGPKVA
	1					LTSTLARIQAGSLARTGGRAYR
		١	0.00.10		1000	WSRSTMLAKSFWCLMAL
25599	55967	A	25740	764	1005	QARPRAPRRAPYPILIRSSIITLIY
	1					/DGQRLGHLDDGTDSWNHVPT
		ł				LNGQCTLVLIHEYVDTRGPEIK TILVISWWNILVFH
25500	55968	١.	25741	463	786	TILVISW WNILVFH
25600 25601	55969	A	25741	3	646	
25602	55970	A	25743	1	3008	MTMLOIVGALILLIAGFAILRLL
25002	1559/0	A	23743	1	3008	FRALISTASALAGLILLCLFGPA
İ		1				LLAGYITERITRLFHIRWLAGVF
		1			İ	LTIAGMIISFMWGLDGKHIALE
		ļ.				AHTFDSVKFILTTALAGGLLAV
		1				PLQIKNIQQNGITPEDISKEINGY
	1					
						YCCFYTAFFLMACSDQRRLRG AMDKRYKFILVGFGEVFVFNLE
1				1		
l		1				SLDSGKKIHLLRRSHEEVMGSV
1	1			1		MRTGTIDKGILPFIHHTRGNEIL
1		1		1		FIPALFILFSLGGAVFGMGEEAV
		$\perp$	L	L	l	AFAIIIA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		_				
25603	55971	A	25744	2	3494	TITNLRPAAPGICEMAQGLSAG
						GEYTGASIFVAEYSPDRRRGFM
						GSWLDLRSIAEIELGAGGVGLIS
						TIVGEANFLDWGWRIPFFIALPL
			ŀ			GIIGLYLRHALEDTPAFQQHVD
			İ			KLEQGDREGLQDGPKVSLKEIA
						TKYWRSLLTCIGLVIATNVTYY
						MLLTYMPSYLSHNLHYSEDHG
i						ALIIIAIMIGMLFVQPVMGLLSD
					İ	RFGRRPFVLLGSVALFVLAIPAF
		l				ILINSNVIGLNLLPAMFPTHIRYS
		l				ALLLEMKN
25604	55972	Α	25745	1	277	
25605	55973	Α	25746	902	1006	
25606	55974	A	25747	2	1265	
25607	55975	Α	25748	409	525	
25608	55976	Α	25749	91	431	NHKPGNIDVARRIQRGFAGDQI
		1				GHLRPVERQCSPDKRRFIAADG
						REIRGKQRAGHIFQLLSRCLLQI
		1				LNHCQRRAAHFRFQLSNQRHQ
						QLLPV/HYHAAEREYPAGACLV
						RWLL
25609	55977	Α	25750	3	71	
25610	55978	Α	25751	1	1212	
25611	55979	Α	25752	Ĭ	2786	MAAVIEQIRRAVLALVTGVVHP
			ŀ			GDIPVVWDIVWNATAAFIAVIII
1		İ		ł		SLLLDESGFFEWAALHVLRWG
			1			YGPGRLPFNRIGLIRRITRRIRQR
		1				LLFGLVTFILLLNRSQNPAQDIQ
						LLAFRARTGKQTAQFIHHLPRM
1						VFTDKTGSSNGLAPQGQCSAQ
		1				GELILNEKLAKQLVTAANWVK
1						MOSDEGEINPVDILRWPGVMA
						AQEQDLDAIAAEILAALDGTLD
						DFIVARETEGOSGLKRVYHSPG
						APDIREFTRDAIP
25612	55980	A	25753	5	402	EIFSVVWIIMTRGDVVTISRWR
		1		[		VSSSPLETWNKRWAKISPAPFS
						LLPISRLEKSEGDWLPETVISAF
	l		1			NMPSSLSLIISSL*FKVRDV*HFF
			ĺ			/RI*TLRGHYRVINWPNFNIVVS
						QGIGKRLANSWLVFTLFHRI
25613	55981	A	25754	48	219	PETCGHLWAYVWPSCAAV\GL
23013	22901	^	20104	70	-17	YFKVHVLG*RSVTPVTDIVKLL
						EFTRLRLPGYTKSIE
25614	55982	A	25755	1	912	El React Of I Rolls
23014	22702	<u>_</u>	23133	l	/12	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last aminu acid	*=Stop endnn, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25615	55983	Α	25756	1	1857	MRVCARACVRTRTRMCVYAH
		1				TCVCVRTYAYVRVRVRVRVHVRA
		1				RVRVCAYARTRVRNSLSILPFIC
		1				LTLATPIHHIHOEEFNIRGIVPVI
	1	1				RRVKPDLAIGIDITPSCDTPDLH
		1				DYSEVRINGGVGITCLNYHGRO
	1	1				TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
		1				GWEIGFSPLALLLAFLCSTSPGF
		1				GDPDGLGVIAYQDTVRPNAAT
		ŀ				AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
		ŀ				KAVTELNQHAPLAMVGDGIND
						APAMKAAAIGIAMGSGTDVAL
		1				ETADAALTHNHLRGLVQMIEL
						ARATHANIRONITIALGLKGIFL
		1				VTTLDDRVVAGSAGRYGGDGA
		1	l			GDSECVKIVAQEIRQTDRNIER
		1				DRSPRPSGERVRVRGKGGIEAN
		1				QPLSTAFTNQITIRQSIRLFSNQF
		l	l			VFHKGISRVVAGSSAIISNVSPG
		ı	l	ł		CILRTPNCRRGFPISCTGEGKAA
		1			1	YGWQRDGGHAEYLLAEEKDLI
						LLPDALSYEDGAFISCGVGTAY
			l			EGILRGEVSGSDNVLVVGLGPV
						GMMAMMLAKGRGAKRIIGVD
			1			MLPERLAMAKQLGVMDHGY*I
			İ			LPDVY/V*IGVARVSWMNGRID
						SELRTRVRAYAHTRTRARTCTR
						TRTRTYAYVRTHTHVCAYTHM
	1	1				RVRVRTHARAHTR
25616	55984	Α	25757	3	1180	SKLGTRRSVVWA*SPSTSPTLW
		1				CSTFSAAGHSSMKRMNEFVDL
				1		LPAQQRMKGENWYRGTADAV
						TQNLDIIRRYKAEYVVILAGDHI
						YKQDYSRMLIDHVEKGARCTV
		1				ACMPVPIEEASAFGVMAVDEN
		1				DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
						RDENSSHDFGKDLIPKITEAGLA
						YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
		1				PAGPPLPLPAARSEAPKAAGTV
						ASVPSIAPARLRPVPDPVELVLV
						AAEFITPGDPTPRLHGSGFIDIR
						QIHHQTRSHLEGVKTGIRFLNH
						FSGNPQGGIAHVNGVARFQVK
		1		1		QCHQAWGQQYAARLRFQARGI
		1				SLQIAIHRVDIIHRFDVRQL
25617	55985	A	25758	16	543	
25618	55986		25759	1	3387	
		1' -				

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25619	55987	A	25760	1688	2234	LSVGKTFPVLVPAAFRKVSATG
		1				AAVPGTPSILALPSYSTTPFGVC
		1		l		TSASMNVPVLTLRIRTRVTGEV
						AAIKPFSMANAPTPDSILPQLGV
		l		l		VSTRCS*TITCANR*STSARGSL
		1				ERLIMATLL/WVAGTFD*SVWF
		1				GHDTDVVTLYRFHEALCYSVT
						LRTPHRRVLRFKSQHPGELACF SPVA
25620	55988	A	25761	905	4762	PPHNWMPSNATPGIAFVWCAY
						GAI/LPGDAPVPVVDDYRKVVR
		i				KDTKGLIARWKYFWMSVIALG
	1	l				VAFALYLAGKDTPATOLVVPFF
	l		}	1	KDVMPOLGLFYILLAYFVIVGT	
		1	į			GNAVNLTDGLDGLAIMPTVFV
	l				AGGFALVAWATGNMNFASYL	
	ļ	l				HIPYLRHAGELVIVCTAIVGAG
1	1	l				LGFLWFNTYPAQVFMGDVGSL
	1	l				ALGGALGIIAVLLRQEFLLVIM
	l				GGVFVVETLSVILQVGSFKLRG	
		l				QRIFRMAPIHHHYELKGWP
25621	55989	Α	25762	1	1448	MCHVLLAGRQRRTAGPEHALT
	1	l				PPECGSAAIGPAVYKWAHATG
	İ	1				VMIPDRPRSPHAGAEERHWHH
		l				PQPELISQRLGSFSSGPTKYIHEF
					1	QYLTLSYNLTWSDLNVILTFILP
						LDEWERVFSLAQSHTDNCRLH
		l				KPDLQEGIREVPQEDPQWNYQ
						ENSPGIARRDYMISCLVEGLKK
		1	1			AAYKAINYDKLKETTQGTDKN
		1				PAQSMACLAATMRHFAALDPE
	l l	1				ALAPHRDVNHGIKLTCKTIRSSI
		l				DISREIRAPRECRSTEMASWHPP
1	1	l				ADLTECPVESGYSVLSGRTDCQ
	ł	l				YSHTVRRACLTTIDSRPAVRQL
		l				LKIREVQLLSLLRGCVRSRRSGS
	1	1				INAQYCRCLERVVTLPFFDSGPS
	1		l			LMNHAPHLYFAWQQLVEKSQL
	1	1	l			MLRLATEEQWDELIASEMAYV
	1	1	l			NAVQEIAHLTEEVDPSTTMQEQ
	1	1	1			LRPMLRLILDNESKVKQVLQIR
	1	1	l			Q\DGLAKLVEQLRHLSKKHHLD
	1	ĺ		l		TDSTSSSLPGVRTPYSPIRGGEE

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25622	55990	A	25763	1029	1665	RPESISSVASKTRLGRSFHGAAR
-		l				RTREYHSSTCNASIAAAATV\A
ł		l				AQGHPDTTSTPPASVDTTATNT
		1		l	1	QTPAVTAPAPAVDPOONAVVS
		l			i	PSOANVDTAATPAPTAATTPDG
		l		l		AAPLPTDQAGVTTPVADPNAL
		l				VMNFTADCWLEVTDATGKKLF
		l				SGMORKDGNLNLTGOAPYKLK
		l				IGAPAAVQIQYQGKPVDLSRFIR
	1	l		l		TNOVARLTLNAEQSPAQ
25623	5599I	Α	25764	658	1307	SNRLYTDVESINEIEGIYMKLRF
		l				ISSALAAALFAATGSYAAVVDG
		l			ŀ	GTIHFEGELVNAACSVNTDSAD
	ł	l				QVVTLGQYRTDIFNAVGNTSAL
1	1	l				IPFTIQLNDCDPVVAANAAVAF
	1	1				SGQADAINDNLLAIASSTNTTT
		l				ATGVGIEILDNTSAILKPDGNSF
	ŀ	1				STN\QNLIPGT\NVLHGLAFRAR
	Į.	1				CVSTANLRVPRPICFDPGSSYQA
						NTIGSGRCADCQPDA
25624	55992	Α	25765	167	232	
25625	55993	Α	25766	441	686	
25626	55994	A	25767	206	331	
25627	55995	A	25768	674	900	VVPICTMLEEALERQNLTASLC
		l	l			G*LKKACGRSWQTSPIKRSLNG
						AKFSRTSIIMGFITAEKWSGWEI
25628	55996	A	25769	41	222	WSARNVTS
25629	55997	A	25770	17	525	ESLECSGPSWNASGTQSGFYCH
23029	33337	^	23770	1''	323	RIAPILPEKRLARMVEKTWGLG
		l		l		LRRRTGFRRQNLGGGTGTLVE
		l				CTSENS\KPSKSSFRKORRGORR
	1	l				EGH*SLRR*IRRERTERMOASR
		l				VTWNSFPQVPAAKKPSSLSESG
1		1				*P*ATNYTREODSMWNCVHHY
						WOPPTSVSRLVHLNSG
25630	55998	A	25771	698	1051	PYLRIRLTALISRSSTVMRILFAI
		1	l	1		SKRPIT*PKRPKPTTMTWGLSSL
l	1		l	l		THGFSSSSSGPLNWRDSHLSTSF
						ISNGVVIMESVTVTSNNAIWSPS
l				l		SSVAAVNTSRTPEAAIKRNTGR
	1		l	1		SK
25631	55999	Α	25772	1	2204	
		_				

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	Incation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25632	56000	IA.	25773	3	891	RYRNQDDHELQIHTGTRFYVEL
23032	30000	^	23113	3	1051	CGFRVNPPWLATDVTHAAMAL
		l				
		l				LTLVTTGLHIVGEWGKHATPPV
					i .	PYSICSNPPRRAAYITVWRNRPC
		1				TLGDHLFSIAYPRGLRYDMGG
		1		1		GGEGTA WANVRQALARTTGR
		1				AQHWTKDNAKSSREARHPRQN
	1	1				KTKTHLGKPVLRWV/DPSFDQS
						KYDSIVWNPI/TYYPVPKPSTQV
						GQKV/LDKILNYTNTEMKEAIA
						H/DTSKEGLQFYEVVPVALVVA
						GTQMATGLRTMDTRLYFEGELI
						DAAPNKPVIKVVRQGEEPDWP
		_				SKGDAGDGEKVPSSLSESG
25633	56001	Α	25774	1	285	
25634	56002	Α	25775	1	302	SFSSFTQRTASVIISSTSTQSRLA
		l				TSPILAIARARTSRRCPEKPQLG
	1				1	YPDSAAHVFQQDRATKYVINR
	1	1				NSKKP*ICSACRSTVSTRQHRR
						WRGSLQPLSQ
25635	56003	Α	25776	307	473	
25636	56004	В	25777	67	809	
25637	56005	A	25778	44	1519	MAIN OUT WATER TO SEE THE
25638	56006	A	25779	1	1519	MINRLQHTVYTHKWNSYRTEP DRRHTALRNSFCLVRLNDSSHS
1		1				
1		ı				RSLDSKQGHTEITFAATEHPPSP
}		1				VSLRIHDVAFDDGRQTSRAPCF
l		1				NLEQPGKLDCTKRLISDCWVM
l		1				HPGESWHGFKDIPDNWSMLDPI
ĺ	1	1	l			KISILAPGMGEDGELEETGVPA
		1				ALVTAWLGRHGIVPTRTTDFQI
ŀ		1				MFLFSMGVTRGKWGTLVNTLC
	İ	1	l			SFKRHYDANTPLAQVMPELVE
	1	1			i	QYPDTYANMGIHDLGDTMFA
	1		1			WLKENYSGARLNEAYS/GLPSII
						ERHVVDAQGYRGGGMLCSCES
		<u> </u>				NFCVSLLRIQAS
25639	56007	Α	25780	461	789	HHVLSELQQLYTAYRSVDHIID
		ļ				HSLAIARAPQRRRCPEKPQLGY
1		1				PDSLQHVFQQDRATKYVINGTS
l						KKP*ICSACRSTVTHGHTDAGE
						EVWNPFAVLVPSGKDARVWG
25640	56008	В	25781	1	990	
25641	56009	A	25782	1	3066	
25642	56010	Α	25783	583	904	WGIRTTDFQIMFLFSMGVTRGK
l		1		1	1	WGTLVNTLCSFKRHYDANTPL
[		1		1	i	AQVMPELVEQYPGR*FTGVRK
l				1	1	KSNN*FRQFGGVDTAGNNL\SEI
l	I	1				FSASASAEIFPANSFCNRLA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25643	56011	A	25784	331	660	TGIQLPGAP*SQPWSTRRRAVV RPLYRVN*AVP*NR*VIRSKRA MPKRTDIKSILILGAGPIVIGQRL GWRDSDGVRLCGVLGSQENVC ELDEKGEERWSISGTSSEFTR
25644	56012	A	25785		798	MSDAEDGARTTLGSGNAVERL ADALSQQNVTVIKSTSLDDGFA ILSSNEAIDCLMFSYQMEHPDE HQNVRQLIGKLHERQLNVPVFL EGAWILEDTADFIAGÏRAVAAM TTYRQQLIPHFSALMKYSDIQ SEYSWAAPGHQGGVGFTKTPA GREYIDYYRLLRVAWVLHKTE CRLINFPETIPFONSFRVDIEVSN ESPDEEVKLRRHHLARCMKNF KTDIYFVSTFEPSTKSVDLLTVE TPAGT
25645	56013	A	25786	211	414	RVCECIQLRRIEIFRFMISSQPNL PEDLHPQIIAKPSQKRLIEQ*SSK LTVTKARRQGSRYKSSRFFS
25646	56014	A	25787	1694	4974	ISLISAKPVYMVPSRNRYGIIG PIVPQEMQPETLQKKISSPLT KDKAGQKPSYCVVTNCTYDG VCYNAKEAQD/LLEKTSDR.HF DEAWYGY/ARNPIYADHYAM RG/EEGDHNGPTASYIHVREGV GRLNFFRR/OAYMMHATTSPL YAICASNDVAV/SMMDGNSGLS LTQEDCWYMHPGESW/HGFKD DGELEE/TGVPAALYSNLCLSSG TTGLSTFALLYSNLCLSSG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25647	56015	A	25788		1709	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSADP ELRIKVVKAVIEOHMSLNQAA AHFMLAGSGSVARWLKVVEE GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQVR FLETRLMYLKKLKALAHPTKK LASALSTMRTLKSVFSEIYHENG GRYGYRRVTLSLHEGKQINH KAVQRLMGTLSLKAAIKVKRY RSYRGEVGQTAPNVLGRFKA TRPNEKWYTDVTEFAVNGRKL VLSPVIDLFNDEVISYSLSERPV MNMYENMLDQAFKKLNPHEH PVLHSDQGWQYRMRYQNILK EHGIKQSMSRKGNCLDNAVVE CFFGTLKSECPYLDEFSNISELK DAVTEVIEYYSRRISLKLKGL TPIEYRNGTYMPRVNCPLFDTL RIPDIGGVVRARIAKLKNDTD MAIIDKRRPRANVSQWHIIIGD
						VAGRDCVLVDDMIDTGGTLCK AAEALKERGAKRVFAYATHPIF SGNAANNLRNSVIDEVV/DLRY HSAER*NQITAERAYSDPVRKI
25648	56016	A	25789	2902	3271	SSAARHCAGCGDVRSVCRSGR ADAPRMHPGESWHGFKDIPDN WSMLDPIKISILAPGMGEDGE/P TRTTDFQIMFLFSMGVTRGKW GTLVNTLCSFKRHYDANTPLA IOVMPELVEQYPAFVINQ
25649	56017	А	25790	185	663	SPVPSSRPSTRHRLPDGSSSSQFS SAIAARKVVNSCILCSKICQN*F NRRAASPLKRLP*SGASGMITP NQPAPAQPAK*LYTRLDEVKP* *KITHGNGVSFCPTG*A*RTGIS ASSRDLEVQSKKRSFPALNWPA VYCCSALGSAPKCKPIPFLRAT V

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25650	56018	A	25791	684	4208	NGLFWLFQPWLFADETRRRLE
23030	30018	^	23791	084	4208	ERFRDRYQIIHHSSQVCHSDQA
		1				VYVLTQERVNERDDIVDIDLFV
ŀ	1	i			i	IDEFYKLAFRQLKSGDIDHQDE
l		ı			i	RVIELNIALSKLLKVSROFYLTG
		1				PFVNSIRGLEKLGYPHTFVSTDF
		į.				NTVALDVKTSASKRMTTKPSS
		1				KRWGKSRTCVDADHIKNGIGI.
		1				HFGALPRALQQYTADQFNAGK
	ì	l				LRFLLCTSTIIEGVNTIAKNVVIY
1	ŀ	l				DNRAGSTRTISADIINSVICGLN
		l				TLKSFDTRWALL
	24010	١.	25792	1	896	ILKSFDIRWALL
25651	56019	A	25792	231	721	IITAEKGRSREQQLAIL\PLNLAD
25652	36020	IA.	25 /93	231	1/21	MROLOOOHSOTRLADTAADGL
		l				RHFTAQQRLMPLQLQAIFVTGQ
	1					ROLMLORVGY/R/LHGSPWRKA
į.						OTHLPVPGSTPEYRRSDPHGPA
		1				LTGCSSHHNPVRARRGMTIAOL
		l				
						AANPDKEYRARSFAIARSRPLA SRSGYETVTPGC
25652	56021	A	25794		933	MLEAAVCLCVFVSCSLAEGRA
25653	36021	l <sup>A</sup>	23/94	1'	933	CCRVAVSIPVSVRARIHLLESDH
1	i					LGRFREPKSIPRKDAQMDTFRT
		1				MVREPATFLDQVDGLQQSDDIL
		l				RLLPPELATLGITELEYEFYRRL
		l				VEKQLLTYRLHGESWREKVIER
						PVVHKDYDEOPRGPFIVCVDTS
						GSMGGFNEQCAKAFCLALMLI
						AIANKWRCY\IMLSS\TEIVRYE
1						LSGPQGIEQAIRFLSQQFRGGTD
1					1	LASCFRAIMERLQSREWFDADA
		1				VVISDFIAQRLPDDVTSKVKEL
		1				QRVHQHRFHAVAMSAHGKPGI
27674	7.6022	_	25505	02	1100	MRIFDHIWRFDTGMRSRLLRR
25654	56022	C	25795	83	1108	
25655	56023	Α	25796	1	747	L

					In a second second	
SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	hod	in USSN 09/540,217	codon for peptide	of pentide sequence	deletion, \=possible nucleotide insertion)
	sequence		02/340,217	sequence	or peparati sequence	accented to possible state conducting critically
		_				
25656	56024	Α	25797	25	1741	IMERLKRMSVFAKVVEFGSFTA
		1				AARQLQMSVSSISQTVSKLEDE
	l	1	Į.			LQVKLLNRSTRSIGLTEAGRIYY
		1				QGCRRMLHEVQDV\HEHLYAL
	l	1		I		NNTPIGTLRIGCSSTMAQNVLA
	ŀ	1				GLTAKMLKEYPGLSVNLVTGIP
	i	l				APDLIADGLDVVIRVGALQDSS
		1				LFSRRLGAMPMVVCAAKSYLT
ļ		l				QYGIPEKPADLSSHSWLEYSVR
	l					TDNEFEL\IAPEGISTRLIPQGRF
		1		i		VTNDPMTLVRWLTAGAGIAYV
						PLMWVINEINRGELEILLPRYQS
		l	}	ł		DPRPVYALYTEKDKLPLKVQV
			Ì			VINSLTDYFVETPTPLSSLTSLPT
						IEICCMVSIPGTNQRLRPFTGFA
						THRLQSDLLLQVMTISRGRFSR
	1	1		i		SARFNGPTPSGRRLIRVIISTESG
		1		i		SRSSNPRTTGCFEEHCDHYRAII
		ı				DSADGLPMVVYNIPALSGVKLT
				1		LDQINTLVTLPGVGALKQTSGD
		1				LYQMEQIRREHPDLVLYNGYD
	1	1				EIFASGLLAGADGGIGSTYNIM
		l				GWRYQGIVKALKEGDIQTAQK
	1	I				LQTECNKVIDLLIKTGVFRGLK
	1	1			1	TVLHYMDVVSVPLCRKPFGPV
						DEKYLPELKALAQQLMQERG
25657	56025	A	25798	1	1005	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25658	56026	Α	25799	1	2392	MEMVAASKMRKSQDRMAASR
						PYAETMRKVIGHLAHGNLEYK
		ŀ				HPYLEDRDVKRVGYLVVSTDR
İ		l				GLCGGLNINLFKKLLAEMKTW
						TDKGVQCDLAMIGSKGVSFFNS
						VGGNVVAQVTGMGDNPSLSEL
				i		IGPVKVMLQAYDEGRLDKLYI
1		ĺ				VSNKFINTMSQVPTISQLLPLPA
		1				SDDDDLKHKSWDYLYEPDPKA
		1				LLEOCSCMLRSPAWGITSTDTT
				1		RARTDLACPIWLLLDPYPKLMG
		1		1		NAPKALASVDKRGVPVNTILVS
		l				ALVTALCVLINYLAPESAFGLL
		l				MALVVSALVINWAMISLAHMK
		1				FRRAKOEOGVVTRFPALLYPLG
		1			l .	NWICLLFMAAVLVIMLMTPGM
						AISVYLIPPLQTNTFNSTTIAMA
i					l	DYQMESLSAEINFAAAKLARA
		l				CADEWTARTPEKPRYVAGVLG
		l				PTNRTASISPDVNDPAFRNITFD
		l				GLVAAYRESTKALVEGGADLIL
I		l				IETVFDTLNAKAAVFAVKTEFE
		l				ALGVELPIMISGTITDASGRTLS
		1				GOTTEAFYNSLRHAEALTFGLN
						CALGPDELRQYVQELSRIAECY
İ		l				VTAHPNAGLPNAFGEYDLDAD
		l				TMAKQIREWAQAGFLNIVRGC
					l	CGTTPOHIAEMSPGRKRLTRAE
						SSSVPSTLPGKAWLEHALPLIAE
		l			I	QL/QGRRSAVFIPF\AGVTQTWD
					i .	DYTAKTAAVLAPLGVSVTGIHS
						VVDPVAAIENAEIVIVGGGNTF
25659	56027	A	25800	412	1115	LAGEVMDLLLLSNSTLPGKAW
25055	2002/	ľ.	2000			LEHALPLIAEQLOGRRSAVFIPF
						AGVTOTWDDYTAKTVAVLAPL
	1	ľ				GISVTGIHSVVDPVAAIENAEIVI
						VGGGNTFQLLKQCRERGLLAPI
						TDVVKRGALYIGWSAGANLAC
	1					PTIRTINDMPIVDPOGFDALNLF
		l				PLQINPHFTNALPEGHKGDPRL
		1				FR\IRELLVVAPELTIIGLPEGNW
		1	1		1	ITVSKGHATLGGPNTTYVFKAG
		1			1	EEAVPLEAGHRF
25660	56028	A	25801	1	360	MDHAIAGIAVQFRGGNLLRFK
23000	30028	l^	23001	I.	1	AFQQRVKYRMCQAERAINRLF
	1	1			1	NIAVKRLTGNRLDDKSKOHIIDI
1		1	1		1	AVDIPKWSDHLHIIRRKHHDPT
		1			1	QDSGTHLPAVADDGFRTSVRN
		1	Ì			RSA*HIRYLTRC*KALNRNKLPP
		1	1		1	
				L	L	RN*TAIPAMA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25661	56029	A	25802	1032	1233	LVQFLRICFHILQRF/LPSH*RQF
				1		DESLRALPVSFLCWRTDSDFPA
		į.		1	l	DISYONYR*YNREPYLPRPDSG
25662	56030	Α	25803	I	1394	MTRDGLANKALAVARTLADSI
23002	50050	1	23003	Ι'	1.371	EIROGLOKKPOESGIQAIAEAV
					1	KRNDLLFIVVTDMQSLRYSHPE
	1				i	AQRIGQPFKGDDILKALNGEEN
				1		VAINRGFLAQALRVFTPIYDEN
				I	1	HKQIGVINDSRWSIIWSVLFGM
1				I		LVGLIGTCILVKVLKKILFGLEP
		1			1	YEISTLFEQRQAMLQSIKEGVV
		1				
					1	AVDDRGEVTLINDAAQELLNY
					i	RKSQDDEKLSTLSHSWSQVVD
		1		1		VSEVLRDGTPRRDEEITIKDRLI
						LINTVPVRSNGVIIGAISTFRDK
				1		EVRKLMQRLDGLVNYADALRI
				1		RSRLEHILHNQRVPFIMKLHHR
						MLRHFIAASVIVLTSSFLIFELV
		1				ASDRAMSAYLRYIVQKADSSFI
						YDKYQNQSIAAHVMRALAAEG
						SEVSPEQRRAICEAFESANNTH
1		1				GLNLTAHK\SRAYAAHYKPHPI
						TATQLWK\RSTITRF*SGSGRQP
	20021		25004		1010	PPG*LRFRSWDGRREISLLSRSL
25663 25664	56031 56032	A	25804 25805	14	219	
25665	56033	A	25805	744	1566	FASWLRVFSITNCAAPVTSESC
23003	30033	l^	23800	/***	1300	ALDLGSAEAKAWIGVENPHRA
						DVLTELRRSTVARVCTGRAGP
1					1	PRTQALLRFLADHSRSKDTVLK
				1		EVPEEWVKAQGLLEVRSEISDK
						NLYLTRPDMGRRLCAEAVEAL
l			l			KAQCVANPDVQVVISDGLSTD
l						
1						AITVNYEEILPPLMAGLKQAGL
l	į.					KVGTPFFVRYGRVKIEDQIGEIL
[		1	i			GAKVVILLVGERPGLGQSESLS
		1				CYAVYSPRMATTVEADRTCIY
				1		NIHQGGTPPVEAAAVIVDLAKR
	45004	<del> </del> -		40.6		MLEQKAF\GINMTR
25666 25667	56034 56035	A	25807 25808	596 151	745 660	ETTERI CODEVRA ANIII UCEC
2300/	30033	l <sup>A</sup>	23808	1,21	000	STTERLGDDFVRAANIILHCEG
l		1	l			KVVVSGIGKSGHIGKKIAATLA
		1				STGTPAFFVHPAEALHGDLGMI
	1	1	1			ESRDVMLFISYSGGAKELDLIIP
1	1	1	1			RLEDKSIALAPNSRTVIT*CWFS
			1	1		AGDGGLPGPDYGQDFAAHPAG
		1		1		AGALYKCRDLINDNILRTVSCQ
	L	1_		L		SHDDGDIRGMAFARQ
25668	56036	A	25809	314	583	
25669	56037	A	25810	Į1	2982	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=passible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25670	56038	A	25811	120	1790	EGLKTKGEKASPPSCLSFCKNE
23070	30036	l^	23011	120	1790	FVISSTDYALSQSQSGGVMHRQ
		1			-	
		ı				SFFLVPLICLSSALWAAPATVN
		ı				VEVLQDKLDHPWALAFLPDNH
		l				GMLITLRGGELRHWQAGKGLS
		l				APLSGVPDVWAHGQGGLLDVV *APDFAQSRRIWLSYSEVGDDG
		l				KAGTAVGYGRLSDDLSKVTDF
		l				
		ı		l		RAVFROMPKLSTGNHFGGRLV
		l				FDGKGYLFIALGENNQRPTAQD
20071	56020	<del>  -</del>	25012	707	1141	HRVPSWYK
25671	56039	A	25812	707	1141	ASHTATSPRPVRLSSSIASITLAV
		l				NATCGMASSRRIR*CTLFSKRA
		l				PSAPAGWERAKSSSLNPRACM1
		l				AIASASPIIRVLTVLEVGAKCIG
l		l				QGSRSDSTELSPFIKMVPPNSLT
		l				TALAVIPPFSLSDTLPEVLISLSL
05600	55040	١.	0.0010	210	2162	YNTLF
25672	56040	A	25813	215	2160	EINSITSRLSIIPRSPCSASAGWT
		l				KKAGVPVLASVAAIFLPMWPD
		ı				LPIPETTTLPSQCKMILAARTKS
		1				SPR/RSNIMTHIRIEKGTGGWGG
		l				PLELKATPGKKIVYITAGTRPAI
		1				VDKLAQLTGWQAIDGFKEGEP
		l				AEAEIGVAVIDCGGTLRCGIYP
		l				KRRIPTINIHSTGKSGPLAQYIVE
ŀ		1				DIYVSGGKEENITVVGDATPQP
		1				SFVGPDYDTSEKLMIVRKKPIG
		İ				VQMLYQVGTVSMLLYTRTIIQT
						KMTPRTIVTISHSVRNAGDSFFS
						IASNOPMPPTAKKIEPLAISLLS
						AEAPTRLSELKARIGEPRWSIEA
						IKPMPISTHKPNMQAITPPARRA
						ILSPCACESRSRQEPCPPGCHCS
						CPNHSCRSRLKGVLSMEQYLL
						QQKHVGTPPGPFRPPDTNQPCW
						KTKPSQREEYTRRVGFTGHSNQ
		1				GAKIIRTHIICRRRTSFALERPGD
						GFQAVVGGTVLMGLPRTKNVG
			l			LPVTILGRVHRRSSERFPRTSES
			I			AINRKDAGPKDPVRQRLAYKK
						HPMERRHGPHVVARTFGRAIPT
	1					LGPHRTVLSTRFQVAKNPLGPI
	1					GPSPLAVLTWTVPRPKNGRRG
	1					GKQRARIICQSRREASCNNVCL
						ARSSGVFKGFSPVSSSGEHTGN
	L					KYSAYSFSLCPLFVFLPLSGRLL

SEO ID	SEO ID NO:	Met	SEO ID NO:	No. of the least	N 1	Amino acid sequence ( X=Unknown.
NO:	of peptide		in USSN	location of first		*=Stop codon. /=possible nucleotide
140.	sequence	liida	09/540.217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25673	56041	A	25814	11	613	RLSSVFVSKSLASWRSCNCSFS
						GPLVRLTIRP\LSPPDVRLLLSPS
						VVHAYNCPHQETQRHHTHHLT
						P/RLPNHGQIAISAMVYSSPATN
			ĺ			SMLRQLLIQHVEQIGSVPLVMD
						AISLVEAHD/RSAAG*SRPLY*R
						AN*SSRY*VSYARKRVRQAKSR
ļ						/HGKPSKKVLAKRAVPNRVCRC
	1					CNRVKRRCICQPKRRKCMTLPV
						RATR
25674	56042	В	25815	1	1920	
25675	56043	A	25816	247	1182	EAVMRQTKTGILLANLGTPDAP
						TPEAVKRYLKQFLSDRRVVDTS
	1					RLLWWPLLRGVILPLRSPRVAK
						LYASVWMEG\GSPLMVYSRQQ
	İ					QQALAQRLPEMPVALGMSYGS
	1					PSLESAVDELLAEHVDHIVVLP
	1	1	İ			LYPQFSCSTVGAVWDELARILA
				i	1	RKRSIPGISFIRDYADNHDYINA
	1					LANSVRASFAKHGEPDLLLLSY
						HGIPQRYADEGDSLRELYAVA
						NPNPGPGMGVLLAYMFFGRGS
	1					AKQSAGGSGLDGLLRRTPPITP
	ł				ļ	GGYFSVFVWKSLGSWRSCNCS
	1		l	l	1	FSGPLVGLTIRPRFTAGRSPTSF
						AQRCTCL
25676	56044	В	25817	1	651	_
25677	56045	A	25818	1	1647	
25678	56046	A	25819	1	1506	

SEOID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25679	56047	Α	25820	645	2161	LDRCALNVTAQPSIECQVANAC
						LSPKGEFEYLOIDAPTPOALLSE
						IEKCWHRHRNVWPDHTINLAL
		l	l			AIHGOVDPVTGVSQTMPQAPW
		1			ŀ	TTPVEVKYLLEEKLGIRVMVDN
			ŀ			DCQLHYCKTAILNWSRKMALS
			İ			ROKFTFERLRRFTLPEGKKOTF
			Ì			LWDADVTTLACRATSGAKAFV
						FOSVYAGKTLRMTIGNINDWKI
			Ì			DDARAEARRLQTLIDTGIDPRIA
					l	KAVKIAEAESLQAESRKTKVTF
						SVAWEDYLQELRTGISAKTKRP
					l	YSTRYIADHINLSSRGGESPGLG
		l				LLLAFTLFGKGMSKRSAPGAMI
						IHFLGGIHELYFPYVLMKPLTII
		l				AMIAGGMSGTWMFNLLDGGL
						VAGPSPGSIFAYLALTPKGSFLA
	l		i			TIAGVTVGTLVSFAITSLILKME
	İ					KTVETESEDEFAOSANAVKAM
						KOEGAFSLSRVKRIAFVCDAG
				i		MGSSAMGATT\FRKRLEKAGL
						AIEVKHYAIENVPADADIVVTH
			ĺ			ASLEGRVKRVTDKPLYGPAVV
25680	56048	A	25821	2	341	ASELORVIROVIDRIETGIAVV
25681	56049	A	25822	218	469	LICAQGRRSPSRESTRQPKVLTL
23001	50045	^	23622	12.10	100	ACHNGSVSVVVLSPNSLYIEVV
						VPS*CNAATGPVVTCLYKGKFC
			l			PILILLYTSTRVSSCI
25682	56050	A	25823	1	3966	112122 11311113331
25683	56051	A	25824	2	728	
25684	56052	Α	25825	528	1123	DAEEGPDHRYLSSAHGGGSAS
						OPPSCAVTACRWPWRGRGCRA
		1	ł			GVWNOPTA AOGRSWPVGKTSO
						*GOGSTCKSQTWGFRGQRLPQ
		ı				DAPAPPASLCASFHLVEAGASA
			ĺ			DSGDTRRMTIR/FASKTVARAK
	1	l	l	l	I	RIIRVLRFSPLWVATRSLASTAI
	1	l	l			KIACCASEPGSFLQLWKPRSMA
	1					PVHRCTWHEACPEGOROMSCV
			1			SSTGL
25685	56053	A	25826	ī	492	

NO.	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
25686   56054   A   25827   1740   3858   ADAAGTEKTATVSRYHFYLI							
25686   56054   A   25827   1740   3858   ADAAGTEKTATVSRYHFYLI		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
PRSCRSVIDVRSWWRFSIMD SRSIPRAISICARGKPVTAKI QGTMPEPSNKAIILPIRFPEPG LMIIKKSGGRWQLSLLASVV AFFLNTAYAWQEYUPTOJI LSTERYTWDSDHQPDYNDIL RIQSSQRALGLEVNLAETPY VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFOD TTLTPDF.WHASVSTLGWRV; RLGDLRPWAQISYNQQFGEN WKAQSGLSRNTATNONGNN DVTVGADMLLANQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITOPALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLGERGVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFA YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVYEKDYT ESMRKPQYWMLAVMFLTAG SGLVIGVAKDLAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLFAPLNAVTFFAALACVAFP GGTTTVFPSLICGSIIASLFGG VTFYVFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 36055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLMPSC ATCPSGAIYKEEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKGIFCYPRIESGOPTVC TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SRCCDROVIERSGOPTOCT TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI	İ				sequence		
PRSGRSVIDVRSWWRESIMD SRSIPRAISICARGKPVVTAKI QGTMPEPSNKAILPIRFPPG LMIIKKSGGRWQLSLLASVV AFFLNTAYAWQGEYIDTDÜ LSTERYTWDSDHQPDYNDIL RIQSSQRALGLEVNLAEETPI VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFGD TTLTDPLWHASVSTLGWRV RLGDLRPWAQISYNQQFGEN WKAQSLSRNTATNNONGNI DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIOPALGSVYTWSLIP ALSAKLDAPVSQVAFSFGLL GLAISSSVGKLQERFQVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWPFPERKGLISAFA VGLGSLGFKFIDTOLLETVG KTFVWGAIALLMIVFGATLM DAPRQEVKTSNGVVEKDYTI ESMRRPQYWMLAVMFLTAG SGLVVIGVAKDIAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLFAPLNAVTPFSLICGSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  WYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSSPYFGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLVEAI SR°CDRVQLMSALQSVLANGS	25686	56054	Α	25827	1740	3858	ADAAGTEKTATVSRYHFYLRY
SRSIPRAISICARGKPVYTAKI QGTMPEPSNKAIIIPIRFFPOX LMIIKKSGGRWQLSLLASVY AFFLNTAYAWQQEYIVDTQI LSTERTYTWSDDIIQPDYNDII RIGQSQRALGLEVNLAEETP VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFQD TTI.TDPLWHASVSTLGWRVI RLGDLRPWAGISYNQOFGER WKAQSGLSRMTATNONGNI DVTVADMLLANQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIQFALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFQVKR MASGILLGLGFFTAHSDNL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLOFKFDITOTLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVYEKDYT ESMRRPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGML LLFAPLNAVTFFAALACVAFP GGTTTVFPSLICGSIIASLFGG VTFYVIFALLILSLALSTTIRQ GKMLHFTYLTTSALFPAGFK GKSCHCFVFYFFALACVAFF ELKARAEKALDDVKKRLLY WRRROICALRRISSSPYDGILG ECIASFDRNFEAMQKEMYG ENTFMMYLFRLCEHCLNPSC ATCPSGATYREEDGIVLIOQ CRGWBLISGCPYKKILY GKSKCHCFVFRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFFTLVLVLPAI SR*CDRVQLKREEGGVUTCU TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFTTLVVLPAI			ľ				PRSGRSVIDVRSWWRFSIMDAL
LMIIKKSGGRWOLSLLASVV AFFLNTAYAWQQEYIVDTQI LSTERYTWDSDIQPDYNDIL RIGSSQRALGLEVNLAEETP VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFOD TTLTDPLWHASVSTLGWRVI RLGDLRPWAQISYNQOFGEH WKAQSGLSRMTATNQNGNI DVTVGAMLLINQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFOVR MASGILGLGFFLTAHSDNL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLGFRFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPRQEVKTSNGVYENDYT ESMRRPQYWMLAWHFLTAG SGLVIGVAKDLQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGMI LLFAPLNAVTFFAAIACVAFP GGTTTYFFSLICGSIIASLFGG VTFYVIFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGFK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRRDICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIIFVHFFTLVVLPAI SRCCDRVQLMSALOSVARAS							SRSIPRAISICARGKPVVTAKFK
AFFLNTAYAWQGEYIVDTOI LSTERYTWDSDHQPDYNDIL RIQSSQRALGLEVNLAEETPY VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFGD TTLTDPLWHASVSTLGWRVI RLGDLRPWAGJSYNQQFGEN WKAQSGLSRMTATNONGNV DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIQFALGSVYTWSLFP ALSAKLDAPVSQVAFSGELL GLAISSSVAGKLQERFGVKR MASGILGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATL DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAK SGLYVIGVAKDIAQSAGYI LSMCKYSNGVVEKDYT ESMRKPQYWMLAVMFLTAK GGTIVFPSLICGSIIASLFGG VTFYVFALLILSLALSTTIRQ QKMLHFTYLTTSALFFAGRK GGTITVFPSLICGSIIASLFGG VTFYVFALLILSLALSTTIRQ QKMLHFTYLTTSALFFAGRK ELAPLANATTSALFFAGRC ENTSMMYLFRLCEHCLNPSC ATCPSGATYREEDGIVLIOG CRGWELCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFFTLVVLPAI SR*CDKVQLMSALGSVLSTAGS							QGTMPEPSNKAIILPIRFFPGVV
LSTERYTWOSDIGPDYNDIL RIQSSQRALGLEVNLAEETP VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFGD TTLTDPLWHASVSTLGWRV) RLGDLRPWAQISYNQQFGEN WKAQSGLSRMTATNNONGNV DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITIOFALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFA VGLGSLGFKFIDTOLLETVG KTFTWGAIALLMIVFGATLM DAPRQEVKTSNGVVEKDYT ESMRRPQYWMLAVMFLTAG SGLVVIGVAKDIAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLTAPLNAVTFFSALIGCSIIASLFGG VTFYVFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGATYKEEDGIVLIOG CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFF*TLVVLPAI SR*CDRVQLMSALGSVARLSS							LMIIKKSGGRWQLSLLASVVIS
RIQSSORALGLEYNLAEETPY VTSSMSMGWNFPLYEQVTTI VAALHYDGTTTSMYNEFGD TTILTDPLWHASVSTLGWRVI RLGDLRPWAGISYNQOFGEN WKAQSGLSRMTATNONGON DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITICPALGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLOFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLA DAPKQEVKTSNGVYEKDYT ESMRRPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAALACVAFP GGTITVFPSLICGSIIASLFGG VTFYVIFALLILSLALSTTIRQ GKMLHFTYLTTSALFPAGFK GKSCHFCVFYUFALLILSLALSTTIRQ QKMLHFTYLTTSALFPAGFK ELARAEKALDDVKKRLLY WRROJCALRRISSPYPGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGATYKEEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKCHFCVPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHFYHTTVLVLPAI SR*CDRVQLMSALQSVLARAS SR*CDRVQLMSALGSVSATAS							AFFLNTAYAWQQEYIVDTQPG
VTSSMSMGWNFPLYEQVTT VAALHYDGTTTSMYNEFGD TTILTDFLWHASVSTLGWRVI RLGDLRFWAQISYNQOFGEN WKAQSGLSRMTATNOQROM DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGITITGFAGSVYTWSLFP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLOERFGVKK* MASGILLGLGFFLTAHSDNLI MLWLSAGVLVGLADGAGYI TLSNCVKFPFERKGLISAFAI YGLGSLGFKPIDTGLLETVG KTFVIWGAIALLMIVFGATLA DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDLAGSLAVLG SDKLARIEVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFF GGTITVFPSLIGGSIIASLFGG VTFYVIFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY WRRRICIGALRRISSPYPGHG ECIASPBRYFFAMGKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOG CRGWBLCISGCPYKKIYPNW GKSSKCIFCYPRIESGOPTVC TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHFFTLVLVEAI SR*CDRVQLMSALGSVARXAS							LSTERYTWDSDHQPDYNDILSQ
VAALHYDGTTTSMYNEFGO TTLTDPLWHASVSTLGWRVI RLGDLRPWAQISYNQQFGEH WKAQSGLSRMTATNQNGNN DVTVGAMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLOERFGVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPEFKGLISAFAI YGLGSLGFKFIDTQLETVG KTFVIWGAIALLMIVFGATLI DAPRQEVKTSNGVYEKDYT ESMRKPQYWMLAWHFLTAG SGLVIGVAKDLOSSAFLOL SAANAVTVISIANLSGRLVLC SDKIARIKVITIGQVISLVGM LLFAPLNAVTFFSALIGCSIIASLFGG VTFYVIFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGFK  25687 56055 A 25828 2 356  WYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRRDICALTRRISSPYPGIG ECIASFDRNFEAMQKEMYGG ENTFMYLFRLCEHCLNPSC ATCPSGAIYKEEDGIVLIOQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIIFVHFFTLVLVLPAI SR*CDRVQLMSALQSVARAS							RIQSSQRALGLEVNLAEETPVD
TTLTDPLWHASVSTLGWRVI RLGDLRPWAQISYNQQFGEN WKAQSGLSRMTATNONGNU DVTVGADMLLNQNIAAYAA QAENTTNINSDYLYTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKQERFGVKR MASGILLGLGFFLTAHSDNLI MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLGSLGFKFUIDTQLLETVG KTFVIWGAIALHMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAC SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKLARIEVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFI GGTTTVFPSLICGSIIASLFGG VTFYVFFALLISLALSTTIRGQ QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSSPYPGIH ECIASPBRNFEAMQKERMYG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOQ CRGWRLCISGCPYKKIYPNW GKSSKGIFCYPRISSGPYTCC TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHFFT-TLVUFAI SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS							VTSSMSMGWNFPLYEQVTTGP
RLGDLRPWAQISYNQOFGEN WKAQSGLSRNTATNONGNU DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TLIGTITOPALGSVYTWSLIP ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKEPPERKGLISAFA YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMYFGATLM DAPRQEVKTSNOVVEKDYTL ESMRKPQYWMLAVMFLTAG SGLVIGVAKDLAGSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIVITIGQVISLVGM LLFAPLNAVTFFSALIGCSHIASLFGG VTFYVIFFALILSLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  WYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSSPYGHG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLMPSC ATCPSGAIYKREEDGIVLIDG CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVLFAI SR*CDRVQLMSALGSVARAS				İ			VAALHYDGTTTSMYNEFGDST
WKAQSGLSRMTATNOMGNI DVTVGADMLLNQNIAAYAA QAENTTNNSDYLYTMGRTR TILGTITIOFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFOVER MASGILLGLGFFLTAHSDNL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLOFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVEKDYTI ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQGSLAHLD SAANAVTVISIANLSGRLVLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFALICASHAL GGTITVFPSLICGSIIASLFGG VTFYVIFALLILSLALSTTIRQ GKMLHFTYLTTSALFPAGFK GKSGTEVGENGAL Z5688 56056 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLLY WRROICALRRISSSPYDGHG ECIASFDRNFEAMMCEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIHVHFF*TLYVLPAI SR*CDRVQLMASLQSVARAS							TTLTDPLWHASVSTLGWRVDS
DVTVGADMLLNQNIAAYAA							RLGDLRPWAQISYNQQFGENI
QAENTTNNSDYL YTMGRTR TLIGTIITQFALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGLGFFLTAISDNLL MLWLSAGVLVGLADGAGVI TLSNCVKWFPERKGLISAFAI YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFSALIGCSIIASLFGG VTFYVIFALILISLALSTTIEQ GTITTYPFSLIGCSIIASLFGG VTFYVIFALISLALSTTIEQ QKMLHFTYLTTSALFPAGFK  25687 56055 A 25828 2 356  25687 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRROJCALRRISRSPYPGIG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFF*TLYVLPAI SR*CDRVQLMSALQSVARAS				ŀ			WKAQSGLSRMTATNQNGNWL
TILGTITTOPALGSVYTWSLFI ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLOERFGVKR MASGILLGLGFFLTAHSDNLI ML.WLSAGVLVGLADGAGYI TILSNCVKWFPERKGLISAFAI YGLOSLGFFKTHDTOLLETYG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFP GGTITVFPSLICGSIIASLFGG VTFYVIFALLISLALSTTIRGO QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGHE ECIASPBRYFEAMQKEMYG ENTFMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIOD CRGWRLCISGCPYKKIYFNW GKSSKCIFCYPRISSGPYTCC TCYGRIRYLGVULYELTAQQ PVWPPDIFVHFFT*LTVLVFAI SR*CDRVQLMASLQSVARAS							DVTVGADMLLNQNIAAYAALT
ALSAKLDAPVSQVAFSFGLL GLAISSSVAGKLQERFGVKR MASGILLGGFFLTAHSDNLL MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFA VGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLM DAPKQEV KTSNGVVEKDYTI ESMRRPQYWMLAVMFLTAG SGLVVIGVAKDIAGSLAHLD SAANAVTVISIANLSGRIJVLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFSAIGCSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK 25687 56055 A 25828 2 356  25687 56055 A 25828 2 356  MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKRRLJY WRRRQICALRRISRSPYPGHE ECIASFDRNFEAMOKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDG CRGWBLCISGCPYKKIYFNW GKSEKGIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFF*TLVVLPAI SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARAS SR*CDRVQLMSALGSVARASQSVARASS							QAENTTNNSDYLYTMGRTRWL
GLAISSVAGKLÖERFÖVER MASGILLGLGFFLTAHSDNLI MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGLISAFAI YGLOSLGFKPIDTOLLETVG KTFVIWGAIALLMIVEGATLA DAPKGEVKTSNGVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANISGRIVLG LLFAPINAVTFFALICUSH LLFAPINAVTFFALICUSH GGTITVFPSLICGSIIASLFGG VTFYVIFALILISLAISTIRQ QKM.HFTYLTTSALFAGRK QKM.HFTYLTTSALFAGRK URRAGVAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA			i	ŀ			TLIGTIITQFALGSVYTWSLFNG
MASGILLGIGFFLTANSDALI MLWLSAGVLVGLADGAGYI TLSNCVKWFPERKGILSAFAI YGLGSLGFKFIDITQLLETVG KTFVIWGAIALIMIVGGATLA DAPKQEVKTSNGVVEKDYTI ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDLAGSLALIG SAANAVTVISIANLSGRIJVLG SDKLARRIVTITGQVISLVGM LLFAPLNAVTFFAAIACVAFI GGTITVFPSLIGGSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  25688 36056 A 25829 I I307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQIGALRRISSRYPGHE ECIASFDRNFEAMGKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEGGIVLIOG CRGWBLCISGCPYKKIYFNW GKSSKCIFCYPRIESGOPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFT-TLVUFAI SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS SR**CDRVQLMASLQSVARAS		ł					ALSAKLDAPVSQVAFSFGLLSL
MLWLSAGVILVGLADGAGYI TILSNCVKWFPERKGLISAFAI YGLGSLGFKFIDTOLLETVG KTFVIWGAIALLMIVFGATLI DAPKQEVKISNGVEKDYTI ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFALICUSIASLFGG VTFYVIFALILISLALSTTIRQ QKMLHFTYLTTSALFPAGPK 25687 56055 A 25828 2 356  25687 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLIY WRRROICALRRISRSPYPGIG ECIASFDRNFEAMQKEMYGG ENTFMMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVVLPAI SR*CDRVQLMASLQSVARAS							GLAISSSVAGKLQERFGVKRVT
TLSNCVKWFPERKGLISAFAI YGLGSLGFKFUDTOLLETYG KTFVIWGAIALLMIVFGATLI DAPKQEVKTSNGVVEKDYT ESMRKPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLC SDKIARIKVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFP GGTITVFPSLICGSIIASLFGG VTFYVIFALLISLALSTTIRQ QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGHE ECIASFDRNFEAMQKEMYGG ENTFMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKGIFCYPRFIESGGPYTCG TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFT-TLVUFAI SR*CDRVQLMASLQSVARAS							MASGILLGLGFFLTAHSDNLM
VGLGSLGFKFIDTOLLETVG   KTFVIWG AIALLMIVFGATLM DAPKQEV KTSNGVVEKDYTI   ESMRKPQYWMLAVMFLTAG   SGLVVIGVAKDIQASLAHLD   SAANAVTVISIANLSGRIJVLG   SDKIARIRVITIGQVISILVGM   LLTAPLNAVTIFFAAIACVAFF   GGTITVFPSLICGSIIASLFGG   VTFYVFFALLISLALSTTIRG   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   SF0555   A 25828   2 356		l	l				MLWLSAGVLVGLADGAGYLL
KTFVIWGAIALLMIVPGATLA   DAPKQEVKTSNGVVEKDYTI   ESMRKPQYWMLAVMFLTAK   SGLYVIGVAKDIAQSLAHLD   SAANAYTVISIANISGRIVLG   SGLYRIGANISGRIVCI   SDKIARRVITIGQVISLVGM   LLFAPLNAVTFFAAIACVAFP   GGTITVFPSLICGSIIASLFGG   VTFVVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGR   QKMLHFTYLTTSALFFAGR   Z5687   56055   A   25828   2   356     25688   56056   A   25829   I   1307   MVETLEEVLRSSGDPADQKY   ELKARAEKALDDVKKRLLY   WRRQICALRRISRSPYPGHG   ECIASFDRNFEAMGKEMYG   ENTFMMYLFRLCEHCLNPSC   ATCPSGAIYKREEGGIVLIOD   CRGWELCISGCPYKKIYFNW   GKSECIFCYPRIESGQPTVC   TCVGRIRYLGVLLYELTAQQ   PVWPPDIFVHFFTLVVLPAI   SR*CDRVQLMASLQSVARAS   SR*CDRVQLMASLQSVARAS   SR*CDRVQLMASLQSVARAS   SR*CDRVQLMASLQSVARAS   SR*CDRVQLMASLQSVARAS   SR*CDRVQLMASLQSVARAS   SR*CDRVQLMASLQSVARAS			1				TLSNCVKWFPERKGLISAFAIGS
DAPKQEVKTSNGVVEKDYTI ESMRKPQYWHLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANI.SGRLYLLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFI GGTITVFPSLICGSIIASLFGG VTFYVFFALLISLALSTTIRG QKMLHFTYLTTSALFPAGPK 25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGHE ECIASPBRNFEAMQKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEGGIVLIOQ CRGWBLCISGCPYKKIYPNW GKSSKCIFCYPRIESGGPYTCG TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHFFT-TLVUFAI SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS							YGLGSLGFKF\IDTQLLETVGLE
ESMRRPQYWMLAVMFLTAG SGLYVIGVAKDIAQSLAHLD SAANAVTVISIANLSGRLVLG SDKIARIRVITIGQVISLVGM LLFAPLNAVTFFAAIACVAFF GGTITVFPSLIGGSIIASLFGG VTFYVIFALILISLALSTTIRQ QKM.HFTYLTTSALFAGFK 25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRLLY WRRROJCALREISRSPYPGIG ECIASFDRNFEAMQKEMYGG ENTFMYLFRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWBLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDIFVHFFTLVVLPAI SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS SR*CDRVQLMASLQSVARAS			1				KTFVIWGAIALLMIVFGATLMK
SGLVVIGVAKDIAQSLAHLD   SAANAVTVISIANIASGRLVLC   SDKIARIRVITIGQVISLVGM,   LLFAPLNAVTFFAAIACVAFF   GGTTTVFFSLIGCSIIASLFGG   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   QKMLHFTYLTTSALFFAGFK   VTFYVIFALLILSLALSTTIRQ   VTFYVIFALLISLALSTTIRQ   VTFYVI				١.			DAPKQEVKTSNGVVEKDYTLA
SAANAVTVISIANLSGRIJVLC   SDKIARIRVITIGQVISLVGM/   LLFAPLNAVTVFSAIAGCVAFF   GGTITVPFSLIGGSIIASLFGG   VTFYVFFALLISLALSTTIRG   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGPK   QKMLHFTYLTSALFPAGFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK   QKMLHFTYLTSALFFK			1	ŀ			ESMRKPQYWMLAVMFLTACM
SDKJARIRVITIGQVISLVGM/ LLFAPLNAVTFFAAIACVAF9 GGTITVFPSLICGSIIASLFGG VTFVVIFALLILSLALSTTIRQ QKMLHFTYLTTSALFPAGPK  25687 56055 A 25828 2 356  25688 56056 A 25829 I 1307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY, WRRRQICALRRISRSPYPGHQ ECIASPDRNFEAMQKEMYGG ENTFMMYLPRLCEHCLPSC A TCPSGAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS				ľ			SGLYVIGVAKDIAQSLAHLDVV
LLFAPLNAVTFFAAIACVAFP							SAANAVTVISIANLSGRLVLGIL
GGTITYPPSLICGSIIASLFGG			1				SDKIARIRVITIGQVISLVGMAA
VTFVVIFALLILSLALSTTIRQ				i			LLFAPLNAVTFFAAIACVAFNF
QKMLHFTYLTTSALFPAGPK   25687   56055   A   25828   2   356     25688   56056   A   25829   1   1307   MYETLEEVLRSSGDPADQKY   ELKARAEKALDDVKKRLLY   WRRROJCALRRISSRYPGHE   ECIASFDRNFEAMQKEMYGG   ENTFMMYLFRLCEHCLMPSC   ATCPSGAIYKREEDGIVLIOP   GKSEKCIFCYPKIYFNW   GKSEKCIFCYPKIFSOGPTYCC   TCVGRIRYLGVLLYELTAQQ   PVWPPDIFVHFF*TLYULPAI   SR**CDRVQLMASLQSVARAS    SR**CDRVQLMASLQSVARAS    SR**CDRVQLMASLQSVARAS							GGTITVFPSL\ICGSIIASLFGGFY
25687   56055   A   25828   2   356							VTFYVIFALLILSLALSTTIRQPE
25688 56056 A 25829 I I307 MYETLEEVLRSSGDPADQKY ELKARAEKALDDVKKRKLY WRRRQICALRRISSRYPGIE ECIASPBRYEFAMQKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRISSGQPYCC TCYCRIRYLGVLLYELTAQQ PVWPPDIEVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS							QKMLHFTYLTTSALFPAGPKRN
ELKARAEKALDDVKKRKLY WRRROICALRRISRSPYPGHO ECIASFDRNFEAM MOKEMYGO ENTFMMYLPRLCEHCLNPSC ATCPSCAIYKREEDGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHEVHPF*TLYVLPAI SR*CDRVQLMASLOSVARAS					2		
WRROJCALRRISRSPYGHG ECIASFDRNFEAMOKEMYGG ENITFMMYLPRLEGHCLIPSC ATCPSGAIYKREEGGIVLIDQ CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGGPTVC TCVGRIRYLGVLLYELTAQQ PVWPPDHEVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS	25688	56056	Α	25829	1	1307	
ECIASFDRNFEAMOKEMYGG ENTFMMYLPRLCEHCLNPSC ATCPSGAIYKREEDGIVLIDO CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRISGOPTVC: TCYGRIRYLGVLLYELTAQQ PVWPPDIFVHFF*TLYULPAI SR*CDRVQLMASLQSVARAS							
ENTFMMYLPRLCEHCLNPSC A TCPSCAIYKREEGGIVLIDQ CRGWALCISGCPYKKIYFNW GKSEKCIFCYPRIESGQPTVC: TCVGRIRYLGVLLYELTAQQ PVWPPDHEVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS							WRRRQICALRRISRSPYPGHQL
ATCPSGAIYKREEDGIVLIDQ CRGWRLGISGCPYKKIYFNW GKSKKCIFCYPRIESGGPYCC TCVGRIRYLGVLLVELTAQQ PVWPPDIFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS							
CRGWRLCISGCPYKKIYFNW GKSEKCIFCYPRIESGOPTVC: TCVGRIRYLGVLLYELTAQQ PVWPPDHYHPF*TLYVLBARA SR*CDRVQLMASLQSVARAS		l					ENTFMMYLPRLCEHCLNPSCV
GKSEKCIFCYPRIESGQPTVC: TCVGRIRYLGVLLYELTAQQ PVWPPDHFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS		1					ATCPSGAIYKREEDGIVLIDQDK
TCVGRIRYLGVLL/SELTAQQ PVWPPDIFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS		1	1				CRGWRLCISGCPYKKIYFNWKS
PVWPPDHFVHPF*TLYVLPAI SR*CDRVQLMASLQSVARAS		1					GKSEKCIFCYPRIESGQPTVCSE
SR*CDRVQLMASLQSVARAS			٠.				TCVGRIRYLGVLLYELTAQQFF
		1					PVWPPDHFVHPF*TLYVLPAPP
I I I I I I I I I I I I I I I I I I I							SR*CDRVQLMASLQSVARASRE
				1			YRWYGFSR*TPRKALALAQLRP
AESSPTAPDCN			L				AESSPTAPDCN

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	-	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
		<u> </u>	1		14460	
25689	56057	A	25830	583	1369	RHQLNSIASPAGGRWKDIGWF
						NFPQSNLCLKREKQDESCSLTQ
						ALPSELKVSADNVSLTGAVSLA
						SMLTEIFLLQQAQGMPEPGWG
						RITDSHQWNTLLSLHNAQFYLL
l						QRTPEVARSRATPLLDLIKTALT
						PHPPQKQAYGGT\LPLPVRFMA
	1					GPDTNLANLGGALKFNWTLPG
ļ						QPDNTPPGGELVFERWRRLSDN
		İ				SQWIQVSLVFQTLQQMRDKTP
						LSLNTPPGEVKLTLAGCEERNA
1						QGMCSLAGFTQIVNEARIPACS
25690	56058	Α	25831	199	543	
25691	56059	Α	25832	1	642	EASIFRRLSVYDNLMAVLQIRD
		1				DLSAEQREDRANELMEEFHIEH
						LRDSMGQ*SARPGRCRAGAQ*
			1			CV*CR*PRSGQPRQTVRRAE*IS
		1				DSQPVRGQFLHG/VRSPPESDCP
		1				MLSRRCSM*NSSISSFARSSRCS
		1				ADKSSRICSTAIRLS
25692	56060	A	25833	3	329	
25693	56061	A	25834	1974	2195	
25694	56062	A	25835	1	615	
25695	56063	A	25836	2	166	
25696	56064	Α	25837	2	189	STPGNWRFTTTYPLNCATRWK
						M*FLIVATMAPSVYWSLPRNIA
		1				AAKPTTPPTPSRRSGARGK
25697	56065	Α	25838	64	354	
25698	56066	A	25839	1123	1845	
25699	56067	Α	25840	1120	2097	
25700	56068	A	25841	124	548	CROMVGTRRGGEQGKEVIDGY
		1				GKPATFYQMQDNGKPVEGHAS
l		1				OMHYELAKDFVVLTGNAYLQ
1		1				OVDSNIKGDKITYLVKEOKMO
		1				AFSDKGKRVTTVLVPSQLAKA
1		1				YKG\VAW*KTSA*PSTPGKLSV
		1				CWGQTVPVRPPLSTWL
25701	56069	A	25842	77	514	CWGQTTT TRITEST WE
25701	56070	A	25843	2487	5738	RRAAGLPGRNDAGLARSHOWA
23,02	155075	1	23043		I	GSADTGSEKQHELQLRIQGEPV
		1				SGOLNLAGSFDRKEERWKG\TL
		1				SNTRFQTPVGPWSLTRDIALDY
		1				
1	1	1			l	RNKEQKISIGPHCWLNPNAELC
		1				VPQTIDAGAEGRAVVNLNRFD
		1	1			LAMLKPFMPETTQASGIFTGKA
1		1	1		I	DVAWDTTKEGLPQGSITLSGRN
		1	1		<b>f</b>	VQVTQTVN\DAALPVAFQTLNL
1		1				TAELRNNRAELGWTIRLTNNG
		1				QFDGQVQVTDPQGRRNLGGNV
	L	L			L	NIRNFNLAMINPIFTRG
25703	56071	Α	25844	538	777	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
25704	56072	IA	25845	489	2797	TRRRRTMIALIQRVTRASVTV
	l			ĺ		EGEVTGEIGAGLLVLLGVEKDD
						DEQKANRLCERVLGYRIFSDAE
						GKMNLNVHQAAGSVLVVSQFT
		ı				LAADTERGMRPSFSKGMSQLP
		l				GLSRETRESIAMYHLRVPQTEE
						ELERYYQFRWEMLRKPLHQPK
	l					GSERDA WDAMAHHQMVVDEQ
		ľ		İ		GNLVAVGRLYINADNEASIRFM
						AVHPDVQDKGLGTLMAMTLES
						VAPYFSGSETGMMTLNRYRLR
						HMAKQGNRSAKRVEKLLRKPD
						RLISLVLIGNNLVNILASALGTI
						VGMRLYGDAGVAIATGVLTFV
						VLVFAEVLPKTIAALYPEKVAY
						PSSFLLAPLQILMMPLVWLLNA
						ITRMLMRMMGIKTDIVDMLLS
		1				VLDLEKM/TVDDIMLPRSEIIGI
		1				DINDDWKSIL/R/QLSHSPHGAIV
	1	İ				LYRDSLDDAISMLRVREAWRL
						MSEKKEFTKETMLRAADEIYFV
						PEGTPLSTQLVKFQRNKKKVGL
	ŀ					VVNEYGDIQGLVTVEDILEEIV
						GDFTTSMSPTLAEEVTPQNDGS
		1			·	VIIDGTANVREINKAFNWHLPE
		1				DDARTVNGVILEALEEIPVAGT
	I	1				RVRIGEYDIDILDKLSFCFRYSN
		1				HRRTNRTTIQRITFLHNAQYVT
l						WRNVIRFHHCDGLMHIRVQWD
l		1				VSFGDHFNAKLTHNIQHRLQRQ
l		1				LNAFNHRRHIRVSFISHFQRTIQ
						AINHRQQFVDEFLQREFVGFFNI
25705	56073	A	25846	87	199	QPASVQTAGAGCRL*LHQRQW
	1	l			l	RECLVLDSKRRGDGVL

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25706	56074	Α	25847	1167	3306	GKSMDKELPWLADNAO\LELK
						YKKGKTPLSHRRWPGEPVSVIT
						GSLIQTLGDELLQKAEKKKNIV
				l		WRYENFSLEWQSAITQAINLIG
						EHKPSIPARTMAALACIAQNDS
		l				QQLLDEIVQQEGLEYATEVVIA
						RQFIARCYESDPLVVTLQYQDE
		l		l		DYGYGYRSETYNEFDLRLRKH
						LSLAEESCWQRCADKLIAALPG
		1		l		INKVRRPFIALILPEKPEIANELA
1		1				VPALREFLAATKMPATCTLKGL
		1			1	GAVEADYPYYLGMLGMHGTK
						AANFAVQECDLLIAVGARFDD
					1	RVTGKLNTFAPHASVIHMDIDP
						AEMNKLRQAHLRDEHSWRYD
	ŀ					HPGDAIYAPLLLKQLSDRKPAD
1						CVVTTDVGQHQMWAAQHIAH
						TRPENFITSSGLGTMGFGLPAA
						VGAQVARPNDTVVCISGDGSF
		1				MMNVQELGTVKRKQLPLKIVL
		1			1	LDNQRLGMVRQWQQLFFQER
		l			l	YSETTLTDNPDFLMLASAFGIH
		l			1	GQHITRKDQVEAALDTMLNSD
		1				GPYLLHVSIDELENVWPLVPPG
		1				ASNYKKHHKLKQTFGVKIIPDV
		1				HDPSQAQPVADVVNVIQLPAFL
		1				ARQTDLVETHGENRPGQMGNI
	1	1				VDKFKEGGNEKVILCDRGANF
ļ	1	1	1			GYDNLVVDMLGFSIMKKVSGN
		1				SPVIFDVTHALQCRDPFGAASG
1						GRRAQVAELARAGMAVGLAG
		<u> </u>			60.5	LFIEAHPDPEHAKCDGPSALPL
25707	56075	Α	25848	I	695	MATRASVTPMSLFSAGTCLLST
						SCVLSPVGDTAEESCWQRCAD
					I	KLIAALPGINKVRRPFIALILPEK
	l	l				PEIANELVGLECPRTHFHSKEW
		1				LKVVANDPTAVRKLEHYWSQD
	i	1				IFSDREASYMSHENHFGYAACA ALLREOGLAAIPRLAMYAHKE
		1				
						DCGSLLVQINHPQVIRTLLLVA
					1	DKNKPSLQRVAKYHKNFPHAT LAALAELLALTEPPA/RPWLSN
1		1	1			HRRQKAACTAKSTR
25708	56076	A	25849	823	1091	CVRFARINCSDRRSRCFAGFNH
25/08	30076	A	23849	023	1071	VLNKALGVHINHFG/YSACAP*
						CRYPPHAAGEFYPDPCRHKGTT
						GYRHROGYPPPGEPPPRASWLD
1					1	LR
25709	56077	A	25850	714	875	EFSSARISRTSRLKYTNGCCRL
23709	55077	<u> </u> ^	23030	l	10,5	WSAFCRLRTATTVPPARP*QLR
				1	1	PDRSRAQCQ
			<u> </u>			

SEQ 1D	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25710	56078	Α	25851	2730	2893	WPVGERLAPGDYPVI*TGQLCT
	ĺ					AAGD/EWRR*KVRRHQPLWRG
						FPNRRYMAWRSA
25711	56079	Α	25852	750	929	SFHPAGRRYLYRHSSRSGNITN
						GCCRLWSAFCRLRTATTVPPAR
						P*QLRPDRSRAQCPV
25712	56080	A	25853	2	2427	CRQHHRWHSGSTAVYRRVLITS
		1				KCWNVFIRTKTWTVSILTTSVV
		İ				CASARRVCVPAPRAVSSRCLSV
		i				TTLIPSASTPW*LAHRISLAAR*
		ł				AFWFNCRIPAGIDNVKVLERIH
		Į.				PDKDVDGFHPYNVGRLCQRAP
		ŀ		1		RLRPCTPRGIVTLLERYNIDTFG
				1		LNAVVIGASNIVGRPMSMELLL
		1		1		AGCTTTVTHRFTKNLRHHVEN
			ļ	ŀ		ADLLIVAVGKPGFIPGDWIKEG
	1	1				AIVIDVGINRLENGKVVGDVVF
		1			i .	EDAAKRASYITPVPGGVGPMT
						VATLIETRYROGKMFDGSSIGG
		1	l			WKGINESDMVLMPDASTAVID
		ı				PFFADSTLIIRCDILEPGTLQGYD
		ı				RDPRSIAKRAEDYLRSTGIADT
		1		l	Į.	VLFGPEPEFFLFDDIRFGSSISGS
		1		ŀ		HVAIDDIEGAWNSSTQYEGGN
ŀ				1		KGHRPAVKGGYFPVPPVDSAQ
l		1				DIRSEMCLVMEOMGLVVEAHH
			i			HEVATAGONEVATRENTMTKK
						ADEIQIYKYVVHNVAHRFGKT
i		1				ATFMPKPMFGDNGSGSPPSOPO
i			1			SQPTPPEILLQALLSAGCFYAVY
i	1					YVTYKTRLRKRVADVPRRPLFT
		1		1		MNRVETNLTWVILMGIALVSV
						GIFFMHNGFLLFRLNSYSQIFSS
						EVSGVALKRFFYFFIPAMLVVY
		1				FLRQDSKAWLFFLVSTVAFGLL
						TYMIVGGTRANIIIAFAIFLFIGII
l						RGWISLWMLAAAGVLGIVGMF
		1				WLALKRYGMNVSGDEAFYTFL
25713	56081	A	25854	502	885	
25714	56082	A	25855	233	738	SNSCKRTKIISDVTSVFHAIFPAI
1		1	1	1		KITAPNSPRLRVNDSATPLTSAG
l		1	1		1	ESSGSTTLQKLCQRVAPSVSAA
		1	1			SSYSGPNLFOHRLHGTHPKRNA
ĺ		1	1			GKGHSHRNPQPCIGDFDIKLRQ
l			1			PFTVKTLYVKEKGQR*GGDRV
l		1	1		1	LPAORVNPSAHOAACGLGSDS
		1	1	1		GLGSTPSADRKRR
L	L	_			I	OLOGIFOADKKKK

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25715	56083	Α	25856	1	2363	MRRQDTGRRGRKRRDAGRWQ WRYWGKGSFTPMNATWDVAC KGEWHDSTITLTDLSTGFDQLQ YGTMTVEKPRLILDKPIVWVRL AQHPSFSGALSLDAGQTLFTGG
						SVLPPSTLKFSVDGRDPTYFLFK GDLHAGEIGPVRVNGRWDGIR LRGNAWWPKQSLTVFQPLVPP DWKMNLRDGELYAQVAFSAA
						PEQGFRAGGHGVLKGGSAWM PDNQVNGVDFVLPFRFADGAW HLGTRGPVTLRIAKQRKEMRN NNLRQFKLLGPDVGFDSINDRP MAEELSKLLSKONEENLLPKTI
						LYCLNPRDNEVLGTMIENGASF AANPLYFDPKNIVELAIEAGCN CVASTYGVLASVSRRYAHRIPF LVKLNHNETLSYPNTYDQTLY
						ASVEQAFNMGAVAVGATIYFG SEESRRQIEEISAAFERAHELGM DGGWIGLMIKPLGRWSLIMEID EGFAVGMSPAELSAEQLLSKL
						WLWEGKAERYGWGRKSMDKI LPRLADNAQLELKYKKGKTPLS HRRWPGEPVSVITGSLIQTLGD ELLQKAEKKKNIVWRYENFSLI
						WQSAITQAINLIGEHKPSIPART MAALACIAQNDSQQLLDEIVQ QEGLEYATEVVIARQFIARCYE SDPLVVTLQYQDEDYGYGYRS
		L				ETYNEFDLRLRKHLSLAEESCW QRCADKLIAALPGINKVRRPFIA
25716	56084	A	25857	1	4440	MNRFDGAKQNVVGADAHHLA DTAVKRNQSLFQLRASGHPRLF AGGGKAVFHGRFAAKKIEAVA FYFRHLIALLVVOMHFKLVKG
						NVDVVFTAQLIDSTVQLIDSTTT VTQFTHIQTQLMRSVEWLTDN GSCYRANETRQFARMLGLEPK NTAVRSPESNGIAESFVKTIKRD
						YISIMPKPDGLTAAKNLAEAFE HYNEWHPHKAGTLTNEQWQQ VTAELHDRMMETVFFALDDAE
						QLFAHHQPTPVTSVDLLGQG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25717	56085	A	25858	1	3705	MEEYGGVDVRLYRIPDPMAFL
		1		ŀ		ROOKNLHRIVVOPOYLGDGLN
		1				NTLTWLWDNWYGKSRRVMOR
		1	ł			TFSSOSRONVTOALPELOLGNA
1		l				IIKPSRYVONNOFSPLKKYPLVK
						QFRYPLWQAKPFEPQQGSRGL
		1				YLVEAMVGGYRATTGGVVSDI
		1				VALSKVSSKELLVWTAGKKOV
		l				NEPGSEIFGLTALRITAENODCA
						SLTPETFLPRIHVIKGVNISTATV
		l				CROCEDAPCANVCPNGAISRDK
						GFVHCEARTLHLFAKT
25718	56086	Α	25859	123	923	TDSPYERGHLMSNLLGPRDAN
						GIPVPMTVDESIASMKASLLKKI
						KRSAYVYRVDCGGCNGCEIEIF
		İ				ATLSPLFDAERFGIKVVPSPRHA
						DILLFTGAVTRAMRSPALRAW
		l				QSAPDPKICIS\YGACGNSGGIF
			1			HDLYCVWGGTDKIVPVDVYIP
						GCPPTP\AATLYGFAMALGLLE
		ĺ				QKIHARGPGELDEQPAEILHGD
			1		İ	MVQPLRVKVDREARRLAGYRY
						GRQ\VADDSFTQLGQGEEQVAR
		-	İ			WLEAENDPRLNEIVSHLNHVVE
25719	56087	A	25860	1337	1516	KLKSKSAKRHKFITPILAWRILI
		1				HYLQRVAV*WGSRLL*LFLITIP
						SRWRLLPHNTGKG
25720	56088	A	25861	1	545	MARLAALKACETVYSMGVRSH
		l				RRSPLEHLWQLKDQLVNEGEL
		l				VLETLVIDGDENTVLVPGDRYA
		l				QMRNVYFIPSALALKNWLKKC
		l				GFVDIRIADVSR/ITTTEEQRRTE
						WMVTESLADFLDPHDPGKTVE
						GYPAPKRARNRNRAEDHRQRL
		1				RHRTRKKQTHGQRRRHRPEPA
		_				QRQPQTGTTD
25721	56089	Α	25862	620	1117	
25722	56090	A	25863	1	1188	
25723	56091	Α	25864	231	407	
25724	56092	Α	25865	1	501	
25725	56093	В	25866	1	2373	
25726	56094	A	25867	1	2211	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25727	56095	A	25868	2093	3589	GGINGKNFWFFLSPFTPCVGRC
						HSRVQLANSHLVDVDETPPSSA
1						AVHLYATDADSIGNCGTDREFO
		ı				PCNPIRRHAFCCERLQNGYHRS
						GYAFHLGHYGDRKVITNFYSLI
						AKNHLSHWLETLPAQIANWQR
						EQQHGLFKQWSNAVEFLPEIKP
						YRLDLLHSVTAESEEPLSAGQI
		l				KRIETLMRNLMPWRKGPFSLY
		l				GVNIDTEWRSDWKWDRVLPHL
		l				SDLTGRTILDVGCGSGYHMWR
		l				MIGAGAHLAVGIDPTQLFLCQF
						EAVRKLLGNDQRAHLLPL/GIE
						QLPALKAFDTVFSMGVLYHRR
İ						SPLEHLWQLKDQLVNEGELVL
						ETLVIDGDENTVLVPGDRYAQ
						MRNVYFIPSALALKNWLKKCG
						FVDIRIADVSVTTTEEQRRTEW
1						MVTESLADFLDPHDPAIFQIWP
	•					CTFMHAYHAFFDPVSHHRACQ
						NLTTFVPDTHQIAIRNTKACSIF
						VSFALRTTHSCAISHSSLEDPPA
				_		LFKIADRMEQNLELLATAGNLG
25728	56096	Α	25869	231	1785	DDEVHRYSELRTRTVPSYPPER
						SGEAKTAAQRAGTAFRRGRGA
			l		l	GVPFNLQQRSDRWCS*RSQQN
			1		l	A*RLIGLHGQNSRSVPQLPMES
				1	l	ASVA*RCGSIIEKTTLSSRPFYW
						CPGCQHYADRFGA

SEQ ID	SEO ID NO:	Mer	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
				<u></u>		
25729	56097	Α	25870	1818	3311	RMAIQFRTLSLRWCWKISLVSS
		1				FTVVKAMTIRIVAMRQLLRQQ
		l				KQRTFVC*SS/TVDGVLSDGLIY
ļ		1				MGNNGEELKAFNVRDGYGIRC
		l				ALTSDIEVAIITGRKAKLVEDR\
		l				LPHWGSLTCIRGSQTN*SPLAIC
	l	l				WKNWRLP/QENVAYVGDDLID
		l				WPVMEKVGLSVAVDDAHPLL
		l		•		GTEIDAYIENADYQYNKKRLRE
						IDRRVRYLTKCLENLKIVDYSP
		1				QQEGKVFFGAWVEIENDDGVT
		1			1	HRFRIVGYDEIFGRKDYISIDSP
						MARALLKKEVGDLAVVNTPAG
1		1			į.	
	ĺ	1				EASWYVNAIEYVKPRLNQTVR
						LLLEHEMGQVWISGEISNFTQP
	i					ASGHWYFTLKDDTAQVRCAM
				l		FRNSNRRVTFRPQHGQQVLVR
				}		ANITLYEPRGDYQIIVESMQPA
						GEGLLQQKYEQLKAKLQAEGL
						FDQQYKKPLPSPAHCVGVITSK
1		1				TGAALHDILHVLKRRDPSLPVII
						YPAAVQGDDAPGQIVRAIELAN
		1				QRNECDVLRPCVWCRRVRCRR
25730	56098	Α	25871	1	3465	
25731	56099	Α	25872	I	3126	
25732	56100	Α	25873	1	1722	MSSLSQAASSVEKRTNARYWI
		l			Į.	VVMLFIVTSFNYGDRATLSIAG
		l			F	SEMAKHIGLDPVGMGYVFSAF
						SWAYVIGQIPGFVDIFSGFGIIV
			l		8	ALFTLRFLVGLAEAPSFPGQSRI
					l	VGDWFPAQDRGTGVSIFTPFIL
						RKGDLRPIWVVILMAGOLHAL
					l	MSTLEDTPFSNKAGMRLRRWI
	ı	1			i	NAAVMRLNPLACLATRSNOVN
	i		1			WLLLTGNISVYPVGSSEPTRRR
				1		STPINSTPHENKTILPINARYSPT
			1			LPSSDGTRWTTRIDDKPTVGHK
					I	FARYWDVELREIP\MRPG\QLFR
	1				1	DPKRMIEGCAENPL\GV\VPTFG
		1			I	
	l		1		İ	VTYAGNYEFPQPLPDALNKFQ
		l	l		1	ADPGIDIDMHIDAASGGFLAPF
					l	VAPDIVWDFRLPRVKSISASGH
1		1				KFGLAPLGCGWVIWRDEEALP
1		1				QELVFNVDYLGGQIGTFAINFS
1		1				RPAGQVIAQYYEFLRLGREGYT
		1				KSTQPARGSPPANNCQAQPETP
		1				DRAVIHPTDGYESAATIIVLSPP
1		1		I	İ	TASDSDPAHRDQRVVKTDAWS
	1					VVPGSTSEYPRRYKAEWFCQPF
		1			İ	AVLPAILAWSAALWRYQPRAR
		1			1	RRKADYGCRALNSLKNELTTP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25733	56101	Α	25874	1	2385	
25734	56102	Α	25875	1	1767	
25735	56103	Α	25876	1	2079	
25736	56104	A	25877	368	1261	TSPRARPAQGSRGAEL/HLTE KGVNRRAFVGJFESSGKRWAT EREYAFRQLVAEEKYRQVVYQ GLETAPENWQHAQNRLADWL QTLPPQTGIIAVTDARARHLQV CEHLHIPVPEKLCVIGIDNEELT RYLSRVALSSVAGGARQMGYQ AAKLLHRLLDKEEMPLQRILVP PVRVIERRSTDYRSLTDPAVIQA MINYIRNHACKGIKVDQVLDAV
25737	56105	A	25878		868	GISRSNLEKRFKEEVGETHAMI HAEKLEKARSLLISTTLSINEISQ MCGYPSLQYFYSVFKKAYDTT PKEVFAIVNSEVML MTSLKNSMKWDEERFGLEYDL
						DIYMIVAVDFFNMGAMENKGI. NIFNSKYVLARTDATADKOYLD IERVIGHEYFHNWTONRYVTCRD WFQLSLKEGLTVFRDQEFSSDL GSRAVNRINNYRTMGLGPAE DASPMAHPIRPDMVIEMNNFYT LITVYEKGAEVIGMITPPLFQGE HCPONVILTCALEDPTRKYVLKP LCRPPLSLCNRKRYMCRIFTSS ASTILLISRGAVCWNSRITIVSM RSSRRVTSVWLSAPTPIILSPAIF IVRWVLLDSNPLIYYKAWSCW CSRK
25738	56106	A	25879	2097	2512	NTPVRPDVGT**TEEHGGAESGE *RNSRELRENDKA*LHQYHAGP DGKNLAEAFEHYNEWHHSAL GYWRTVD/DMRGR*PQEPSLMI RAGRSSSPVQWQRIPLLIPGRKG DRMQKTVIPGSLFAGMPYAQPS IKTELAG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25739	56107	A	25880	71	2613	QRKPTSSRKGLSARMMSGLTG TITTVSTGWCTTRGHMMSSRW SKVAJFTTRSGGRVAKRVWRR ERDLTGWMSLSRKPQVTWYG GSFTPLIRVETATAVRRRRWQ WGIPAGTVQMLDGHLESEILADR WGIPAGTVQMLDGHLESEILADR WSEESRRWLASCGLTVEQMKK TSIHASIVRHKLLTAEQALKLL KEFAQLAFKNOPMMYGNWAQ SILHGGVIASALDVAAGLVCVG STLTRHETTISEDELRQRLSRMGT IDLRVDYLRPGRGERFTATSSL TAGGNKVAXAVELINEEGLIY ASATATYMSKSMFLAVATILIS KSSLSRLTYAEGFVHYHRQNRH LERRDSVRPYDASFVVVLLNRR SYHITRYPDTVATHRQDLVTAIF TLYGGFQCGGVLGTQLEDVTND DTTFDQQFTLAIRAWIASHHVT DICNFRGSDLAIPVDAEVFTID CYSTSSETIFRRYDDLTVALEDVTN SYSTSTAFTRRYDDLTVALE SYSTSSTAFTLATGROEPSTR SYGTTAYERSVALTPLEPGPDSTR SQFGCFGVLGTQLEDVTN STSSETIFRRYDDLTVALE TLYGGFQCFGVLGTQLEDVTN STSSETIFRRYDDLTVALE TLYGGFQCFGVLGTQLEDVTN STSSETIFRRYDDLTVALE STSTETAYERSVALTPLEPGPDSTR SQFLCTAYAGLASPSSII DNRSRQHLNDVGLTAWDCVIIS GNIGFIGPQARTIATTQAYLCHP
25740	56108	A	25881	71	3478	VRWLPGLEIQNYADASLFADES LRWRSSYEVEKLPEEHTKSSTA CCLSSHPSTTATALRSLSPVRK
						WPKISALIPWEWAMCSLLSHGL MLSGRSLVAWCWTVI.VQNAS TSGRSISGRCHPCCKASSISLVD SALSFILFTLRFLVGLAEAPSP GNSRIVAAWFPARKGTGINEUS PLANTALEGLGGSGDALCTQC EAEGRHITTYLDRPDVLARTT TKILADKIKYPPLLSNGNR VG ELENGRHWVQWQDFPKPCYL FALVAGDFDVLRDTFTTRSGRE VALELYVDRGN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25741	56109	Α	25882	90	629	PGDWGRRQLIGS*KTPGSVFKK
	1	i .				GKSSTPN\DPFLKDKTQDRSGL
	1			i		ATFTMDGQI\RLFYQ\DISGNHS
						GK\QSLPPAQVIVSNSVDHLKIT GVEDHKPIFAGAGKPYQNLRQF
						IDEGNYTSGDNHTLRDPHYVED
						KAHKYLV/FEANTGTENGYOG
İ		l				EESLFNKAYYGGGTNFFRGSSR
		1				VDLOAC
25742	56110	A	25883	I	3066	TELQITE
25743	56111	A	25884	104	547	LFPRLLSCLTTPPHCSFSICFVIC
20110		1		1		SRTLILKGSSLMYVFCLPNTAIV
		ļ.				MALSPRGWRSKFGMPVDSKGP
						PWLFKFLKNGLNFLLHSVGTRD
l				ĺ		LSRLSTILSPLYNTVAPGAN*CR
		l l				ELKLVLDADDVLSTEVKRVITS
		1				SASNITPAFFCS
25744	56112	Α	25885	3	4288	
25745	56113	Α	25886	2	2222	DFADFGTTIKQDFRLLGQTSVD
	1	1				RLLQLSQGQAVKGNQLLPVSLP
		ı				QHTIPDVFIWMLSNNRRVAYA
		ı	1	i		RIASKDLLYSPVAGQMGKHCG
		ı				KIKTHFLKIPKQQQNEKYQVPQ
		1				FDQSTIKNIESAKGLDVWNSWP
		1				LQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYOKDFRLL
		1				GOTSVDRLLQLSQGQAVKGNQ
						LLPVSLVKRKTTLAPNTOTASP
	1	1				RALADSLM/SWHDRFPDWKAG
1		1				RILPISEPPSNRIFACWGKPAWT
		1				ACCNSLRARR*RAISCCPSHW*
		1				KEKPPWRPIRKPPLPARWPIH*C
						SWHDRFPDWKAGRKGSDAHRF
		1				GSWKFQLQRVSG\SATFTWGG
	1					KIR\LYSADYSGNHYGKQSLPS
	1	1				GQVNGSNSDDTLKINGVEDHK
	1	1				TILDGDGKTYQNVQQFIDEGNY
	İ					TSGDNHTLRDPHYVEDKGHKY
						LVFEANTGTENGYQGEESLFNK
	1	1	1			AYYGGGTNFFRKESQKLQQSA
		1	1			KKRDAELANGALGIIELNNDYT
	1	1	1			LKKVMKPLITSNTIRKSDGTLQ
		1		1		EHDGICEIHVAKYAEIFGLTSAE
1	1		1			ASKDIRQALKSFAGKEVVFYRP
1	1		1			EEDAGDEKGYESFPWFIKRAHS
						PSRGLYSVHINPYLIPFFIGLQNR
	1		1			FTQFRLSETKEITNPYAMRLYES
	1	1	1			LCQYRKPDGSGIVSLKIDWIIER
						YQLPQSYQRMPDFRRRFLQVC
	1	L		ļ	0.00	VNEINSRTPMRLSYRMGVRGK
25746	56114	В	25887	1	2640	ſ

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
0.57.47	56115	<u> </u>	25000	Linos	1629	
25747 25748	56115	A	25888	1291	2925	NSLORSHPNAANS/WHNKLWR
25748	20110	Α	25889	1187	2923	SHSDSDLSDHHEPICKPGLELN
						KKDITTSADQIAEVKTMESHPPI
						PPVFVEHMVPQDANQKGLCTK
						ERMICLEFTSREFHAGQIEDELN
						LNDINGCSSGSTLEDPQFNDDSP
						EARKITRRWRIGEAADLVGVSS
	i					QAIRDAEKAGRLPHPDMEIRGR
						VEQRVGYTIEQINHMRDVFGTR
	1			1		LRRAEDVFPPVIGVAAHKGGV
	l					YKTSVSVHLAQDLALKGLRVL
	l					LVEGNDPQGTASMYHGWVPD
	1					LHIHAEDTLLPFYLGEKDDVTY
						AIKPTCWPGLDIIPSCLALHRIET
	ì		ŀ			ELMGKFDEGKLPTDPHLMLRL
	ļ.					AIETVAHDYDVIVIDSAPNLEDP
	ŀ					RVGVMARGNAITLPVCGRDVK
	ŀ					FTLEVLRGDSVEKTSRVWSGNE
						RDQELLTEDALDDLIPSFLLTGQ
	İ					QTPAFGRRVSGVIEIADGSRRR
ĺ				l		KAAALTESDYRVLVGELDDEQ
		1				MAALSRLGNDYRPTSAYERGO
		l		l		RYASRLONEFAGNISALADAEN
		l	ŀ			ISRKIITRCINTAKLPKSVVALFS
						HPGELSARSGDALQKAFTDKEE
	l	ı		l		LLKOOASNLHEOKKAGVIFEAE
	1	1		i		EVITLLTSVL
25749	56117	В	25890	1	1954	
25750	56118	Α	25891	1	454	MERRNRRTGRTEKARIWEVTD
1					l	RTVRTWIGEAVAAAAAADGVTF
		l			l	SVPVTPHTFRHSYAMHMLYAG
		l			l	IPLKVLOSLMGHKSISSTEVYTK
		ı			1	VFALDVAARHRAIR\VPRQQGD
		1				YRTRIWKFEDGLSNVLVIOLNK
	1	1	l	1		LIICVMCLVRDCDVLKTYFHL
25751	56119	A	25892	10	144	FLFIGKGFLKGIT*PGOIVORG*E
23,31	130117	l^	12072	1."	l	KKSNT*FRQFGGVDTAGNNLT
I	1	1	f		ı	KKSINI TRQEGOVDINGINILI

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25752	56120	Α	25893	888	892	TVDLDACTKGVLTFTTALLAG
				1		GANQAFAKENTKKAYKETYGV
						SHITRHDMLQIFKQQQNEKYQV
		l				PQFDQSTIKNIESAKGLDVWDS
ĺ						WPLQNADGTVAEYNGYHVVF
						ALAGSPKDADDTSIYMFYQKV
1						GDNSIDSWKNAGRVFKDSDKF
						DANDPILKDQTQEWSGSATFTS
		l		l		DGKIRLFYTDYSGKHYGKQSLT
						TAQVNVSKSDDTLKINGVEDH
		l l				KTIFDGDGKTYQNVQQFIDEGN
						YTSGDNHTLRDPHYV/EDKGH
						KYLVFEANTGTENGYQGEESLF
						NKAYYGGGTNFFRKESQKLQQ
İ						SAKKRDAELANGALGIIELNND
		1		l		YTLKKVMKPLITSNTVTDEIER
				l		ANVFKMNGKWYLFTDSRGSK
						MTIDDLWKFELENDDLEYLVE
				l		ENSKQKTIQDVIWLFLTAYTHI
				!		RGATQAFAKENNQKAYKETYG
				1		VSHITRHDMLQIPKQQQNEKYQ
1						VPQFDQSTIKNIESAKGLDVWD
				1		SWPLQNADGTVAEYNGYHVVF
				ŀ		ALAGSPKDADDTSIYMFYQKV
l						GDNSIDSWKNAGRVFKDSDKF
l						DANDPILKDQTQEWSGSATFTS
						DGKIRLFYTDYSGKHYGKQSLT
	1	l				TAQVNVSKSDDTLKINGVEDH
					1	KTIFDGDGKTYQNVQQFIDEGN
1					i	YTPGDNHTLRDPHYVKTKAMR

SEO IP	SEO ID NO.	Dito:	SEO ID NO.	Nucleotida	Nucleatide location of last	Amino acid sequence (X=Unknown,
SEQ ID NO:	of peptide	hod	SEQ ID NO: in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence	1	
25753	56121	A	25894	1424	3807	HPLWKWLEGDMNMNIKKIVK
						QATVLTFTTA/LLAGGATQAFA
						KENNQKAYKETYGVSHITRHD
				l		MLQIPKQQQNEKYQVPQFDQS
		1				TIKNIESAKGLDVWDSWPLON
		1				ADGTVAEYNGYHVVFALAGSP
		l				KDADDTSIYMFYQKVGDNSIDS
						WKNAGRVFKDSDKFDANDPIL
1		1				KDQTQEWSGSATFTSDGKIRLF
		1				YTDYSGKHYGKQSLTTAQVNV
		1		1		SKSDDTLKINGVEDHKTIFDGD
		1		1		GKTYQNVQQFIDEGNYTGDPL
		1				EAETAVINHKKRKNSPRIVQSN
				1		DLTEAAYSLSRDQKRMLYLFV
		1				DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIROALKS
						FAGKEVVFYRPEEDAGDEKGY
		1		l		ESFPWFIKRAHSPSRGLYSVHIN
		1				PYLIPFFIGLQNRFTQFRLSETKE
		1				ITNPYAMRLYESLCOYRKPDGS
						GIVSLKIDWIIERYQLPQSYQRT
		1				PDFRRRFLQVCVNEINGAVIGIP
		1				CVSIRKPDGSGIVSIKIAWIIERY
						QPPQSYQRMPDFRRRFLQSRPA
		1				CMHDWLCAEALAWSIQTASYL
		1				VTMQVNLTSLSSDTDRDLSVVS
				1		NSGWVSSGSLVRFNTIKTSSGEI
		1		•		KRTVPRILPDPDDPRSAIAEAPS
		l				EMPGHEVPVEEHFPEAGTNSGS
		1				PQGARKGDESMTKASDSSSPSC
						SSGPRVPKGAAPGSQTGKKQQS
		1				TALOASTLAPANLLPKAVHLA
25754	56122	١.	2000	3	2356	TAEQASTEAT ANEET KA VIIEA
25755	56123	A	25895 25896	1	2610	
25756	56124	A	25897	1	2496	
25757	56125	В	25898	1	3198	
25758	56126	A	25899		5274	
25759			25900	1		
25760	56127	A_			585	
	56128	A	25901	1	2469	
25761	56129	Α	25902	1	1914	
25762 25763	56130	A	25903 25904	1367	2259 1959	VI Ved ID ADI OND VICOVOCO
25/63	120131	A	25904	1367	1959	KLVTLHMDLSWR\NSGYQSQE
		1				T*K*PANRPVKRPH*GGI*\FSRD
	l	1	l	1		QKRMLYLFVDQIRKSDGTLQE
	l	1	l	1		HDGICEIHVAKYAEIFGLTSAEA
	l	1	1	1		SKDIRQALKSF/DGEGSIYSR*A
	1	l		1		HGAA*PSHRKDRESADLGSDG
1		1	1	1		QNDKGH\QYLVFEANTGTENG
			1	1		YQGEESLFNKAYYGGGTNFFR
			l	1		KESHKLQQSAKKLDAELSNGA
L	1	1	l	I		LGFIE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25764	56132	Α	25905	1	2418	
25765	56133	Α	25906	3	1918	
25766	56134	Α	25907	1242	1463	
25767	56135	Α	25908	1907	5097	TSKKIVKQAPVLTFTTA/LLAGO
		1				AIQAFAKENNHKAYKETYGVS
						HITRHDMLOIPKOOONEKYOVE
		l				OFDOSTIKNIESAKGLDVWDSW
						PLONADGTVAEYNGYHVVFAL
		l				AGSPKDADDTSIYMFYOKVGD
						NSIDSWKNAGRVFKDSDKFDA
						NDPILKDOTOEWSGSATFTSDG
						KIRLFYTDYSGKHYGKOSLTTA
						OVNVSKSDDTLKINGVEDHKTI
						FDGDGKTYONVOOFIDEGNEGI
						LPISEPPIKODFRLLG
25768	56136	A	25909	610	2303	SLPNLDNAAICSSSSSPTRTR*SI.
23700	20120	ľ	20,00	010	2505	SEGATQ\AFAKEKYPHKHTKKR
						SGVFHITRHDMLQIPKQQQNEK
						YOVPOFDOSTIKNIESAKALDV
						WDSWPLONADGTVAEYNGYH
						VVFALAGSPKDADDTSIYMFY
						OKVGDNSIDSWKNAGRVFKDS
	i	l				DKFDANDPILKDOTOEWSGSA
						TFTSDGKIRLFYTDYSGKHYGK
	1					OSLTTAOVNVSKSDDTLKINGV
	1					EDHKTIFDGDGKTYONVOOFID
	l					EGNYTSGDNHTLRDPHYVEDK
					i .	GHKYRGPLESPSTHQAEFNPTS
						CVSSLGTLQGFPAPAWLALAHP
						VHPLKHKSGGSNRLSAAIWGIK
		l				RKPARVCPGTGIHASSQIQGEW
	ŀ			1		RTECAVGPKAKAKATAGWRR
						GNNQHISSTYDINRADTQVRRA
		1				VNNYDIIVMSNSFNGQSEHQTY
		l				ESIVIDSAPNLGIGTINVVCAAD
						VLIVPTPAELFDYTSALQFFDM
				1		LRDLLKNVDLKGFEPDVRILLT
ĺ			İ			KYSNSNGSQSPWMEEQIRDAW
		1				GSMVLKNVVRETDEVGKGQIR
	l	ĺ				MRTVFEQAIDQRSSTGAWRNA
						LSIWEPVCNEIFDRLIKPRWEIR
25769	56137	Α	25910	1	2103	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
25770	56138	A	25911	i	2124	MNMNIKKIVKOATVLTFTTALL
					i	AGGATQAFAKENNQKANKETY
		l			·	GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFFKR
						GAIFRVHKHAVNPMSPKCRRPC
ŀ						GRQAYPLVNWEDRNGRSQKTV
				i		HTEGDMNMNIKKIVKQATVLT
ŀ						FTTALLAGGATQAFAKENNQK
						AYKET/YPKQQQNEKYQVPQF
İ						DQSTIKNIESAKG\LDVWDSWP
						LQNADGTVAEYNGYHVVSALA
ŀ						GSPKDADDTSIYMFYQKVGDN
						SIDSWKNAGRVFKDSDKFDAN
						DPILKDQTQEWSGSATFTSDGR
1	1					RSLESTTTAARPIWRKDVGGDQ
						TQEWSGSAPFTSDGKIRLFYTD
					1	YSGKHYGKQSLTTAQVNVSKS
				l		DDTLKINGVEDHKTIFDGDGKT
į.				1		YQNVQQFIDEGNYTSGDNHTL
						RDPHYVEDKGHKYLVFEANTG
					1	TENGYQGEESLFNKAYYGGGT
ŀ		1	i			NFFRKESQKLQQSAKKRDAEL
1						ANGALGIIELNNDYTLKKVMKP
						LITSNTVTDEIERANVFKMNGK
			i	i		WYLFTDSRGSKMTIDGINSNDI
İ						YMLGYVSNSLTGPYKPLNTTG
ł		l	i			LVLQMGLDPNDVTWASLEPHE
1			l	l		SFQWVRGLASSGVKLQTSVVL
1			l	l		QLIKAMWTQRVSSSKVYCKEQ
						MNNASTMSKRTSAGCHCWQG
25771	56139	Α	25912	1	3987	
25772	56140	Α	25913	1	2235	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
		<u> </u>				
25773	56141	A	25914	1	1950	MNMNIKKIVKQATVLTFTTALL
	ŀ					AGGATQAFAKENNQKAYKETY
	l.	1			i	GVSHITRHDMLQIPKQQQNEKY
				l		QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
				l		VFALAGSPKDADDTSIYMFYQ
1	1					KVGDNSIDSWKNAGRVFKDSD
1				l		KFDANDPILKDQTQEWSGSATF
	i i	1			i	TSDGKIRLFYTGSLNSSKTEKY
1	1	1				QVPHIDQSTIKNIESAKGLDVW
		1		l		DSWPLONADGTVAEYNGYHV
1				1		VFALAGSPKDADDTSIYMFYO
						KVGDNSIDSWKNAGRVFKDSD
1	1	1	į .			KFDANDPILKDQTQEWSGSATF
						TSDGKIRLFYTDYSGKHYGKQS
1					i .	LTTAQVNVSKSDDTLKINGVED
				i		HKTIFDGDGKTYQNVQQFIDEG
	i					NYTSGDNHTLRDPHYVEDKGH
	İ					KYL/VFEANTGTEEHPQPQ\ERP
	1					RTOSFTSAFAERRECIPNVPADT
	1				l .	KLSKIKTLRLATSYIAYLMDLL
	1	l			l	AKDDQNGEAEAFKAEIKKTDV
						KEEKRKKELASKCLDLEQLGAS
						VEPTGNLRTKITKEKPRHTGPPE
					i	VVVPGCCPHRSRAYKSDKYAH
	1	1				TLTVTASQHAPPPPTHMEGFEL
					i .	FHLPDLCSPSQDAQTTGRTQMK
	1					PDHSPRPSHRVPQAKGNNVVIT
					1	SYMTNRGFFEDKKATFAPSFLM
		L				NIKGNKTSVVKNSILEQGQLTV
25774	56142	Α	25915	1	2448	
25775	56143	A	25916	1312	1974	
25776	56144	Α	25917	2	1778	
25777	56145	A	25918	1366	2673	
25778	56146	В	25919	1	1938	
25779	56147	В	25920	1	2262	
25780	56148	A	25921	1	2100	
25781	56149	В	25922	7145	7154	
25782	56150	A	25923	2085	11232	VNSEGSEPADRKKPVHTEEAM
	1	1	ł			NMTIKKIVKQATVLTLTTALLA
	1			l		EGATQAFAKENNQKAYKETYG
	1	1	į	l		VSHITRHDMLQIPKQQQNEKYQ
	l .	1				VPQFDQSTIKNIESAKGLDVWD
1	1	1	l	1	1	SWPLQNADGTVAEYNGYHVVF
1	1	1		1	ŀ	ALAGSPKDADDTSIYMFYQKV
	1	1	l			GDNSIDSWKNAGRVFKDSDKF
		1	l			DANDPILKDQTQEWSGSATFTS
						DGKIRLFYTDYSGKHYGKQSLT
1	1	1	l	I		TAQVNVSKSDDTLK\INGVEDH
	1	1	l			KPILDGGGKTYQNVQQFI
25783	56151	A	25924	153	293	
23.03	1-2.2.	11	1	1	E	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25784	56152	Α	25925	420	687	
25785	56153	A	25926	242	491	WLHVQPLHDEHHCWI*YPADT DGVRPAFQRSPALSPEHGCVPY TPARQGSVRSKGPCTSALLYVE CSIAAPDRKHSCHKSDQS
25786	56154	Α	25927	2	113	
25787	56155	A	25928	779	862	NSTLPRCASTTFARY*AIPIKVFS ILP
25788	56156	A	25929	282	443	FSAGFLNLRYAQKFPSSYPPV** CYRPIYYPASDPCRNRLLYPAD VPYQALLD
25789	56157	Α	25930	3	89	
25790	56158	Α	25931	614	823	
25791	56159	Α	25932	1229	1427	
25792	56160	A	25933	1965	2682	FAVPCRTSFGSIETVSIPGRDT* SA*AYRVQVDSHRPRLAHNVQ HRT*RGEVLLAGVPRHVAEREI ATLAGSFSLHEQNIHNLPRDQG PGNTVSLEVESENITERFEVVGE KRVSAEVVAAQLVKEVKRYLA STAAVGEVLADQLVLPMALAG AGEFTVAHPSCHLLTNIAVVER FLPVRFSLIETDGVTRQLLGVSY RILAMGHAEFLQIADMRNDGG WRDFQFSGNLVMDEPNRSAQT YIKLVKSRLGTTKR
25793	56161	A	25934	261	563	RHSRGRSALRQISPEC*IHVCSPP PVQQLHPGYGNAIPLSYGHRNQ PDESDDAPVPPGWCQRYNLHQ KSTAHCGGYTIHADLVKTRCW LAPHRLPPGPGR
25794	56162	В	25935	1	1329	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hed	in USSN	lucation of first		*=Stop codon, /=possible nucleotide
l	sequence		09/540,217	codon for peptide		deletion, :-possible nucleotide insertion)
			1	sequence		
25795	56163	A	25936	761	3224	RGGAVTAKAPPDISAISALTAV
25.55	50105	ľ.	20,50	" "		KHGNCSSLTPLLNPPGSDVIVC
1		1			1	AEMDEOWGYVGAKSRORWLF
	1	1				YAYDSLRKTVVAHVFGERTMA
	1					TLGRLMSLLSPFDVVIWMTDG
		l				WPLYESRLKGKLHSNEGDAVL
		ĺ				LEIEQEVSSVDSSFNSTLGPTFN
				l		TRTIQNAVLVKTGETVVLGGLL
				l		DDFSKEQVSKVPLLGDIPLVGQ
						LFRYTSTERAKRNLMVFIRPTII
	ł			l		RDDDVYRSLSKEKYTRYROEO
		1				QQRIDGKSKALVGSEDLPVLDE
		1		l		NTFNSHAPAPSSRWALAQRIGV
1		1				SRVDMQQHVRRPPVNLSPKRE
						NVIAGYLSNSVARKORHIOTGT
						VFHQLMNLLRDGINIIFMNFKY
						OFIVYLHFLLSPKWVMYNRKC
		į .				VNGMLLIASVPATWMLSRYRS
						SHRWIAKEIPMGKTOPLPILLLG
						/GGRRIGLALA\WHFIIQKQPVIV
		1	i			SYRTHYPAIDGLINAGAQCIQA
		1				DFSTTDGVMAFADELLKSTHG
		ı				LRAILHHASAWMAEKPGAPLA
		l				DVLACMMQIHVNTPYLLNHAL
		l				ERLLRGHGHAASDIIHFTDYVV
		l				ERGSDKHIAYAASKAALDNMT
		1				RSFARKLAPEVKRQTATRAGH
		1				RGINQLSRYYRRALARQNQRR
		1				MVELRSLRFMYRHRPRSFVLW
		1				QATRLHRLNIAVRHRKPDARPL
		1				PAIQRNTDIAIKQPKRAVITGNH
				1		HRSTFVPTRLAQTGSEIRRHAM
25796	56164	Α	25937	3	543	
25797	56165	Α	25938	209	343	LSPPMSSFLATVFRSIAWLLTAK
						SIRYRTT*RWIRCAAVWLTMD
25798	56166	A	25939	547	640	
25799	56167	A	25940	174	583	
25800	56168	A	25941	2001	2610	DVLV\RKHNGHWTVELYSDSIP
1						RLQINQHYASMCNNARNDGDS
	1	1		1		QFIRSNLQDAKWLIKSLESRND
	1			1		TLLRVSRCIVEQQQAFFEQGEE
				I		YMKPMVLADIAQAVEMHESTI
	1	1		I		SRVTTQKYLHSPRGIFELKYFFS
		l				SHVNTEGGGEASSTAIRALVKK
		1		l	1	LIAAENPAKPLSDSKLTSLLSEQ
	1				1	GIMVARRTVAKYRESLSIPPSN
				İ	1	ORKOLV
25801	56169	A	25942	329	484	TROLSLLVRMTL*AFVRKRRSS
		ľ				LA*KPLWSWLSSVKSQPGWKL
		1				MLARWKSF
		-				

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25802	56170	A	25943	1	1785	
25803	56171	Α	25944	2493	2696	
25804	56172	Α	25945	1	1861	
25805	56173	Α	25946	456	700	
25806	56174	Α	25947	1	2413	MPVIKVRENEPFDVALRRFKRS
						CEKAGVLAEVRRREFYEKPTTE
1		l				RSRYDLVDRNNNIVLEYRKKEL
1						VRLTLTDPVTGKSGEVKSLVSS
l						LQTKYALKGYNVEATALEAAG
ł						GKVVTTGKDILVRKPTLDLPLE
			İ			VRRKMWFKPFMQSYLVVFIGY
	ļ					LTMYLIRKNFNIAQNDMISTYG
						LSMTQLGMIGLGFSITYGVGKT
						LVSYYADGKNTKQFLPFMLILS
						AICMLGFSASMGSGSVSLFLMI
1						AFYALSGFFQ\ST\GGSCSYST\IT
1		İ				\KWTPRKKRGTFLGFWNISHNL
l						GGAGAAGVALFGANYLFDGH
	ļ				1	VIGMFIFPSHALIVGFIGLRYGS
1						DSPESYGLGKAEELFGEEISEED
			1			KETESTDMTKWQIFVEYVLKN
1						KVIWLLCFANIFL\YVVRIGIDQ
						WSTVYAFQELKLSKAVAIQGFT
		1				LFEAGALVGNGCSYAQGMWG
						KTAETSDLQDLLIAALQGLSAW
		1				AVKAREYGIINHDVDSFAPRAF
						FSTLTNVNFDSPRIVGYAREAIA
1						LREALKAQCLAVDANARVDNP
						MADLQLVSDDLGELQRQAAEF
						TPNKDKAAIGENILGLRLLCLY
						GLKVFNGREDQLDSCYHGNRQ
		1				LRGSLRLLFLAFIRQRLRDLIITA
ì		1				HRVIRVNRQHAALGVKHCRLP GITGNRIQRQATQYRDRRGTGQ
		1				NOCMRGDMOOLFADIANVAN
		1				TFAOIIAGRGRKFGANLLHIAD
0.000	26186	-	0.5040		2720	TFAQIIAGRGRAFGANLLHIAD
25807 25808	56175	B A	25948 25949	1518	3738 2124	DCFCGSRHDKLPSAHQCSAKPG
25808	301/6	A	23949	1318	2124	SDRFWRSHADAAYAHDGGIQP
						VLCASRSNGCLQKPKCHTIVSG
		1				RCPLQQIGS\SVFPSGDAANVAS
			1	1		FSCACDNAGSAQHRTLLLGKQ
		1		1		FFNCRNAFHFNRNSRQTALKSG
		1		1		ISWVTFQLILKQQPRPVIMTKM
		1		1		AIGFRKV*SQRNIIRHLLVYIFKF
		1		1		ADGGCFVVIFLCLQRFIETGINN
				1		KMG
25809	56177	С	25950	1	747	
25810	56178	Ā	25951	168	332	CAWRAVCAAW/PTGASC/CNN
		1	1	1		DRFVFQILRSFEHDNSEDKPGP
		ı		1		GMPPHGWRTQFWGG

SEO ID	ICEO ID NO	IMa:	SEQ ID NO:	Nucleotide	Nucleatide Inesting of last	Amino acid sequence ( X=Unknown,
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
NO:	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			,	sequence		
25811	56179	A	25952	l l	2706	
25812	56180	A	25953	1	1062	
25813	56181	A	25954	<del>li</del>	855	
25814	56182	c	25955	1	2412	
25815	56183	Ā	25956	279	713	RCDAAAGAVLHSAGLLRHCGY
23013	30183	^	23930	219	1/13	WORGKPDRWSRRPGNYADRIC
l		1				RRWFCAGGVGDROYELCOLLA
Į.	1					YTVSATRRGTGYCLYRDSRGR
ŀ	1	1				TGLPVV*HLSGAGLYGRCRFAG
						VRWCVRHYRRTATSGIPAGDY
						GGRVRGRNAFCHPAVAP
0.001.6	27104	<del>  -</del>	25957	,	769	MDFAETELEFIKFWGDIITNKLN
25816	56184	Α	25957	1	/69	
						EALAAQGDNVVINLASDEYFKS VKPKKLNAEIIKPVFLDEKNGK
1				1		FKIISFYAKKARGLMSRFIIENR
İ						
						LTKPEQLTGFNSEGYFFDEDSSS
		i				NGELVFKRYEQRAECRIVTRHL SFSGDVCLDHDRRDDHEELSY
1						GGAAVAAVLVIEPNKLAFDGS
		1				
		1				GYLAWEGLICMQEIGKC/YRRT
						SGDCA*VAGRAQTG*VSGWAL
		İ				SRGKNQPGVGCEAGARRHARE
2 - 2 - 2	44104	-	05050	Į. —	2472	ARIGDERHRLAPRDML
25817	56185	В	25958 25959	11200	4492	DCGGVRSORPDOR*DWNR*GA
25818	56186	Α	25959	4300	4492	
1		1	1			GGESDS*SLATGGQAAEGVAV WRYSARWR*PLFAGRCARAGG
1		1	1			
24010	46107	-	25050	40	2000	D
25819	56187	B	25960 25961	49 266	3000 812	LLRWRPGALALGHKLVAGEIR
25820	20198	I <sup>A</sup>	25961	200	812	OORMDAWRAACLONPOGILCC
	1	1				ARGGQRSHIVQSWLHAAGIDY
1		1				PLVEGGYKALRQTAIQATIELA
1		1				OKPIVLIGGCTGSGKTLLVQQQ
1	1	1				ANG/VDLEGLARHRGSAFGRTE
		ı				DELGKLAQTSTSSPAHWRETSK
		ı				CGGFLCPIFLTNMRTPLPVCAT
1	i .	ı				VLPYLAIATV
25821	56189	1	25962	761	874	VLFILAIAIV
25821	56190	A	25962	2	304	MAAYGSGIFAQTYIEAFGISTIQ
23822	30190	I^	23963	1	304	PASCSPVNQYITAAFVLFGNVA
	1	ı				HALLIALORRNRRHLORRKGA
		ı				VIVIAFNTSOGA/VPAFCCOP*S
	1	1	1			RYASPPCCSFSTA
26022	56191	<del> </del> -	25964	109	777	KIASIFCCSFSIA
25823 25824	56191	A	25964	5	187	ITHKKPPPSWRSALLPAAGVFS
25824	30192	Ι^	23903	l <sup>3</sup>	107	RRYMPALCE*HWAS*RMRAEA
		1				
25026	56102	١.	25066	,	711	TETFSDCTMPIIGMMMS
25825	56193	A	25966	1	711	
25826	56194	A	25967	757	1026 750	
25827	56195	A	25968	1	/30	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25828	56196	A	25969	l  1	1065	MKVLEKRNNASSEPEEKNEIRA
		1				AREHAGFTLOELVCLGASGRK
		ı			i	VQGEAANAEEEVAAGELDNIA
		l				KITNEGSYTEOOIFNEGYMWLS
	]	l				TLMKIKENKISCSWATOSHFOG
						SIDAGELEHLTPERVWKETESA
						LTTRNPQVFFQVLRDCGALRVL
		İ				FPEIDALFGVPAPAKWHPEIDT
					1	GIHTLMTLSMAAMLSPOVDVR
		1		i		FATLCHDLGKGLTPPELWPRH
		ł				GHGPAGVKLVEOLCORLRVPN
		ŀ				EIRDLARLVAEFHDLIHTFPML
		1				NPKTIVKLFDSIDAWRKPORVE
	1					OLALTSEADVRGRTGFESADYF
						OGRWLREAWEVAOSVPTKAV
		1		1		VEAGFKGVEIREELTRRIAAG
		ı		1		LRG*VSRSHPHLPNAEPKNH/AS
		1				NYLIPSMPGVNRSVSSNWR*PA
						RLTCAAE/HGFESADYPQGRWL
İ						REAWEVAQSVPTKAVVEAGFK
		1				GVEIREELTRRRIAAGLRGMPT
25829	56197	Α	25970	2373	2597	SADDKADSVA*YLRLASA*TNS
		1				CRPYRRPSAPVCRRAPAI*G*TP
						QNYGPPSSCPAGGFWRYPVDPF
1			İ			RFSGFVH
25830	56198	Α	25971	2616	2777	TSVRKRFSTLSGKPVAKAGRKR
					1	PPPCR*TPTANGHPKPCRPPVW
						CHPAPVARP
25831	56199	В	25972	1	1449	
25832	56200	Α	25973	1076	1477	CAVRRSITWCKLSSKTPVRPLR
						PSTYRDCLTVSIALTPPASEKVK
		1				RRPVPAVKSAMKVPPGAAQSR
ŀ		1				KRVWLVSPFPTCEFLASNSRGK
		1				KISVSLSALSPRWTS*PKARWA
		1				ARRLTTNLVVRH*TATSVLMK
						KK
25833	56201	Α	25974	1	3552	
25834	56202	Α	25975	196	493	KRCRFADRPGDPGRQGTPAATT
		1				FGGMSFVTILPAPIPELSPMVTP
		1	1			GLITT*LPIQTLLPIVIGKEYISPF
		l				FLNSWCTGCPVTERVTLGAIST
1	1	1		1		LSPIVTV

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
				sequence		
25835	56203	A	25976	1	3917	MTDKHQQHRYVAAPGPFVGD
					\	KCOVAGDPLMLRRALSNLLSN
						ALRYTPTGETIVVRCQTVDHLV
		1				QVIVENPGTPIAPEHLPRLFDRF
		l				YRVDPSRQRKGEGSGIGLAIVK
						SIVVAHKGTVAVTSDARGTSGL
						DDFFIDVVYWVRRIKRKLSVYR
		l	i			RIPRMSYRELYKPDEQPLAIMV
						PAWNERASSAIWRAGGTTLDT
						KFLFVGLPGPILGSCKVPFEFLE
						VACPPSGGPVGPPWRRPCRGA
						AAAICASPAAIILAPT
25836	56204	A	25977	3	292	GDMQRLNSLFC/SVAYSVLEQP
						DEDEGRDSINIVNPSGRPHVSSG
						ATPAVREYAAHGFHLYGLRQR
	İ					VGEVRVDLQREQIYASKPCGST
					-	IGISLVVR
25837	56205	Α	25978	2	181	SARRLR/RSKHRFRILNRRYSHA
						HS\MLGDMQRLNSLFC/SVAYS
						VLEQPDEDEGRDSINIVN
25838	56206	A	25979	I	2781	
25839 25840	56207 56208	A	25980 25981	I 635	2554 741	
25840	56208	A	25981	91	501	LWIRLAKRSGKAIKERRDFIFRL
23641	36209	^	23982	191	301	CTHRVRQGTALLRLFQHSGGN
				l		RLMKLDNQHLRLRISNHRAFHF
			ł	i		RHRTTVKQSQQTFRYPWLYRV
						RHWGQKPKTDNFHGLLARIFG
		1				NSRSKTWGENR*EHSVLEOPDE
						DEGRDEY
25842	56210	A	25983	2153	3062	APVMPPERLPVIAVROYPTANC
		1				CSDCLAAASRFFLASVAAPEOT
				l		DADTRRSRVAVGRRKTRSNSA
		l				NOPRPRRDWRELOLMDRLARV
			l			AQARASFAARETLRIGDAMEQ
		1				MMEGLNKVMHGEPRQEKELR
						KLADDINVLYTAIKLYLARMPK
		1		l.		EELAEEESRRWAEIIEMSLNLEQ
						ASDIVERMG\GELVDKSWAAR
						RAFSLDGLKELDALYEQLLSNL
			1	İ		KLAMSVFFSGDVTSARRLRRSK
						HRFRILNRRYSHAHVDRLHQQ
				1		NVQSIETSSLHLGLLGDMQRLN
L		L				SLFCSVAYSVLEQPDEDEGRDE
25843	56211	Α	25984	135	308	KLSLRLGIFPRPSLFPRPTPSPST
						PAPAS*PAPS*VSPSPRTATPSCP
		L	L			TSYSSFPCH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25844	56212	Α	25985	3	663	ARGKKPPRRGKEDFWDLSIATR
			Ì			VSVNPIKFPVEA*PFLKP\LQQV
						S\GPLGGRLPLPIPGNLLLQVAD
			l			GTLSLTGTDLEMEMVARVALV
			l			QPHEPGATTVPARKFFDICRGL
			l			PEGAEIAVQLEGERMLVRSGRS
		1				RFSLSTLPAADFPNLDDWQSEV
			l			<b>EFTLPOATMKRLIEATOFSMAH</b>
	l					QDVRYYLNGMLFETEGEELRT
				1		VATDGHRLAVCSMPIGQSLPSH
25845	56213	Α	25986	1	1077	,
25846	56214	Α	25987	I	1323	MHSGTFNPQDFGWQGLTLTPA
		1				AAIHIRELEILDEYGIPNAWQGE
		l				TNFWGSTAVSIDRLAAYKDVD
						VLCFDHDNSKDMDALMATPL
	1					WQAMPFVRAGRFQRVPAVWF
						YGATLSAMHFVRVLDNAIGVIV
			Ì			ATALTWMNFSQALPRSOWAQ
		1	l	1		AAWSPDIDVIEOMIFHYSLLPRL
						AISLLVGAGLGLDVRYYLNGM
						LFETEGEELRTVATDGHRLAVC
			ŀ			SMPIGQSLPSHSVIVPRKGVIEL
						MRMLDGGDNPLRVQIGSNNIR
			ŀ			AHVGDFIF\TSKLVDGRFPDYRR
			l			VLPKNPDKHLEAGCDLLKOAF
						ARAAILSNEKFRGVRLYVSENO
						LKITANNPEQEEAEEILDVTYSG
			l			AEMEIGFNVSY\VLDVLNALKC
			l		ł	ENVRMMLTDSVSSVQIEDAAS
				1		OS\AAYVVMPMRLEGSPPLGNP
						EFOKISSPCALYIALCSKARHHT
			ŀ			GRYLGLCGL
25847	56215	Α	25988	211	475	GAIGVFTAGKLTRASVYHQAR
						RFMQRETVWLVEDEQGIADTL
			ŀ			VYMLQQEGFAVEVFERGLPVL
			ŀ			DKARKQVPDVMILDVGLPDISG
			1	1		FELCROLLALHPALPVLFLTAR
				1	1	SEEVDRLLGLEIGADDYVAKPF
				1		SPREVCARVRTLLRRVKKFSTP
				1		SPVIRIGHFELNEPAAQISWFDT
			l			PLALTRYEFIVLKT\LLKSPGRV
			1	1		WSRQQLMDSVWEDAQDTTSH
	1			1	1	VVAFATILQGISRDLRRRILPYCI
	l	l	l	1	ł	RCRRERCTGTALWQ

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide scquence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25848	56216	A	25989	1661	2499	OMAHDEOWLTPRILUTAATLC NQNAPROGSPLWLGVUDLGTCD VYSMYVDRDGQPVAVCLDWA DVVRDGIVWDFFGAVTIVRRHE DTLEQQFGRERSHAATSFDG DPRISINVLESAGLEVSHVLDEP TAVADLLQLDNAGVVDIGGGT TGGAIVKKGKYTYSADEATGGH HIFLTFAGNRISI.EEAEQYKRG HGEEIWPAVRVYEKMADIVA RHIEGQGITDLWLAGGSCMQP GVAELFRKQPFALQHLPQHSL HTPLIAISSGREKAEGLYAK
25849	56217	А	25990	915	1518	ISGHAPDLNGAPATAHIQPGGR YPAPRSVRRATDNGYPAGDPLE WRSTAQVFVSSRRRVSLENDRK TVLTRCWSAAH*FALPAPLCAG RTGERKNRRFHTPTRCGGEQF APAASRCAGRRGDASGRSTTS RRPAPSHCPVQ*GGHRSTTSTS TSRRPGQSARPYSGPEYRE*Y CSAQRFFINDGSRPPVVRQAGR AQFP
25850	56218	A	25991	1	1254	
25851	56219	A	25992	675	835	VRWCWIFPSQ*TLFQKRAGHA APSADVLHESCQHFLNLLNRLG RHYDFGEGEP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25852	56220	Α	25993	1	2255	MRESPTRDDSKNTVNTTIRIRIH
						NSYTEOLOIVTNSYCTKOWHV
						HHTAKPYAHIQRPATPDAQLTK
l		1		l		MOEEEEVEPEPEMEAEVEPEPN
				I		PEEAETESESMNORDVRGTVRI
		1				VLKTFNNCRDTVFVAFEVNNT
ĺ		l		1		VSLLVATTDMTSGDTAIVVTTT
		ı				GFAVFFQQRSKSAANEVQILAF
						FQGDVSFFPVATTTDTLSVTFN
		1				FPFNYQGVNDFDFDFKQFLHSS
		1				FDFCFGRVFSNFEYLHGARAHA
		1				CIPPSACIGEVLETSSFDIRVSVY
		l				RSSCVCVRLRESSTGDRYFGGL
		l				SLQMMRKATGLTDITSDTPGNT
		l				DDQRWHPEHGLTQRMQKEQE
		l				LVKEPEGAARDGDGEAEAWGE
-		l				VKAKSSGCVGTRASSHLFRCNV
		1				CELHFKESSELLQHPCTPSGERP
		l		1		FRCGECQKAFKRPSG\LRQHER
		1		l		THSAERPFKCDLCPMGFKQQY
	1					ALMRHRRTHKTEEPFKCGLCE
	ĺ	1		l		KGFGQPSHLLYHQHVHTLETLF
						KCPVCQKGFDQSAELLRHKCLF
		1				GAAERPFKCPVCNKAYKRASA
		1				LQKHQLAHCAAAEKPLRCTLC
						ERRFFSSSEFVQHRCDPAREKPL
		1				KCPDCEKRFKYASDLQRHRRV
		1				HTGEKPYKCPNCDKAFKQREH
1		1			l	LNKHQGVHAREQQFKCVWCG
		ł				ERFLDVALLQEHSAQHSAAAA
		1				AAEGAYQQTLHHPRRQQQQY
						WQLLCARNNVKLCMHILFSPH
25853	56221	Α	25994	98	596	YSGIIMAQSKLYPVVMAGGSGS
		l			1	RLWPLSRVLYPKQFLCLKGDLT
		1				MLQTTICRLNGVECESPVVICN
						EQPRFIVAHQMRQLNELSENIIL
						EPAGRTTAPTIAPAALAANRHS
						PESAPLMLVLATDHVIANEDAV
		1			1	RAPVK\NAIPYPKKGKLVTFGIG
				1		LDGRVPRYNM
25854	56222	A	25995	3	554	
25855	56223	Α	25996	1	222	

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
		$\vdash$				
25856	56224	Α	25997	I	1043	MKVKVLSLLVPALLVAGAANA
		1				AEVYNKDGNKLDLYGKVDGL
		l				HYFSDNKDVDGDQTYMRLGFK
						GETQVTDQLTGYGQWEYQIQG
	1	l				NSAENENNSWTRVAFASLKFQ
		l				DVGSFDYGRNYGVVYDVTSW
	i	l				TDVLPEFGGDTYGSDNFMQQR
						GNGFATYRDTDVFGLVPTRLHF
		l				ARVCCALRELKDAGADRIWYI
						ADAFRAGLSVDGVFNLTNIDR
		l				WFLHINRAKDKNHMIISIDAEK
1		l				AFDKIQQPFMLKTLNKLGIDGT
		l				YFRIIRAIYDKPTANIILNGOKLE
		l				AFPLKTGTRQGCPLSPLLFNIVL
						EVLARAIRQEKEIKGIQLGKEEV
		1				KLSLFADDMIVYLENPIVSAON
		l				LLKLISDFSKVSGYKINVQKSQT
						FLYTNNRQTESQIMSELPFTIAS
		ı				RRIKYLGIQ*IRY*WDVFQNNK
						SYL*QTHSQYHTEWAKTGSIPF
						ENWHKTGMPSLTAPIOHSVGSS
						GOGNOAGEGNKGYSIRKRGSOI
						VPVCRRHDCLSRKPHRLSPKSP
25857	56225	A	25998	1	3339	VEVERHDELSKREHKLSERSE
25858	56226	A	25999	1440	1880	AAQHASVYLYQNRIRGAVPPV
23838	30220	l^	23999	1440	1880	RFFHADQRTRRDGADGKORHA
1						TETLCRIAEKISSSREQDWLHCD
						ERQSLYEWTW*PYSPHSGRSQK
						EKROT*TAILDAYCADCFRCGR
						GVFARRERRTKRDRPGNAGTG
25859	56227	ļ	26000	ļ. ——	2277	GDCPCWLRRQYECVRL
25860	56228	A A	26000	1	1845	
25861	56229	A	26002	56	113	OOOPNPTRDQLQLAILHNIRGIR
23801	30229	Ι^	20002	36	113	
25862	56230	c	26003	1	2317	KIYG*IQSATREAG*GHSPQY
25862	56231	A	26003	3	2168	
25864	56232	A	26005	670	2541	
25865	56233	A	26005	98	944	YSGIIMAOSKLYPVVMAGGSGS
23803	30233	I <sup>A</sup>	20000	98 '	944	
						RLWPLSRVLYPKQFLCLKGDLT
						MLQTTICRLNGVECESPVVICN
ļ						EQHRFIVAEQLRQLNKLTENIIL
						EPAGRNTAPAIALA ALAAKRHS
		1		1		PESDPLMLVLAADHVIADEDAF
		1		I		RAAVRNAMPYAEAGKLVTFGI
	1	i		1		VPDLPETGYGYIRRGEVSAGEQ
		1		1		DMVAFEVAQFVEKPNLETAQA
		1				YVASGEYYWNSGMFLFRAGRY
		1				LEELKKYRPDILDACEKAMSAV
1			1			DPDLNFIRVDEEA/FLACPEESG
		1				DYAAMGRTGDAVVPLSLGAH
					1	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown. *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25866	56234	A	26007	3	417	
25867	56235	А	26008	507	717	WPEAEYLDNADAVLAMYHD/Q GLPVLKYQGFGRGVNIT/LGLPF IRTSVDHGTALEWRTCKPMVP DSIVSCIL
25868	56236	А	26009	5	378	MAVCSSLSPRRSPAFL/HDFTDV WTHHLVFGVNP*RGLHIGTALT DHVG/ENGNYSSD*HGTALTD HVGKTETILPTKYANIYSINTSK DRFLTKPAFAEVVLFLHPRELQ TCSFFLSQNMLVKVGHQRHWF TEVDVTLTEITOLA
25869	56237	A	26010	I	469	MQKEYAYWMÖGLKTCKPDNR KNALSNFGWYPSQPLLGRSRY ATTESWVEDIATAKSNPNRLPL KFTATCALPLRLAGFQ\PRWMD NPQQLNTLAPPASYRSI*TA*CL K*KNPRPRQQSCRR*RDGNQYE TLNPRPRQGIEKTCGTINKAG MPITT

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25870	56238	Α	26011	2	1854	CGGTLARACDGCLNGEFAA/LI
		1				TGPVHKGVINDAGI/PFTGHTEF
						FEERSQAKK/VVMMLATEELRV
		1				ALATT/HLPLRDIADAITPALL/H
						QPKYLDNADAVLAMY/HDQGL
		1				PVLKYQGFGRGV/NITLGLPFIR
		l		ŀ		TSVGHG/TALELAGRGQ/ADVG
		1				SFIRPYSAIK*L*NAGASVRWLS
						ERRICRAITGPVHKGVINDAGIP
						LPVIPSFSKSVRRRKRCDDAGD
		1				RRTSRGAGNDALPLRDIADAIT
						PALLHNRNILITPTPCWRCTRSG
						SSRAKIPGLRARCDITLGLPFIRT
				ł		SVGHGQPLNWRDVANRCWQF
				l		YTPLFCHQMIVKPMHNRIPRAT
						YRGAVKSAIGLGCCCLKASATF
						CAYRWRRSGRRDQSRFRYFEIA
		1	Ì			GIRSRGINFIACPTCSRRNLMLS
	İ	i		i		VRLTRWSNAWRYHHSDGRFD
						YRLRGECPGEALVSTLGVTGG
						NKKAASMKMGAQRPSGQQDM
		l				IDQLEARIRAKASQRTKRVELT
		ł				FSRLKNNNVEKQDTALFALYQ
		1				RRLRCVRKVRRYVMAAVSAGO
		1				GGGVCAVSAYMPLNRLPNAQE
		l				ANNEYTSFENCIKCTVCTTACR
		I				VTLRNNDPKLPYLVKAGLKMK
		1				RVTRSPRRYCAAASATHRFNDE
i	1	Į.				RAGKVQGMPDINKLPADRETC
	ł	1				STLTCARSRQNQTNPYPANRAA
1		1				NAYQVVLATKALEKVSMKSP
	1	1	1		1	WQHKVSSPAAVRHLPSITQRRT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25871	56239	A	26012	1	1504	MGIVASASVQAAEIYNKDGNK
2.5071	30237	ľ.,	20012	ľ	1	LDVYGKVKAMHYMSDNASKD
		1				GDOSYIRFGFKGETOINDOLTG
					1	YGRWEAEFAAWTDMFPEFGG
					İ	DSSAQTDNFMTKRASGLATYR
						KTTSSAYRWPELNLQYHRCTS
						AARAMLLSGRPVMQINERTAV
						RRQMTVYLRVERIHEIDPLVSL
				ļ		SHSMSVIPIDVERPIAAAPCTPG
						LWRTKTPLRVPSTYPLRLPGRA
						RVVCHRTFRLHLCKDWVFMFS
				ŀ		GLLIILVPLIVGYLIPLROQAAL
		1				KVINQLLSWMVYLILFFMGISL
		l l				AFLDNPRPYLADSVPDROLLAP
		ı		1	ŀ	VNSISRYKTIEWLNYIATELHK
		l		1		GFTPLFRPDTPEEYKPTVRAHSE
		l		l		KKLOYVNEALKDEHWICGORF
		l				TIADAYLFTVLRWAYAVKLNL
1		1	1			EGLEHIAAFMORMAERPEVOD
	ļ	1				ALSAEGLKGSRHLSAGARRLIL
		1				GIIVTFSLILALICVTQPFNPLAQ
						FIFLMLLWGVALIVRRMPGRFS
		1				ALMLIVLSLTVSCRYIWWRYTS
						TLNWDDPVSLVCGLILLFAETY
		1				AWIVLVLGYFOVVWPLNROPV
		1		l		PLPKDMSLWPSVDIFVPTYNED
		l				LNVTPDELKQVLDVAAALKAL
1		1				RAENISTKVFNSGLGISVFRDNS
		l		l		TRTRFSYASALNLLGLAQQDLD
		i				EGKSQIAHGETVRETANMISFC
İ		1				ADAIGIRDDMYLGAGNAYMRE
						VGAALDDGYKQASGFSEPAMR
25872	56240	A	26013	2903	3024	
25873	56241	Α	26014	123	335	
25874	56242	Α	26015	2634	2787	
25875	56243	Α	26016	1477	2485	NPEQLMVKTQRVVITPGEPAGI
						GPDLVVQLAQREWPVELVVCA
1						DATLLTNRAAMLGLPLTLRPYS
						PNSPAQPQTAGTLTLLPVALRA
						PVTAGQLAVENGHYVVETLAR
						ACDGCLNGEFAALITGPG\HKG
						VINDAGIPFTGHTEFFEERSQAK
						KVVMMLATEELRVGLATTHLP
		1	1	1	1	VRDIADAITPALLHEGIAILHHD
						LRTKFGIGEPRILV\GGLNPHAG
		1		1		EG\GPMGTEEIDTIIPVLNELRA
						QGMKLNGPLPADTLFQPKYLD
		1				NADAVRPMYHDQGLPVLKYQ
		1	1	1	1	GFGRGVNITLGLPFIRTSVDRGT
		1		1		ALELAGRGK\ADVGSFITALNL
	1	l	l			AIKMIVNTQ

SEQ ID	lero in vo	Tar.	SEQ ID NO:	No. of cast de	Numberside togetion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	· .			sequence		
0.0000		15	26017		3432	
25876	56244	В	26017	1385	2536	KSSQSHLITGMLEHVFVKSGDT
258//	36243	A	26018	1383	2550	
						PSR/LPELMNGAQALANQINT/F
					į.	VLNDADGAQAIQLGAN/HVWK
						LNGKPDDRMIED/YAGVMADTI
						RQHGADGL/VLLPNTRRGKLLA
						AKL\PDASRTGETH/TVEWQAP
						AVAITRTATQARQSNSVDLDK
	i					ARLVVSVGRGITDSQTLRLYYI
						RLPPSLMGMRLTVFLLPICGFH
						RVGPPTLLSVLATNRNRNAKVF
1						AHKNAPKFRSHTASEQWKSSIA
1						HNKGVHPRVTSHTHARHSLME
		1				TDIPHNIHSGHASPADITRHRAQ
					l	VFNSVPKMASPIGDRVPTLHTQ
		l				HNSPANTGKAQSLLTCGPAAES
				1	l .	CCRLIPRQMVSLVFRLKARLLLI
				i		TTELPKGLVPVATISGTGNFGN
		<u>.                                    </u>			1000	TQSANPYRPSENTDLSLS
25878	56246	A	26019	926	1293	LSPNPKEPSCRTRLKKSGFFTRI
	l					SAGAEPLMAIPARLSNSLACGA
		1				RDSAAKE/GFVVVPVCVAVEA
		1				DIAELDDEERDEFMADVGFT\V
				ŀ		GVKEVRAWTIPVGATAPQAAG
25879	56247	A	26020	,	1278	KIHTDFEKGFIRAQT
25880	56248	A	26020	678	1526	ERNTNTCEVVPNRKRAYASHD
23000	30248	^	20021	070	1320	MELSISPVGKGASKGEVNPADD
						IEVINTELALADLDTCERAIHRV
						OKKAKGGDKDAKAELAVLEK
						CL\PQLENAGMLRALDLSAEEK
	ŀ	1				AAIRYLSFLTLKPTMYIANVNE
						DGFENNPYLDQVREIAAKEGSV
						VVPVCAAVEADIAELDDEERDE
						FMOELGLEEPGLNRVIRAGYKL
1	1	1				LNLQTYFTAGVKEVRAWTIPV
	1					GATAPQAAGKIHTDFEKGFIRA
						QTISFEDFITYKGEQGAKEAGK
						MRAEGKDYIVKDGDVMNFLFN
25001	66240	<u> </u>	26022	1177	1605	MRAEGRDTIVKDGDVMNFLFN
25881 25882	56249 56250	A	26022	1177	644	MDNHIALDFLLASECGSVYVY
23882	30230	^	20023	1	044	ATTHGRNMAGARALWRATGM
1	]	1			1	
	1	1			1	TDADFGKPIIAVVNSFTQFVPG HVHLRDLGKLVAEQIEAAGGV
1	1	1			1	AKEFNTIAVDDGIAMGHGGML
1	1	1			I	YSLPSRELIADSVEYMVNAHCA
1	1	1			1	
	1				1	DAMVCISNCDKITPGMLMASL
	1				1	RLNIPVIFVSGGPMEAGKTKLS
	1				I	DQIIKLDLVDAMIQGADPKIN/D
25883	66261	В	26024	1	1944	YQSRGRRCPNRCFRCKNQAGS
23883	56251	B	20024	J <u>.</u>	1394	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25884	56252	A	26025	1 '	1488	
25885	56253	Α	26026	1	1919	MNKAHFVSNLGATKCCPLSFLF
						YRWRRVIAFVVAFYFRHLIDLL
1				1	i	VVQMHFKLVKGNVDVVFTAQ
		l				LIDSTVQLIDSTTTVTQFTHIQT
1		ŀ		1		QLMIQRAGTKCRKEDFRHCVGI
1		l				LEPEWYPIIVVRVVVDVSQFEV
		ŀ				RSQSLIFAVGEGITCIYTQFITHA
					i	VVRLTVNFHVVAQLSSPDWNR
		ŀ				PETLPVRSHVTSITQFEVVTGFQ
						TEAPSVGVGATVNVSTVAHGC
		ŀ				RQVVVEVRVAQATINKDVVRE
						VSRRVDVGSLAVLIHLTRTVIH
						VTFSEACSRTDDPLSVVTVNFG
						NTDHDAVNILIIVDGAVVAVEV
						TTEVAYPCAAVISQAMTRVGQ
						TSTNGVWTISSVNAFQIRTGAA
		i				RSLAPPWSLTEKVFCGTTMER
		ĺ				MRAALEAIMPFTESSSATQAPY
						LPCGRECGLAVRQFFGRGEGIE
				l		TVAYLFRIIRVVRTRVLSIGGFS
			ļ.			RTRISSTPVKIATLRQNRSDCHA
		l l		l		AMIADTYRQVTPTDPFSRHPFS
		ŀ				RVLRGLFFIIFKDTKAHNGIGMI
		l				GGVNRRADYLNLLEKVFGDRV
		l			}	SSPQWQATLKAIVPSYGRKLNG
		l				DVAATERELQYTSEVVGLNYD
		l				KPQAADNNRQHKVRAARSRRQ
1						NRPDRGSQIADSTAGARCRFQT
		l	ļ.	l		PTAGDGA*SAASTAAPI/MLNLL
		l				EKVFGDRVSSPQWQATLKAIVF
1		l		I	1	SYGRKLNGDVAATERELQYTS
						EVVGLNYDKPQAADNNRQHK
25886	56254	Α	26027	I	2130	
25887	56255	Α	26028	1144	1309	PGGSTPMAVEDPDFRSSERVLR
1		l		l		FQPAVSVYGPEQPAV*DYAQTS
		_				YLRTRPRRSDP
25888	56256	Α	26029	1	3546	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
25889	56257	Α	26030	1097	3332	TRVLVLDHRLLRCLYATVCAG
				l		ASWGMNPVVCSQQIDPQFHTM
		1				LMICASEEAQRMQQASEDEFN
						RALNIAFDNRLGLCKVESARQV
				1		FPLTGRYARQFASHRLALVGD
		l				AAHTIHPLAGQGVNLGFMDAA
				ļ.		ELIAELKRLHRQGKDIGQYIYL
						RRYERSRKHSAALMLADSFVR
			1	l		TTHALRRSHGGFPRLDDAAAL
				ŀ		RFANRRTSCERNDDNTWSRSL
						YADLKNGTAQNIRAKFVFIGAG
}						GAALKLLQESGIPEAKDYAGFP
İ			1			VGGQFLVSENPDVVNHHLAKV
		l				YGKASVGAPPMSVPHIDTRV\L
						DGKRVVLFGPFATFSTKFLKNG
1		l				SLWDLMSSTTTSNVMPMMHV
		1				GLDNFDLVKYLVSQVMLSEED
		1				RFEALKEYYPQAKKEDWRLW
		1				QAGQRVQIIKRDAEKGGVLRL
			ŀ			GTEVVSDQQGTIAALLGASPGA
					1	STAAPIMLNLLEKVFGDRVSSP
		l	İ	1		QWQATLKAIVPSYGRKLNGDV
		1				AATERERKTLHVIFNDLRPEOC
		1	ŀ			EAGKSPSRVQLQTWTNGGMLN
		1	Į.	ļ		APLSLRLTLVEKLASMLDPGHL
		ŀ				ALTQIAQHLALLQKMDHRQHS
		Į				AFPELPQQIAALYEWFSARCRW
						KEKALTQRGLLVQAGDQSEQIF
		1				TRWRAGAYNAWSLPGRCFIVL
			ŀ			EELRWGAFGDACRLGSPQAVA
		1		1		LLLGDLLEKATQHLAESINAAP
		1				TTRHYYHQWFASSTVPTGGEH
25890	56258	Α	26031	115	654	HATQTMTPWFLYLIRTADNKL
23890	30236	l^	20031	1113	054	YTGITTDVERRYQQHQSGKGA
						KALTGGSARSPLIKKALAEOLP
						GIPIAGGDDFGSVTAGLAR*RF
		1				HORHGPCWSMKAESLOLCRAD
		l				CORREQPMSFGGHFRHYRLSVC
		ļ				
		1		l		WRYRFIRPEHKTAFTARFPVDN
		1	1	l		RLGQMVAKPFHLLNATTGNIC
25001	56250	-	26022		240	GCFNTKRP
25891	56259	A	26032	1	348 906	
25892	56260	A .	26033			
25893	56261	В	26034	59	910	
25894	56262	A	26035	1	3684	
25895	56263	A_	26036	l	2634	

SEQ ID NO:   SEQ ID NO:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   No:   Nucleotide   Nucl	de nucleotide eleotide insertion) ARCFSARSED PNGRNVLSQ
Sequence   Sequence	ARCFSARSED PNGRNVLSQ
23896 36264 A 26037 1162 3478 LVRFGLLPLAYS, RPKDECETCCIKY EIHQVFVLNGIOS NELASMGGLVDY AREAFSHSIDLA RYWLAEHINNT GYLAEHINNT GYLAEHINNT GLGRAPGSDORT GLGRAPGSDORT SGDIDNFPRDV AI DPILEPTHORRIL GYTRGVEPTTOPI GYTRGVEPTTOPI	PNGRNVLSQ
RPKDECETCCIK\ EIHQVFVLNGIQS NELASMQGLVD\ AREAFSHSIDLA RYWLAEHHNMT GYLAANTTILHL HSPLVIAEPGTI GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRL GYTPGVEPTTDPI	PNGRNVLSQ
RPKDECETCCIK\ EIHQVFVLNGIQS NELASMQGLVD\ AREAFSHSIDLA RYWLAEHHNMT GYLAANTTILHL HSPLVIAEPGTI GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRL GYTPGVEPTTDPI	PNGRNVLSQ
EIHQVFVLNGIQS NELASMQGLVD' AREAFSHSLDLA RYWLAEHHNMT GYLAANTTITLHL HSPLVJAEQFGTU GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRL GYTPGVEPTTOPI	
NELASMOGLVÖ AREAFSHSLOLA RYWLAEHENMT GYLAANTITLHL HSPLVIAEQFGTL GLGRAPGSDQRT SGDIDMFRDV AI DPILEPTHNGRRL GYTPGVEPTTGP	
AREAFSHSIDLA RYWLAEHINMT GYLAANTTILHI HSPLVIAEQFGTI GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHORRIL GYTPGVEPTTOP	
RYWLAEHHNMT GYLAANTTILHI HSPLVIAEQFGTI GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRI GYTPGVEPTTOP	
GYLAANTTILH. HSPLVIAEQFGTI. GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRI. GYTPGVEPTTDPI	
HSPLVIAEQFGTL GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNORRL GYTPGVEPTTGPI	
GLGRAPGSDQRT SGDIDNFPRDVAI DPILEPTHNGRRL GYTPGVEPTTOP	
SGDIDNFPRDVAI DPILEPTHNGRRI GYTPGVEPTTOPI	NTLYPGRIDL
DPILEPTHNGRRL GYTPGVEPTTGPI	MMALRRHM
GYTPGVEPTTGPI	ELVDWFDAR
	CSTVRHPRM
	LGQGLANAV
I I I I GLAIAERTLAAQI	FNQPDHEIVD
HFTYVFMGDGCI	MEEGWFTD
DTAKRFEAYHWI	HVIHEIDGHD
POAVKEAILEAO:	SVKDKPSLIIC
RTVIGFGSPNKAG	
GEEEVALAROKL	
KEIYHAWDAREK	
NEKFAAYKKAHI	
MSGGLPKDWEK*	
ANPAKIATRKASI	
MLPELLGGSADL	
SVSLKEDPAGNY	
MTAIANGIAHHG	
MFVEYARNAARI	
IMVYTHDSIGLGI	
OLASLRLTPNFST	
AVGWKLAVERH	
ONLAQVERTPDO	
VLKDSGGKPDIIL	
QAAEKLAGEGRY	
AAGGDEDREKEI	
KQKGLGLAAGW	
ASQLPPPPTHPIPC	
QHLLSTLWTNVC	
GGWCMNLDMDI	
RRHWDTGGIKPH	
TLSEREEIRAGLS	
ALNRSPSTISREV	
KAVDANNRANRI	
DQNLPLRKLVLE	
OISGWLRRTKPRO	QKTLRISPETI
	NHLNIQ\HLA
YKTLYFRSREALI	NRNGERGPV
YKTLYFRSREALI	RTSVKRALGQ

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
1				sequence		
25898	56266	A	26039	797	1440	PAMRLTAMRCISMKSRLPASR
25070	50200	ľ.	20033	1.77		MOFCATVRWKYRCHREPTLSA
				l		QHGAFRSINPTPRNSRGNCWKK
		1				REMKWANWPIWCR*KN*RERS
		1				LSAICCASRK/TGQFVLPPARYH
i i		1		l		LRRSHSLRHGRRHTRKGERGTI
						NIVNGTPIHERSRNIDNRRSLGH
1		1				WEGDLVSGGVGTVIGVVTGVII
						FTVINYGLTYIGVNPYWQYIIK
		1				GAIIIFAVALDSLKYARKK
25899	56267	A	26040	687	1106	GSLSLTALLPDTAEREEIRAGLS
123077	50207	ľ`	200.0	007		AKMSI/RAIATALNRSPSTISRE/
		1				VORNRGRRYYKAVDAN/NRAN
				l		RMAKRPKPCLLDQ/NLPLRKLV
						LEKLNIQHLRRSHS/LRHGRRHT
						RKGERGTIN/IVNGTPIHERSRNI
						DNSALVTVLR
25900	56268	A	26041	1	2851	MKTLIARHKAGEHIGICSVCSA
25500	50200	ľ.	20011	ľ		HPLVIEAALAFDRNSTRKVLIEA
						TSNOVNOFGGYTGMTPADFRE
1						FVFTIADKVGFARERIILGGDHL
1	ļ					GPNCWOOENADAAMEKSVEL
						AVVIDLWSRAVIGWSMSPRMT
	l	l				AQLACDALQMALWRRKRPRN
	1					VIVHTDRGGQYCSADYQAQLK
		i				RHNLRGSMSAKGCCYDNACVE
						SFFHSLKVECIHGEHFISREIMR
	i				1	ATVFNYIECDYNRWRRHSWINS
1	1					LLSQKRNTQGRIEDGRQH
25901	56269	В	26042	1	1048	222411111421122211411
25902	56270	Ā	26043	323	1290	GTSMNTVGTPLLWGGFAVVVA
						IMLAIDLLLOGRRGAHAMTMK
l						QAAAWSLVWVTLSLLFNAAF
1		1				WWYLVOTE\GRAVADPOALAF
1						LTGYLIEKSLAVDNVFVWLML
1		1		Ì		FSYFSVPAALORRVLVYGVLG
}				ĺ		AIVLRTIMIFTGSWLISQFDWIL
1		l		ļ		YIFGAFLLFTGVKMALAHEDES
						GIGDK\RWCAGYA/VHLRMTDT
ł					İ	IDNEHFFVRKNGLLYATPLMLV
1						LILVELSDVIFAVDSIPAIFAVTT
1	i					DPFIVLTSNLFAILGLRAMYFLL
						AGVTKRFSMLKYGLAGILVFIG
1	1	1	1	1		IKRLIVNFNLLQTRACLGGGWA
	1	1		l		FGETLIIKPGEYRMKTAGG
25903	56271	A	26044	28	96	
25904	56272	A	26045	1	777	
23,04	302,2	Ľ.	1200-13	ı	17.7.	

SEO ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25905	56273	A	26046	77	532	I KPSRPEISKGKSVKPAASRRARE
23903	36273	Ι^	20040	l''	332	CAVQALYSWQLSQNDIADVEY
1		1				
						QFLAEQDVKDVDVLYFRELLA
						GVATNTA\YLDGLMKPYLSRLL
l						EELGQVEKAVLRIALYELSKRS
						DVPYKVAIKEAIELAKSFGAED
		<u> </u>				SHKFVNGVLDKAAPVIRPNKK
25906	56274	A	26047	3	175	
25907	56275	Α	26048	85	440	YSSSSLWAARKRRQMVLSARR
	1					FATSDRVCRCVLVWSAGTSRA
		l				KSKSTGWLSMASKAIGVSS*TK
		1				TPTARRVSSSSLPCGMAIPLPIP
l		1				VLPIFSRVRIASKTT*GSSLSCFA
		_				ARSLMTS
25908	56276	A	26049	80	706	KLIQVAVVIGGGQPLGAFLCHG
						LAAEGYRFPVVDIQSDK\AANV
1			ļ.			AQEINAEYGESMAYGFGADAT
i		1				SEQSVLALSRGVDEIFGRVDLL
ļ						VYSAGIAKAAFISDFQLGDFDR
						SLQVNLVGYFLCAREFSRLMIR
1						DGIQGRIIQINSKSGKVGSKHNS
1			1	l		GYSAAKFGGVGLTQSLALDLA
		1		l		EYGITVHSLMLGNLLKSPMFQS
						LLPQ*KTKLGIK
25909	56277	Α	26050	741	893	TGCSGKRSLQQRREERRRNPVQ
ŀ						KIRCTV*RVRNGRIRYCSPRAGF
						YSRYR
25910	56278	Α	26051	269	987	
25911	56279	Α	26052	1	1268	MDAKCDRSRFPWLWPTKRPRG
						CFATFVPIGIPYDQTKTHLHTLS
						LVAKRLADKTICRRLRAAQSDE
						ELYQIITDTEGTPDEARCEEKQY
1				l		MVLMIVSGRSGSGKSVALRAL
				l		EDMGFYCVDNLPVVLLPDLAR
1				l		TLADREISAAVSIDVRNMPESPE
1						IFEQAMSNLPDAFSPQLLFLDA
						DRNTLIRRYSDTRRLHPLSSKN
						LSLESAIDKESDLLEPLHGFPDY
						DTVGFSCKRRIDYVCRIKHSRRI
						RQVVLLNFAKSGAFSTTRGTDD
1						KTRRSLLVTL/VAYFLCAR/EFS
1						RM/MIRDGIHVRIIQINSKSGKV
		1		I		GSKHNSGYSAAKFGGVGLTQS
		1		I		LALDLAEYGITVHSLMLGNLLK
		1	l	1		SPMFQSLLPQYATKLGIKPDQV
	1					EQYYIDKVPFKRGCDYQDVLN
		1				MLLFYASPKA\SY\CTGQSINVT
25912	56280	A	26053	1	168	LKVFILVIFTLSRE*EHAMFGFL
1	1	ſ		I		FLC*FAENDGFQLHPCPCKGHE
			ŀ			LILFYGCIVFH
25913	56281	A	26054	2	253	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25914	56282	В	26055	319	3780	
25915	56283	Α	26056	513	762	
25916	56284	A	26057	375	550	GVGLCGRSSIRRNM*CK**G*/L SPKIALMACGRRHTRSLFMTSK DLSRMMRLQKEIRL
25917	56285	Α	26058	662	1033	EPKRASGCMWPVGAHCHHPLL LLACQQKLGPPSHQASSRS*NIQ TLDRLCMSSWIPQEHSSSQSWH RSCFLNVTRPWSFYSPVGKNR WMGPFWSFSLDALLLFFTLHSY VAWPVEMMALNLLG
25918	56286	В	26059	1	2034	
25919	56287	Α	26060	369	515	HAKPPGGLGHCSLCPSHYSCIH G*KGPRYVSVSCSRGWKPEAT KAFMW
25920	56288	Α	26061	352	2631	
25921	56289	В	26062	10	351	
25922	56290	Α	26063	321	537	EPLDTGRGTSHTRACHGVGYW GRDSVRRYT*CK*RINGYSTPT WHMHEYVTNLHIVHMYPRTYS IIIKKMSD
25923	56291	A	26064	788	912	VHTHLSERTRKCLPPPAPS*WV TCHHGDCCLPTRLRAPQGP
25924	56292	Α	26065	1348	1799	
25925	56293	A	26066	606	2219	ATYPSAHYPDHNRGEFLWPSL GLGKELDITFWSSLYPFGSPVSA VSRELVRKFSLGGTVDSTGSLP VSGDISPVSDVA/ACTKEPLRFR LQVGDRYITLMDLPGVGESGA RDTEV AALYREQLPRLDLVLW LIKADDRALTVDEHFYHQVIGE GQLSTAQKQNISRKICLLHELFQ PVHPVCAVSVRLQWGLKVMA EKMIKCLPREATSPVVSQLHPSF RTTVVREQARSDFGETVGAVL DSISAPFLIPAPVRAVIQAVRTT VVSFAASVTLLLLPLRSTPVEKS PTCLIPASETFPLLVVMLNPVAS LTLTLTSPVLDTSCPHISLSAAQP NLIQLSGNNNISFVVNRAVVTN VLNTMRTACNSQATIQIYNADI ARDFGTRGIFSINSGFSTVYSRRI GHQSPEVTGEAMALTLSQPSG GHGSPEVTGEAMALTLSQPSG DIDGLIAVANUTDTGLRIGGDARQ KAITAGYPVVDTDKCRIRLR RIRHEQCADENSYQATNYCRP
25926	56294	A	26067	543	741	
	1			4		

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mct hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25927	56295	Α	26068	3	373	VYTGLKPRTIDAQYTPINVV/W KFLSLTHHAYSPLLVVINKAKF DGLSPEFQQALVSSAQEAGNY QRKLVAEDQQKIIDGMKEAGV EVITDLDRKAFSDALGNQVRD MFVKDVPQGADLLKAVDE
25928	56296	Α	26069		1107	MGAFTGKTVLILGGSRGIGAAI VRRFVTDGANVRFTYAGSKOL AKRLAQETGATAVFTDSADRD AVIDVVRKSGA*ILILKRRSISSA FNSRASPKTPIPAFTTRISNAPLL RTTSMTASLSALSVNTAVAPVS CARRLAASFDPA
25929	56297	Α	26070	39	254	
25930	56298	Α	26071	1432	1845	
25931	56299	A	26072	674	1614	AVIVVAILVSKSTGAWVAFSIR MPSITFSHNSVVAGVASARKDS SPSYGDPLESAIPKLNVKRSRSG LSKSLLTLTSCSTIWINWITGQT PIKPCSVTGSVYPKA WRSPSTL TTMTTR*PFTLPA/LDTFISRPAG CTYANECHAPEDSAITRINDVAAR PCNCAQCAALDCVSVFVTIRHS CSSVYSAPGILVAALQAGHKPV ALVGGATGLIGDPSFKAAERKL NTEETVQEWVDKIRKQVAPLP DRKNISPADSRLSPDGRYRGYV HPAPPIPDSHLIRHHRCVIYQQ CLAQFRLNGWAASRSQSICKI GCD MSSSCIEEVSVPDDNWYRIANE
25932	56300	A	26073		3476	MSSSCIEEVSYPDONYRIANE FERRYLQEGSLGLGESYMDGW WECDRLDMFFSKVLRAGLENQ LPHHFKDTLRIAGARLFNLQSK KRAWIYGKEHYDLGNDLFSRM LDPFMYSCAVWKDADNLESA QQAKLKMICEKLQLKPGMRVL DIGCGWGGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGL DVTILLQDYKDLNDGPENKYSV QMEHYDRFNYDTYFAVVDR
25933	56301	A	26074	200	1100	
25934	56302	Α	26075	1	2061	
25935	56303	Α	26076	1	3294	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25936	56304	A	26077	11	2064	MNYSLKOLKVFVTVAOEKSFS
						RAGERIGLSQSAVSHSVKELEN
	ı					HTGVRLLDRTTREVVLTDAGO
1	l	I				OLAFRLERLLDELNNTLRDTGR
ŀ		1				YGATTERSARYSASLPAPTSGR
		ı				SEPAALVQNSSSQPSSLKENIM
		l				KLRSVTYALFIAGLAAFSTFFLA
1	İ	l				\AOSIRCGYETSQADSOHSGAK
	l	l			1	KFNDLLOERPKGELKLKLFPDS
		1				TLGNAQAMISGVRGGTID\MEM
		1		l		SGSNYFAGLSPVMNLLDVPFLF
						RDTAHAHKTLDGKVGDDLKAS
	1	l				LEGKGLKVLAYWENGWRDVT
	l .	l				NSRAPVKTPADLKGLKIRTNNS
	i					PMNIAAFKVFGA\NPI\PMPFAE
		1				VYTGLETRTIDAOEHPINVVWS
						AKFFEVOKFLSLTHHAYSPLLV
	1					VINKAKFDGLSPEFOOALVSSA
						QEAGNYQRKLVAEDQQKIIDG
	i					MKEAGVEVITDLDRKAFSDAL
						GNOVRDMFVKDVPOGADLLK
						AVDEPGWAERDIWAFAPAFFY
		1				PLFISDFNRVRLEFVGHYODVC
		ı	ľ			EKPASTTLWLDVGRSSGLDLTY
		l				OTLNVKNDLSHFPVPFFDPSDN
		l				RTNTLPMVFAGAPDVGLOOAS
		l				AIVASWFGSRSGWRGQNFPVL
		l				YNOLPDRNAIVFATNDKRPDFL
		1				RDHPAVKAPVIEMINHPONPYV
	1	1	1	1		KLLVVFGRDDKDLLQAAKGIA
1	1	1		i		OGNILFRGESVVVNEVKPLLPA
		İ				GSOPVWSSSASESRCCFYA
25937	56305	Α	26078	I	480	LGNTKTVKGWLAQLPAKYHQ
23931	50505	^	20070	l'		RATCMFDRHGLLALLAGRFLA
					1	FVRTLLPTMAGISGLPNRRFQFF
					1	KAKLR\WLS*PTRIAAALAFMP/
		1				FMDDHHPRLMQTVILQILQRRG
	1	1	1		1	TGDRLKIMVERRYAHVGFCRQ
						LLDAQVFGVFILNPFQHAANQT
						EVSLATDORO
25938	56306	A	26079	1	2184	ETOLATDONO
23938	20300	IA_	20079	11	12104	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	l	09/340,217	sequence	or peptide sequence	detection, (~possible nucleonide insertion)
25939	56307	Α	26080	1429	2152	NLFREVVFPTHCPVCGSDVERV
						EGEAVARCTGALICGAQRKESL
				i		KHFVSRRAMDVDGMGDKIIDQ
						LVEKEYVHTPADLFKLTAGKLT
						GLERMGPKSAQNVVNALEKAK
	ł					ETTFARFLYALGIREVGEATAA
	ŀ	l .		1		GLAAYFGTLEALEAASIEELQK
		l l			1	VPDVGIVVASHVHNF\LPKKAT
	i .					AMSSASCWRKVFTGLRRSLSTR
	i i					KRLTARLLVKPWCLRAASGTP
		1		1		LKRASLLMFSGCFSHTSGLAMY
25940	56308	Α	26081	1	2448	
25941	56309	A	26082	125	741	AHLNRTRWKVCWIR*RKISPW
						AKRNTKTVKG\WLAQLPAKYH
		1				QRATCMF\DRHGLLALLAGRFL
						AFVRTLLPTMAGISGLPNRRFQ
	1					FFNWLSGLLWVSVVTSFGYAL
						SMIPFVKRHEDQCRNGVFGKR
						KGGIAAALILTRLRRRFVSSWK
						RFRELRRKSSQADDMNVFGILE
		1				DFTHQFIGGAFLRADISGAAKM
		<u></u>				SCLAKAQASSSMH
25942	56310	Α	26083	1066	1359	
25943	56311	Α	26084	256	952	RLKRCSTGKSMAVIQDIIAALW
1						QHDFAALADPHIVSVVYFVMF
						ATLFLENGLLPASFLPGDTLLIL
						AGALIAQGVMNFSGLRIAVLDP
						RNQVRGGGLSIFKGRWLGNPK
		1				TVKG\WLAQLPAKYHQRATCM
	1	ı		1		FDRHGLLALLAGRFLAFVRTLL
	1	!				PTMAGISGLPNRRFQFFNWLSG
	1	1				LLWVSVVTSFGYALSMIPFVKR
		İ				HEDQVMTFLMILPIALLTAGLL
						GTLFVVIKKKYCNA
25944	56312	В	26085	1	1290	

SEO ID	SEO ID NO	Mes	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
25945	56313	A	26086	1	1839	MRCQNA WWIMQHSSGSERLSS
						VLLHFRRTNLADSNDRIQYHSL
		l				RFFDEDGAOWLVILGDVLNHG
						PRNALPDGYAPRKVAERLNEV
						AHKVIAVRGNLRQRVDQMLLI
						SRAINRLVASNWNRRSAQMRC
						PISGKNLAWIPVQLPVYWQNN
	İ					CRRLLMRSHRKHGSGTNLPGE
						LMAIKLIAIDMDGTLLLPDHTIS
						PAVKNAIAAARARGVNVVLTT
1		1				GRPYAGVHNYLKELHMEQPGI
l						YCITYNGALVQKAAD/GYDDY/
1						RF/LEKLSREVGSHFHALDRTT\
1		1				LYTAN\RDISYY\TVHEFLRCHQ
		1				FPLVVCDGGRMTPRAMFLFSSA
i	1					HILMPLNYHNSHINTLFPVAGT
						LMVEPTESESKVELDRFIDAML
						AIRAEIDQVKAGVWPLEDNPLV
						NAPHIQSELVAEWAHPYSREV
						VFPAALVTGGSRGIGRATALLL
						AQEGYTVAVNYQQNLHAAQE
						VMNLITQAGGKAFVLQADISDE
1						NQVVAMFTAIDQHDEPLAALV
1		1				NNAGILFTQCTVENLTAERINR
Į.						VLSTNVTGYFLCCREAVKRMA
						LKNGGSGGAIVNVSSVASRLGS
						PGEYVDYAASKGAIDTLTTGLS LEVAAQGIRVNCVRPGFIYTEM
		1				HASGGEA WTRRSR
25946	56314	A	26087	2	1275	VNFSPKSSQIHHALRTVAGRFA
		1				VKSIDYFWHDSCNASKRFHIWE
						SIMLELLFVIGYLVMLMVTGVS
İ						LLGIIAALVVATAIMFLGGMLA
						LMIKLLPWLLLAISVVWVIKAI
						KAPKVPKYQRYDRWQLAVRRS
1						PLLPDHTISPAVKNAIAAARAR
						GVNVVLTTGRPYAGVHNYLKE
						LHMEQPGDYCITYNGAL/VYRK
						AAGWLAPLAAKLLLKLMDELI
						GFLEKLSREVGSHFHALDRTTL
ł						YTANRDISYYTVHESFVATIPLV
						FCEAEKMDPNTQFLKVMMIDE
						PAILDQAIARIPQEVKEKYPVLK
1			l			APNLQQPHGSSGSSFHREIFFSS
			l	1		RSEDKRRGGLVVSGISLLVVSA
1						GPWVRNANEPLGQLKTWFSLS
1	1		l			HTLTLTYTRAPACRLTSTQTEP
1		1				RARPCLSPLSSEPRDRSLTPRLG
L						QRFIYLAVQ
25947	56315	В	26088	1	1509	
25948	56316	Α	26089	1	1323	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \*=possible aucleotide insertion)
25949	56317	В	26090	I	5073	
25950	56318	Α	26091	249	531	CWAMRMDSKVGVITPIRMWSA
	1					SGPFAMGTLVPTFAAVTDIPTK
			l	l		SVTTCLRQICERWQAPSTR*SRF
				l	<b>!</b>	ASLSQPAPRFTPSPITLALVLLP
						ARRC
25951	56319	A	26092	3	1038	LVLFGVAETYPVANDFAAGAG
						AYVRGRYAAGVRAWPTIITRK
						TMKTLVVALGGNALLQRGEAL
		i				TAENQYRNIASAVPALARLARS
	ŀ					YRLAIVHGNGPQVGLLALQNL
						AWKEVEPYPLDVLVAESQGMI
						GYMLAQSLSAQPQMPPVTTVL
		l	ľ			TRIEVSPDDPAFLQPEKFIGPVY
						QPEEQEALEAAYGWQMKRDG
						KYLRRVVASPQPRKILDSEAIEL
						LLKEGHVVICSGGGGVPVT\ND
						GAGSESVIHKDLAAALLAEQIN
		1				ADGLVILTDADAVYENWGTPQ
İ						QRAIRHATPDELAPFAKADGSM
			1			GPNVTAVSGYVRSPVQMHHRQ
						FQPVIIHIATNQIDHHRRIIHHWL
25952	56320	A	26093	1	3639	MKRLIVGISGASGAIYGVRLLQ
						VLRDVTDIETHLVMSQAARQT
		l		l		LSLETDFSLREVQALADVTHDA
		1				RDIAASISSGSFQTLGMVILPCSI
					1	KTLSGIVHSYTDGLLTRAADVV
						LKERRPLVLCVRETPLHLGHLR
				ł		LMTQAAEIGGNTGEIDEEELES
			Ì		1	LLYAIAKGNVFNFQTILHLPVA
	1		1		1	VQNDTIDFYQMFARIWSSHPQ
				1	1	WLTLYLAQHRAVIIPDDAKLHR
				1	1	NLLRWYSAGRLDIPELLDYAQS
_	L	L	L			WRETEPDNEDAPY

SEQ ID	SEQ ID NO:	I Mar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
	1	<u> </u>			1.000	
25953	56321	Α	26094	I	1260	AWARQDRRLSVKQWGKPPVD
ĺ	1	1		ľ		ETIPAKEQVRILRKLFDRYYGE
	1	1				VAGRGDGFCSPHVARYVGRVA
	i	1				G*RPCRLGPGHPTNRTPFVAPL
ŀ		1				LEALDIAKYFSVVIGGDDVQNK
	İ	1				KPHPDPLLLVAERMGIAPQQMI
		1			1	FVGDSRNDIQAAKAAGCPSVG
	!					LTYGYNYGEAIDLSQPDVIYQSI
		1		:		NDLLPALGLPIAKIRNRKMTKPI
	ı	l				VFSGAQPSGELTIGNYMGCTEA
		1		İ		DRQFAFNFNNFVLIQLLTNGGP
	1	1				DRLGTTTPAGYTDLLVNYTYRI
		1				AFEGGGGQDFGLAAAIATLIFL
		1				LVAIMFPLLMVVAISLRQGNFA
,		1				TGSLIPEQISWDHWKLALGFSV
		1				EQADGRITPPPFPVLLWLWNSV
						KVAGISAIGIVALSTTCAYAFAR
l	ŀ	l				MRFPGKATLLKGMLIFQMFPA
		1				VLSLVALYALFAPRVRAALCY
25954	56322	Α	26095	I	3240	
25955	56323	Α	26096	494	792	ATRLRHGVTSVGGDGGLQLTV
Į.	l	1				MDKLDVILLMSV/NPGFGGQSFI
	į	1	r			PQTLDKL/REVRRRIDESGFDIR
		1				L/EVDGGVKVNNIGEIAA/AGA
		1				DMFVAGSAIFDQPDAR
25956	56324	Α	26097	1624	2390	RTSERRWHAKALLKLFSAHHA
		l				GFVCCKEEEERLATGKVGWLP
		i				VETLLAQQHIEGHYQVDPSLFK
	ı	l				PNADCPVRVSGMSMKDIGIMD
		l				GDLLAVHKTQDVRNDPLLVPL
		l				FTLIREGKLAANWPLEQDELLT
		l				RLOKSCDMTQVSADYNALFIG
		l				DECAVPPYRSAWVEGATEAEV
	1	l	1	l		RAFLSERGMPLADTPADHIGTL
	1	1	l		1	LLAASWLEDQSTEDESEALETL
	1	l				FKRGA/LPKSLCLWGKAPAPHG
		1				SPVGGFSKGPKTWAPHEGAS
25957	56325	В	26098		534	
25958	56326	Ā	26099	67	399	
~>>>٥	20020	10	20077	I * *	12	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25959	56327	Α	26100	8	1016	PESRRKAVMTQPVLDIQQLHLS
		1				FPGFNGDVHALNNVSLQINRGE
					į.	IVGLVGESGSGKSVTAMLIMRL
						LPTGSYCVHRGQISLLGEDVLN
						AREKQLRQWRG/ARVAMIFQEP
						MTALNPTRRIALQMMDVIRHH
		ı				QPISRREARAKAIDLLEEMQIPD
						AVEVMSRYPFELSGGMRQRVM
						IALAFSCEPQLIIADEPTTALDVT
						VQLQVLRLLKHKARASGTAVL
		l				FISHDMAVVSQLCDSVYVMYA
						GSVIESGVTADVIHHPRHPYTIG
						LLQCAPEHGVPRQLLPAIPGTV
						PNLTHLPDGCAFRDRCYAAGA
						QCENVPALTACGDNNQR\GAC
						WYPQQEVISV
25960	56328	A	26101	3	102	ISRLNTQQHFG*RTRQISPHSPQ
						GCSRCPLHS
25961	56329	A	26102	290	490	SSLNSCMAVWDKTRLIRQ*LV
		1				MWSY*SPSPCR*PAGYRHMKL
						RSTSLVLSTPSRLFLAVIPPVVVI
25962	56330	Α	26103	1	3255	
25963	56331	A	26104	119	634	
25964	56332	A	26105	1640	1770	HLDSNRRVHDSTCNWCCNLS*
						QRLLWSG*WSELCCSVPRQKR
						A

SEO ID	ISEO ID NO-	Met	SEQ IĎ NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25965	56333	A	26106	281	2108	RESLKQKVGGRPQLSPFPPPDS
		1			[ · · · ·	WALDPGGGRARETPRGVSNAT
i		l			i	KEPISVAQHGN/GGDKEIRRELK
		l				YYAHLGRRLKDWSGIPRYHGT
i		l				VETDCGTGYVYDVIADFDGKP
						SITLTEFAEQCRYEEDIAQLRQL
						LKQLKRYLQDNRIVTMSLKPQ
						NILCHRISESEVIPVVCDNIGEST
		l				LIPLATWSKWCCLRKQERLWK
		l				RFIAOPALAIALOKDLOPOATE
		l				ASGAENMASIASGNIARTDPDM
		l				LSIPLSKKICCFGDRIIEIPETIDO
1		1				PVRFWVLTGPVVDMGIYACYL
1		l				SSPQWGWYAERDAEIENETVR
		l				REVEELROASETDLOPGTIEYE
		l				RHRLTRAQADAQELKNARDSA
		l				EVVETAFCTFVLSRIAGEIASIL
						DGIPLSVQRRFPELENRHVDFL
		l				KRDIIKAMNKAAALDELIPGLL
						SEYNRADRQYAGGSRVAARFA
			Ì			ASPRVAVLSVITGLIPRHVCAPY
		l				LLCGDPCCLSTPEDMTPRFRRY
		l				AVRSGNRSTPGLDHRCDACOR
		l	l			SAYELADLRCRPPPSTLFLLPEA
						DKNDFSDALPAVADAMYAAPP
			1			RRKAAPSKPEKAVVSPLRSVRK
		l	l		ł	ARHGSVCSLRPDOYAVRNLPA
		l				YRSCSSPDLQFMVWCALA
25966	56334	A	26107	1	2880	THE COOK DE STATE OF THE STATE
25967	56335	В	26108	61	5101	
25968	56336	Α	26109	80	561	IRPLPPRFKTESRSLPGPCLQPGT
		ļ				FLWSRNRRVLGFPSMNGEDMG
		1			i	LLFLCSEWERSSEGWLCNREGG
		1				SGHSIEPHCCTFLHLTHRSLAFS
		1				LLAGVSCTCASSCKCKE\CKCTS
		1				CKKSECGAISRNLGLWLKVGR
		l				EPKAVPEVRASGEPAFLCPCRL
						SLPV
25969	56337	A	26110	Ĭ .	277	
25970	56338	A_	26111	902	1006	
25971	56339	Α	26112	2	1265	
25972	56340	A	26113	409	525	
25973	56341	Α	26114	91	431	NHKPGNIDVARRIQRGFAGDQI
			1	I		GHLRPVERQCSPDKRRFIAADG
l		l		ĺ		REIRGKQRAGHIFQLLSRCLLQI
		1		l		LNHCQRRAAHFRFQLSNQRHQ
		1				QLLPV/HYHAAEREYPAGACLV
						RWLL
25974	56342	A	26115	3	71	
25975	56343	Α	26116	1	1212	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25976	56344	A	26117	ı	2786	MAAVIEQIRRAVLALVTGVVHI GDIPVVWDIVWNATAAFIAVIII SILLDESGFEWAALHVILRWG YGFGRLPFNRIGLIRRITFRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLFGLVTFILLLNRSQNPAQDIQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQGGLKRVYHSPG APDIREFTRDAIP
25977	56345	A	26118	48	219	EIFSVVWIIMTRGDVYTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI PETCGHLWAYVWPSCAAVIGL
						YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25979	56347	A	26120	1	912	

3498

TCVCVRTYAYVRVRVRY RVRVCAYARTRVRNSLSI LTLATPIHHIRQEFFNIRG RRWKPDLAIGIDITPSCIDT DYSEVRINQOG/GTCLNY TLAGLITPPRLIRMLEDTA IPVQREVAPQVITETGYIC GWEIGFSPLALLLAFLCSI GDPDGLGVIAYQDTVRPP AISELNALAVKGVILTDD AAAIAGELGLEFKAGLLP KAAVTENOHAPLAMVGI APAMKAAAIGIAMGSGTI ETADAALTHNILRGLVQ ARATHANIRGNITIALGLI VTTLDDRVVAGSAGRYG GDSECVKIVAQGIROTDR DRSPRPSGERVRVGKGG QPLSTAFTNQTITRQSIRLI VFHKGISRVVAGSSAIISN CILRTPNCRRGFPISCTGE YGWORDGHAFVLLAFE LLPDALSYEDGAFISCGV EGILRGEVSGSDNVLVVG GMMAMMLAKGRGAKRI MLPERLAMAKQLGYMDI LPDVVY*ISVARYSWM SELRTRVAAVAHTRTRAF TRTRTYAVRTHTHVCA RVRVETHARAHTR TRTRTYAVRATHTHVCA RVRVETHARAHTR LPAQQRMKGENWYRGT- TQNLDIRRYKAGVEYVILL YKQDYSRMLDHVEKGA ACMPYPIEGASAFGVMA DKIEFVEKPANPPSNPNE LASMGTYPDADVLYFLL RDENSHDFGKDLIPKITE YAHPPFLSCVGDDPADF CGYAGNFMESPRSGLIR PAGPPLPLPAARSEAPKA ASVYSIAPARLEGVKTGR PAGPPLPLPAARSEAPKA ASVYSIAPARLEGVKTGR FSGNPOGGIAHVNGVAT GFHORMOGNARLEFG SLQHHHTTSSHLEGVKTGR FSGNPOGGIAHVNGVAT GFHORMOGNARLEFG SLQHHHTTSSHLEGVKTGR FSGNPOGGIAHVNGVAR QCHQAWGQQYAARLEFG SLQHHHTTSSHLEGVKTGR FSGNPOGGIAHVNGVAR QCHQAWGQQYAARLEFG SLQHAHRVDIHREDVKQ	SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25981 56349 A 26122 3 1180 SKLGTRRSVVWA*SPSTS CSTFSAGHSSMKRMSEI LPAQQRMKGENWYRGT: TQNLDIIRRYKAFYVILL YKODYSRMLDHVEKGA ACMPVPIELASAFGYMA' DKHEFVEKPANPSMPNE LASMGTVFDADVLYELL RDENSSHDFCKDLIPKITE YAHPPELSCVGDPDAFP CGYAGNFMESPRSGLIR PAGPPLPLARSEAPKA. ASVPSIAPARLRPVPDPVE AAEFITGGDFTPRLHGSG QHHOTTRSHLEGVKTGIR. FSGNPGGGIAHVNGVARI QCHQAWGQQYAARLRF SLQJAHRVDIHRFDVRQ 25982 56350 A 26123 16 543	25980	56348	A	26121		1857	MRVCARACVRTRTRMCVYAH TCVCVRTYAYVRVRVRYHVRA RVRVCAYARTRAYVRVRVRVHVRA RVRVCAYARTRAVRNSLSILPIG LTLATPHHHHIGEFNIRGIVPVL RRVKPDLAIGIDITPSCDTPDLH RVKPDLAIGIDITPSCDTPDLH DYSEVRINOGYGITCLNYHGR GTLAGLITPRLIRMLEQTALEIN IPVOREVAPOVITETGYIQLFLP GWEIGFSFLALLLAFLCSTSPG GDPDGLGVIAYQDTVRPNAAT AISELNALAVGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV KAYTELNGHAPLAMVGOGIND APAMKAAAIGIAMGSGTDVAL ETADAALTHNHLRGLVQMIGI TADAALTHNHLRGLVGMIGI VTTLDDRVVAGSAGRYGGDG GDSECVKIVAQEIRQTDRNIER STEPRSPERSFERVYRGGGGEN QPLSTAFTNQTIRGUSILFSNOG CILRTPNCRRGPPISCTGEGKAA YGWQRDGGHAEYLLAEEKDLI LPPDALSYEDOAFISCGYGTAY EGILRGEVSGSDNVLVGLGPV GMMAMMLAKGRGAKRIIGVD MLPERLAMAKQLGVMDHGY*I LPDLYVPIGVARYSWMNGRIIO MLPERLAMAKQLGVMDHGY*I LPDLYVYN*IGVARYSWMNGRIIO SELRTRVRAYHTETRATTCTR
CSTFSAAGHSSMKRMME  LPAQQRMKGENWYRGT TONLDIJRRYKAEYVVIL YKQDYSRMIDHYEKGA ACMPVPIEASAFGVMA DKIIEFVEKPANPPSMPNI LASMGIYVFDADYLYELI RDENSSHDFCKDLIPKITE YAHPPLSCVQSDPDAEP CGYAGNFMESPRSGLIR PAGPPLPAARSEAPKA ASVPSIAPARLRPVPDPVE AAEFITGOPTPRICHGSG QHHQTRSHLEGVKTGIR FSGNPQGGIAHVNGVARI QCHQAWGQQYAARLRFG SSON A 26123 16 543							TRTRTYAYVRTHTHVCAYTHM RVRVRTHARAHTR
							SKLGTRRSVVWA*SPSTSPTLW CSTFSAAGHSSMKRMNEFVDL LPAQQRMKGENWYRGTADAV TONDLIIRRYKAEYVVILACDH YKNDDYSRMLIDHVEKGARCTV ACMPVPIEEASAFGVMAVDEN KUIEFVERPANPESMPNDPSKS LASMGIYVFDADYLYELLEEDE ROENSSHDFCKDLIFKITEAGLA CGYAGNFMESEPRSGLIRVSCM PAGPPLLPAARSEAPKAAGTV ASVPSIAPARLRPVPDPVELVLV AAEFITGGDFTPRLHGSGFIDIR GHHQTRSHLEGWKTGIFELNH FSGNPOGGIAHVNGVARFGVK QCHQAWGGQVAARLRFQARGI SLQIAHRVDIHRFDARGA
125083 156351   A 126124   I   13387							
25765 50551 A 20124 1 2507	25983	56351	Α	26124	1	3387	